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Sequence 24, Sequence 24, Sequence 27, Sequence 27, Sequence 27, Sequence 25, Sequence 25, Sequence 26, Sequence 45, Sequence 17, Seque

US-07-853-913-2 US-08-149-809-24 US-08-247-9028-2 US-08-247-9028-2 PCT-US93-1054-12 PCT-US94-01149-5 PCT-US94-01149-5 US-08-097-831-6 US-08-097-831-6 US-08-290-301-82 US-08-290-301-82 US-08-290-301-82 US-08-290-301-82 US-08-290-301-82 US-08-25-4598-44 US-08-72-8791-1

US-07-640-476-5 US-08-112-703-1

5290690-2

ALIGNMENTS

```
APPLICANT: Yao. Zhengbin
APPLICANT: Yao. Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
CORRESPONDENCE: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98101

ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
SOFTATING SYSTEM: Apple Operating System 7.5.5
SOFTATANEE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION NUMBER: USN 08/410,535
FILING DATE: 33 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08620694A Patent No. 5869286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein

US-08-620-694A-2
1477
18055
2285
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5548
684
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CITY:
STATE:
 Sequence 2, Appl.
                                                                                                      July 5, 2001, 11:47:02; Search time 61.79 Seconds (without alignments) 5.216 Million cell updates/sec
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Sequence 1
Sequence 1
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. /cgn2_6/ptodata/2/laa/5B_COMB.pep: *
. /cgn2_6/ptodata/2/laa/6A_COMB.pep: *
. /cgn2_6/ptodata/2/laa/6B_COMB.pep: *
. /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep: *
. /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep: *
. /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep: *
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-022-257-2
US-08-144-121-10
US-08-735-893-10
US-09-029-213B-25
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US-08-620-694A-10
US-09-022-255-10
US-09-022-696-10
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US-09-022-257-10
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US-08-735-893-3
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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78
1 RADEEQQQALSSQMGF 16
                                                                           - protein search, using sw
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Match Length DB
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Perfect score:
Sequence:
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Maximum DB
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Sequence 2, Application US/08978773
Patent No. 6083906
GENERAL INFORMATION:
APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                              Yao, Zhengbin
Spriggs, Melanie
Fanslow, William
VENTION: No. 6072037el Receptor That Binds IL-17
EQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                  COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION DATA: 05/09/022,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
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ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 3;
Pred. No. 76;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PROR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
"FIFTHONE: (206)587-0430
                                                                                  ATTLE OF INVENTION: NO. 6072037el TITLE OF INVENTION: NO. 6072037el NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.0
Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-09-022-696-2
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                                                                                                                                                                        STREET: 51 Univ
CITY: Seattle
STATE: WA
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CITY: Seattle
                                                                                                                                                                                                                                                  98101
                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-08-978-773-2
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                                                                                                                                                                                                                                                                                         APPLICANT: Yao, Zhengbin
APPLICANT: Sprigs, Melanie
APPLICANT: Sprigs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: Immunex Corporation
STREET: 51 University Street
                        Score 39; DB 2; Length 864;
Pred. No. 76;
6; Mismatches 3; Indels
                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 864;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION NUMBER: US/09/022,255
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76;
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Pred. No. 76;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               US-09-022-255-2
; Sequence 2, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
                      50.0%;
Ouery Match
Best Local Similarity 40.00,
e. hea 6; Conservative
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781 SEEEQRQSVQSDQGY 795
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                2 ADEEQQQALSSQMGF 16
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781 SEEEQRQSVQSDQGY 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
> MOLECULE TYPE: protein
US-09-022-255-2
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Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: S
STATE:
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US-09-022-696-2
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Gaps
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Patent No. 6100235

GENERAL INFORMATION:
APPLICANT: You, Zhenghin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Panslow, William
TITLE OF INVENTION:
OCRRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 864;
                                                                                                                                                                                                                                                               Length 864;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
                                                                                                                                                                                                                                                                     DB 3;
76;
                                                                                                                                                                                                                                                                   Score 39; DB 3
Pred. No. 76;
6; Mismatches
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION APPLICATION APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION APPLICATION APPLICATION NUMBER: 23 MARCH 1995
CLASSIFICATION INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
               TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAN: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TYPE: protein
US-09-022-253-2
                                                                                                                                                                                                                                                                   50.0%;
                                                                                                                                                                                                                                                                 Query Match 50.0
Best Local Similarity 40.0
Matches 6; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                ::|||:|: | |:
781 SEEEQRQSVQSDQGY 795
                                                                                                                                                                                                                                                                                                                                                      2 ADEEQQQALSSQMGF 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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Microsoft Word for PowerMacintosh, Version 6.0.1
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Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATE: US/09/022,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 3;
Pred. No. 76;
6; Mismatches
                                                                CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TLING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PERKIN: PERKIN: PATICIA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A
TELEFOMMUNICATION INFORMATION:
TELEFONN (206) 507-0430
TELEFAX: (206)
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
TOWN A SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.0
Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-978-773-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ADEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
SOFTWARE:
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COUNTRY:
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 APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
UNDER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08144121
Patent No. 5610031
GENERAL INFORMATION:
APPLICANT: Burgeson, Robert E.
APPLICANT: Wagman, David W.
TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
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Pred. No. 76;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
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60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                           ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34 695
REFERENCE/DOCKET NUMBER: 2617-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
PARDIA PAPLICATION NUMBER: 08/620,694
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 40.0.
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781 SEEEQRQSVQSDQGY 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-022-257-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 60 State Stre
CITY: BOSTON
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ADEEQQQALSSQMGF 16
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                                                                                                                STATE: WA
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                      Gaps
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                                                                                                                                                                 Sequence 2, Application US/09022259; Patent No. 6191104; Patent No. 6191104; GENERAL INFORMATION: APPLICANT: Yea, Zhengbin APPLICANT: Panslow, William TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS; ADDRESSE: Il University Street SI University Street CITY: Scattle
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                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                    3;
                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
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   Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/022,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMONICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
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40.08;
Best Local Similarity 40.0 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (206)
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::|||:|: | |:
781 SEEEQRQSVQSDQGY 795
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781 SEEEQRQSVQSDQGY 795
                                                       2 ADEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / MOLECULE TYPE: protein US-09-022-259-2
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                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                 us-09-022-259-2
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                                                                                                                              Gaps
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APPLICANT: CHRISTIAN, Peter D.
TITLE OF INVENTION: RECOMBINANT HELICOVERPA BACULOVIRUSES
TITLE OF INVENTION: EXPRESSING HETEROLOGOUS DNA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 323; 37;
                                                                                Length 40;
                                                                                                                         Indels
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Patent No. 5907082
GENERAL INFORMATION:
APPLICANT: O'Nell, Sharman
APPLICANT: Nadeau, Jeanette
TITLE OF INVENTION: O'VUE-Specific Gene Expression
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,213B FILING DATE: 31-AUG-1998 CLASSIFICATION: 424
                                                                                  DB 2;
                                                                                Score 38; DB;
Pred. No. 3.4;
                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McDermott, Will & Emery
                                                                                                                                                                                                                                                                                        US-09-029-213B-25; Sequence 25, Application US/09029213B; Patent No. 6180098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Joseph Hyosuk Kim
REGISTRATION NUMBER: 41,425
REFERENCE/DOCKET NUMBER: 501
TELECOMMUNICATION:
TELECHONE: 202-756-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 600 13th Street, NW CLIY: Washington STATE: District of Columbia COUNTRY: USA
                                                                                48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.7%;
58.3%;
                                                                                Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 48.7
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-756-8087
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                 2 ADEEQQQALSSQMGF 16
                                                                                                                                                                                                        21 AEGASEQALSAQEGF 35
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168 DDEQQQRASSEL 179
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; FRAGMENT TYPE:
US-08-735-893-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-560-398-2
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APPLICANT: Wagman, David W.
TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 66 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; Length 40;
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PRIOR APPLICATION DATA:
PELLING DATE: 27-OCT-1993
CLASSIFICATION NUMBER: US 08/144,121
FILLING DATE: 27-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REFERENCE/DOCKET NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10:
                          CURKENL AFFLALCALON WINDER: US/08/144,121
PILING DATE: 27-0CT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 35,965
RELECHONE: (617) 227-5941
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TTPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,893
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
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Patent No. 5914317
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 60 State Street
CITY: BOSTON
STATE: Massachusetts
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ADEEQQQALSSQMGF 16
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US-08-735-893-10
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Gaps
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APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 2; Length 866;
Pred. No. 1.1e+02;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA: US/09/022,255
                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 WARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 WARCH 1995
ATOCNEY AGENT INFORMATION:
                                         NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operatir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 10, Application US/09022255 ; Patent No. 6072033
                                                                                                                                                                                                                                                                                                                                                                     48.78;
                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                              INFORMATION FOR ESQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 866 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206)587-0430
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                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 866 amino acids
                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-620-694A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||:|:: | |:
783 EEEQRQSVQSDQGY 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 DEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-022-255-10
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Sequence 10. Application US/08620694A

Patent No. 5869286

GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MICTOSOft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TRW PC compatible
COMPUTER: Patentin Rolease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,398
FILING DATE: 17-NOV-1995
CLASSIFICATION: 435
Townsend and Townsend and Crew LLP
                    Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFO $32

ATTORNEY/AGENT INFO $43

NAME: Bastian, Kevin L.

REGISTATION NUMBER: 34,774

RETERENCE/DOCKET NUMBER: 023070-063300US

TELECOMUNICATION INFORMATION:
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 amino acids

TYPE: amino acid
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FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/620,694A FILLING DATE: 21 MARCH 1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.20,
           STREET: TWO EMECOCITY: San Francisco CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-560-398-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DEEQQQALSSQMG 15
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US-09-022-255-10

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Job time: 316 sec
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                                                                                                                                                                                  RESULT 15
US-02-696-10
is Sequence 10. Application US/09022696
is Patent No. 6072037
is GENERAL INFORMATION:
is APPLICANT: Yao, Zhengbin
is APPLICANT: Fanslow, William
is TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
is NUMBER OF SEQUENCES: 10
is CORRESPONDENCE ADDRESS:
is ADDRESSEE: Immunex Corporation
is TREE OF INVENTION: No. 6072037el Receptor That Binds IL-17
is CORRESPONDENCE ADDRESS:
is ADDRESSEE: Immunex Corporation
is TREET 51 University Street
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Pred. No. 1.1e+02;
5; Mismatches 3; Indels
    Length 866;
  Score 38; DB 3; Length 866
Pred. No. 1.1e+02;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: APPROVE Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
FILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206)
TELEFAX: (206)
INFORMATION FOR SEG ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 866 amino acids: TYPE: amino acid: "noPoLOGY: linear propology: linear property."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity .42.9%;
Matches 6; Conservative
Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-696-10
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783 EEEQRQSVQSDQGY 796
                                                                                                       3 DEEQQOALSSOMGF 16
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Search completed: July 5, 2001, 11:47:02

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	July 5, 2001, 11:48:37; Search time 79.63 Seconds (without alignments) 15.306 Million cell updates/sec	US-09-462-480-13 score: 78 e: 1 RADEEQQQALSSQMGF 16	table: BLOSUM62 Gapop 10.0 , Gapext 0.5
	OM protein - pr	Run on:	Title: Perfect score: Sequence:	Scoring table:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

two-component regu probable ClpA/B-ty ntpl protein - Ent hypothetical prote O-acetylserine syn protein-glutamine hypothetical prote hypothetical prote homeobox protein ( hypothetical prote villin - chicken DNA43 protein hypothetical phypothetical phypothetical phypothetical phypothetical phypothetical probable two-c otnA protein Description SUMMARIES S71478 A31822 T10032 T35682 G83635 B53610 A83169 S19680 B42463 T13215 T04449 F82650 548384 T34491 T20492 н83397 % Query Match Length DB 827 838 1286 83 83 555.1 553.3.8 553.3.8 551.3.8 550.0 500.0 500.0 500.0 500.0 500.0 500.0 449.4 449.4 448.7 448.7 448.7 448.7 468.7 Score 40.5 338 Result 

probable acyl-CoA homeotic protein,	laminin Blk chain nestin - rat	carboxypeptidase A hypothetical prote	Similar to 'MADS b chorion protein s3	tropomyosin - migr tropomyosin, exon	tropomyosin II, mu tropomyosin, exon	tropomyosin, exon dihydroorotate deh	multiubiquitin cha hypothetical prote
D83583 S71477	A53612 A34736	825833 874964	F96/99 A37349	A60364 C25242	A25561 B25242	A25242 F82541	T05691 T45615
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601 768	1170	149	281	283 285	285 286	286 359	386 405
48.7	48.7	47.4	47.4	47.4	47.4	47.4	47.4
38	3 8 8	37	37	37	37	37	37
30	33.5	3. S. S.	37	8 6 8 6	40 41	4 4 3 2	44 45

#### ALIGNMENTS

RESULT

219241

Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

H70802
hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C, Accession: H70802
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A; Reference number: A70500; MUID:98295987
A; Accession: H70802
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-100 <col/>
A; Cross-references: GB: AL022120; GB: AL123456; NID: q3261558; PIDN: CAA17966.1; PID: q296
A; Experimental source: strain H37Rv
C, Genetics:
A;Gene: Rv3874
Query Match 100.0%; Score 78; DB 2; Length 100;
ative 0;

85 RADEEQQQALSSQMGF 100 1 RADEEQQQALSSQMGF 16 ò g

A;Residues: 1-1263 <MIN> A;Cross-references: EMBL:U29082; NID:9861384; PID:9861386; PIDN:AAA68402.1; CESP:C14F A;Experimental source: strain Bristol N2 C;Genetics: A;Gene: CESP:C14F5.3 A;Introns: 21/3; 34/2; 740/2; 852/2; 881/2; 902/3; 970/3; 1005/2; 1041/3; 1093/3; 112 hypothetical protein C14F5.3 - Caenorhabditis elegans
C; Species: T15496
R; Minx, P.
Submitted to the EMBL Data Library, June 1995
A; Description: The sequence of C. elegans cosmid C14F5.
A; Reference number: Z18361
A; Reference number: Z18361
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA homeotic protein H hypothetical prote hypothetical prote hypothetical prote gas vesicle operon tail fiber assembl Vib
 prote prote hypothetical prote actin-related prot prote prote

Gaps

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A;Title: Demonstration of three distinct calcium-binding sites in villin, a modulator A;Reference number: A92418; MUID:83062892
A;Reference number: A92418; MUID:83062892
A;Note: Gly-32, Asp-34, Ser-36, Lys-38, Asn-40, and Ser-43 may be involved in calcium R;de Arruda, M V.; Bazari, H.; Wallek, M.; Matsudaira, P.
J. Biol. Chem. 267, 13079-13085, 1992
A;Title: An actin footprint on villin. Single site substitutions in a cluster of basi A;Reference number: A42816; MUID:92317005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 751-826 <PRI>
K;Glenney Jr., Jr.; Geisler, N.; Kaulfus, P.; Weber, K.
J: Biol. Chem. 256, 8156-8161, 1981
A;Title: Demonstration of at least two different actin-binding sites in villin, a cal
A;Reference number: A92333; MUID:81264203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1.826 CBAZ>
A; Cross-treferences: GB:J03781; NID:g212862; PIDN:AAA49133.1; PID:g212863
R; Cross-treferences: GB:J03781; NID:g212862; PIDN:AAA49133.1; PID:g212863
R; Pringault, E.; Arpin, M.; Garcia, A.; Finidori, J.; Louvard, D.
EMBO J. 5, 3119-3124, 1986
A; Title: A human villin cDNA clone to investigate the differentiation of intestinal
A; Reference number: A91057; MUID:87133467
A; Recession: A25703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Comment: Villin is abundant in the microvilli of intestinal epithelial cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: calcium-regulated actin-binding; in vitro, bundles actin at low C;Superfamily: villin; gelsolin repeat homology; villin headplece homology C;Keywords: actin binding; calcium binding; duplication F;2-826/Product: villin #status experimental <MAT>
F;17-836/Product: gelsolin repeat homology <GELL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A31822; A25703; A03082; A42816
C;Accession: A31822; MULD: Wallek, M.; Smeal, T.; Jakes, R.; Ahmed, Y.
Proc. Natl. Acad. Sci. U.S.A. 85, 4986-4990, 1988
A;Title: Villin sequence and peptide map identify six homologous domains.
A;Reference number: A31822; MUID:88276884
                                                                                                                                                                                                                                             A;Introns: 26/3; 118/2; 157/3; 336/3; 371/3; 502/1; 592/3; 621/3
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;102-158/Domain: homeobox homology <HOX>
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:L32873
A;Note: this sequence has been revised in reference S71449
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB Pred. No. 20; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 751-826 <GLE>
R; Hesterberg, L.K.; Weber, K.
J. Biol. Chem. 258, 365-369, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.1%;
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 DEKQRQQLSKQLG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: villin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 DEEQQQALSSQMG 15
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A, Molecule type: protein
A, Residues: 1-11;128-132
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villin - chicken
                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                     A:Gene: GL2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Bansen, N.F.; Hudhes, B.; Huizar, L.
Nature 408, 1816-1820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, B.; Sakano, H.
A; Authors: Salzberg, S.L.; Sakano, H.
A; Authors: Salzberg, S.L.; Sofwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A; Note: this is a revision to the sequence from reference A53900
B; Rerie, W.G; Peldmann, K.A.; Marks, M.D.
Genes Dev. 8, 1388-1399, 1994
A; Title: The GLABRA2 gene encodes a homeo domain protein required for normal trichome A; Reference number: A53900; MUID:95011550
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C; Species: Arabidopsis thallana (mouse-ear cress)
C; Date: O5-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999 C; Accession: S71478; S71449; A53900
R;Di Cristina, M.; Sessa, G.; Balma, S.; Ruberti, I.; Morelli, G. submitted to the EMBL Data Library, October 1995
A; Description: Athb-10/GLABRA2 is a member of the HD-Zip protein family.
A; Reference number: S71478
                                                                                                                                                                                                                                                                                                                                                                                    homeobox protein (GLABRA2), 66648-63167 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                 Gaps
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              Length 1263;
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              DB 2;
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                                                                                 4; Mismatches
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              Score 49;
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                                              Pred. No
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A; Accession: D96829
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61.5%;
          62.8%;
60.0%;
                                                                              Conservative
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                                                                                                                                                 2 ADEEQQQALSSQMGF 16
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28 SDEEEQYSSSSQLGF 42
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                                          Best_Local Similarity
Matches 9; Conserv
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Best Local Similarity
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A; Residues: 3-747 <MAR>
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A; Residues: 1-747 <DIC>
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A;Cross-references: GB:AE004447; GB:AE004091; NID:q99945902; PIDN:AAG03480.1; GSPDB:GN A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0090
C;Superfamily: endopeptidase Clp ATP-binding chain
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J. Biol. Chem. 269, 11037-111044, 1994
A;Title: Sequencing and characterization of the ntp gene cluster for vacuolar-type Na
A;Reference number: A53610; MUID:94209269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-664 <TAK>
A;Cross-references: GB:D17462; NID:g487271; PIDN:BAA04270.1; PID:d1004790; PID:g48727
                                                                                                  Sistover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; J. Olson, M.V. M.V. Mature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic jA;Reference number: A82950; MUID:20437337
A;Accession: G83635
A;Accession: A;Accession: A;Accession A;A
          C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83635
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C;Species: Enterococcus hirae
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 01-Dec-2000
C;Accession: B53610; B54392
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34491
R;Latreille, P.
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A; Title: Operon of vacuolar-type Na(+)-ATPase of Enterococcus hirae. A; Reference number: A54392; MUID:94193617
A; Recession: B54392
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Pred. No. 38;
5; Mismatches
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36;
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Pred. No.
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Best Local Similarity 57.11
استو 8; Conservative
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205 RADESRMEEIASRYGF 220
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Best Local Similarity 43.8
Matches 7; Conservative
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C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C; Date: 110032
R; Eiglmeier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 199-206, 1993
A; Title: Use of an ordered cosmid library to deduce the genomic organization of Mycobact
A; Reference number: 216917; MUID:93188700
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A;Residues: 1-100 <ELG>
A;Cross-references: EMBL:Y14967; NID:92370268; PIDN:CAA75210.1; PID:92370280
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C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 31-Jan-2000
C;Accession: T35682
R;Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A;Reference number: 221587
A;Reference number: 221587
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F;17-49,398-430/Region: repeats a, a'
F;62-78,174-190,295-311,443-459,554-570,658-674/Region: repeats b, c,
F;398-715/Domain: gelsolin repeat homology <GEL2>
F;763-826/Domain: villin headpiece homology <VHH>
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C; Genetics:
A; Gene: SCOEDB:SC7C7.04
C; Superfamily: ompR protein; response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein MLCB628.13c - Mycobacterium leprae
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A;Molecule type: DNA
A;Residues: 1-224 <HAR>
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                                                                                                                                                                                                           Score 43; DB Pred. No. 22; 3; Mismatches
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                                                                                                                                                                                                        Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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85 KTDDEANQLLSSKMNF 100
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             306 EEKQQAMSRALGF 318
                                                                                                                                                                                                                                                                                                                                          4 EEQQQALSSQMGF 16
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G83635
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Gaps

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C; Species: Vibrio cholerae
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998
R;Bik, E.M.; Bunschoten, A.E.; Willems, R.J.L.; Chang, A.C.Y.; Mooi, F.R.
Mol. Microbiol. 20, 799-811, 1996
A;Title: Genetic organization and functional analysis of the otn DNA essential for ce
A;Reference number: $70952; MUID:96386047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein AAF98405.1 [imported] - Arabidopsis thaliana Cipotein AAF98405.1 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Daccession: F86238
C;Accession: F86238
C;Accession: F86238
C;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.Authors: Hunter, J.L.; Jakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A.Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X90547; NID:g1469276; PIDN:CAA62140.1; PID:e194955; PID:g110 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
  A; Title: Retinol-induced morphological changes of cultured bovine endothelial cells and Reference number: A34446; MUID:90037069
A; Accession: A34446; MUID:90037069
A; Accession: A34446
A; Status: preliminary
A; Molecule type: protein
A; Molecule type: protein
C; Superfamily: protein-glutamine gamma-glutamyltransferase
C; Saperfamily: protein-glutamyltransferase
C; Superfamily: protein-glutamyltransferase
C; Superfamily: protein-glutamyltransferase
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C;Genetics:
A;Map position: 1
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59;
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2; Mismatches
                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             otnA protein - Vibrio cholerae
                                                                                                                                                                                                                                                                                                                   Query Match 51.3
Best Local Similarity 46.7
Matches 7; Conservative
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152 SDEERQEYVLTQQGF 166
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A; Residues: 1-911 <BIK>
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Matches 8; Conserv
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K.; Lim,
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A;Reference number: A82950; MUID:20437337
A;Accession: A83169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 GSTO>
A;Cross-references: GB:AE004799; GB:AE004091; NID:g9949981; PIDN:AAG07203.1; GSPDB:GN001
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A;Reference number: S19680; MUID:92037637
A;Accession: S19680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: cysE; PA3816
C;Superfamily: Bacillus serine acetyltransferase; serine acetyltransferase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O-acetylserine synthase PA3816 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                   A;Cross-references: EMBL:U29244; PIDN:AAC71091.1; GSPDB:GN00020; CESP:ZK1248.10 A;Experimental source: strain Bristol N2; clone ZK1248 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.; Hickey,
A.; Larbig,
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A;Introns: 26/3; 86/2; 224/3; 271/3; 317/2; 445/2; 527/1; 682/3; 803/1; 850/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - bovine
N;Alternate names: 25K retinol-induced protein
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Oct-1999
C;Accession: S19680; A34446
Ex:Nakanishi, K.; Nara, K.; Hagiwara, H.; Aoyama, Y.; Ueno, H.; Hirose, S.
Eur. J. Blochem. 202, 12-21, 1991
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A; Residues: 1-687 <NAK>
A; Residues: 1-687 <NAK>
A; Cross-references: EMBL:X60686; NID:9817; PIDN:CAA43097.1; PID:9818
R; Nara, K.; Nakan1shi, K.; Hagiwara, H.; Wakita, K.; Kojima, S.; Hirose, J. Biol. Chem. 264, 19308-19312, 1989
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submitted to the EMBL Data Library, June 1995
A; Description: The sequence of C. elegans cosmid ZK1248.
A; Reference number: 221534
A; Accession: T34491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-856 <LAT>
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47.4%; Pred. No. 16;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Pred. No.
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nilarity 50.0%;
Conservative 2
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542 RIPRESQONLTDQLGF 557
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Best Local Similarity
'-haq 8; Conserv?
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Matches 9; Conserv
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RESULT 15
344028
actin-related protein - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C; Accession: $44028
K; Frankel, S.; Heintzelman, M.B.; Artavanis-Tsakonas, S.; Mooseker, M.S.
J. Mol. Biol. 235, 1351-1356, 1994
A; Title: Identification of a divergent actin-related protein in Drosophila.
A; Reference number: $44028; MUID:94141930
A; Accession: $44028
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-398 <FRA>
A; Cross-references: EMBL: L25314; NID:9408943; PIDN: AAA17685.1; PID:9408944
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Query Match 50.0%; Score 39; DB 2; Length 355; Best Local Similarity 57.1%; Pred. No. 42; Matches 8; Conservative 1; Masmatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: FlyBase:Actr13E
A;Cross-references: FlyBase:FBgn0011741
C;Superfamily: actin
                                                                                                                                                    100 DDEQGQLFVSNMGF 113
                                                                                                                   3 DEEQQQALSSQMGF 16
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Search completed: July 5, 2001, 11:48:38 Job time: 377 sec

1 RADEEQQALS 11 | |||||| :| 264 REDEEQQMVS 274

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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 5, 2001, 11:51:46; Search time 41.8 Seconds (without alignments) 13.112 Million cell updates/sec Run on:

US-09-462-480-13 78 1 RADEEQQQALSSQMGF 16 Title: Perfect score: Sequence:

93435 segs, 34255486 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		_		P51176 bos taurus	_		Q9tlu9 bacteriopha	P26699 bacteriopha	P32354 saccharomyc	Q13751 homo sapien	P21263 rattus norv		loci					-	-		P08587 cavia cutle	P46582 caenorhabdi	070240 rattus norv	O88566 mus musculu				Q9kgs5 vibrio chol	O51728 borrelia bu	_	Q46497 desulfovibr		P57593 buchnera ap
SUMMARIES	ID	HGL2_ARATH	VILI_CHICK	NTPI_ENTHR	TGLC_BOVIN	ACTU_DROME	GVG1_HALN1	TFA_BPMU	TFA_BPP2	DN43_YEAST	LMB3_HUMAN	NEST_RAT	CBPA_PIG	TPMM_LOCMI	TPM1_DROME	PSD4_ARATH	CBPA_BOVIN	IAP1_DROME	TPM5_DROME	TPM4_DROME	SELB_MOOTH	TGLC_CAVCU	YLB8_CAEEL	AXN2_RAT	AXN2_MOUSE	RB15_RAT	P30_MYCPN	RIBD_BACSU	TIG_VIBCH	Y788_BORBU	YQC1_CAEEL	SELB_DESBA	TGLC_HUMAN	EFG_BUCAI
	Length DB	745	826 1				83 1															689 1							433 1		89			702 1
df	Query Match I	55.1	S	$^{\circ}$	51.3	0	49.4	8	48.7	æ.	œ	8	47.4	7.	47.4	47.4	47.4	47.4		~	~	_	^	9	46.8	9	9	9	9	46.2	46.2	46.2	46.2	46.2
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Q61087 mus musculu P16916 escherichia	P16918 escherichia P16917 escherichia	P37671 escherichia	Q22915 caenorhabdi P04727 triticum ae	PO4725 triticum ae	P26346 proteus vul	P26344 erwinia car	erwinia
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	RT	"The GLABRA2 g	ene ence	odes a h	omeo do	main	prote	i ui	reguli		r nor	nal
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	RC	STRAIN=CV. COL	UMBIA;									
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Protein Sci. 6:1197-1209(1997).
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Markus M.A., Matsudaira P., Wagner G.;
"Refined structure of villin 14T and a detailed comparison with other
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; 'Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDIINE-88276884; PubMed-2839826;
Bazari W.L., Matsudaira P., Wallek M., Smeal T., Jakes R., Ahmed Y.;
"Villin sequence and peptide map identify six homologous domains.";
Proc. Natl. Acad. Sci. U.S.A. 85:4986-4990(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94191534; Pubmed-8142900;
Markus M.A., Nakayama T., Matsudaira P., Wagner G.;
"Solution structure of villin 14T, a domain conserved among actin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-83082892; PubMed-6848508;
Hesterberg L.K., Weber K.;
"Demonstration of three distinct calcium-binding sites in villin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-81264203; PubMed-6790532; Glenney J.R. Jr., Geisler N., Kaulfus P., Weber K.; Benosy J.R. Jr., Geisler N., Kaulfus P., Weber K.; Demostration of at least two different actin-binding sites in villin, a calcium-regulated modulator of F-actin organization."; J. Biol. Chem. 256:8156-8161(1981).
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                                                                                                                                                                                     Score 43; DB 1; Length 745; Pred. No. 12;
                                                                                                                                                                                                        2; Indels
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01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                              826 AA
                                                                                                                                                                                              Pred. No. 12;
; Mismatches
or send an email to license@isb-sib.ch)
                                                                                                                  Homeobox; DNA-binding; Nuclear protein.
                                                                                                                                                HOMEOBOX
                EMBL; L32873; AAC80260.1; -... EMBL; Z54356; CAA91183.1; ALT_INIT. EMBL; AC011717; AAF09047.1; -... EMSP; PO2365: 2HDD.
InterPro; IPR001356; -... InterPro; IPR002913; -... Pfam; PF00185; START; 1... Pfam; PF00165; HOMEOBOX; 1... PROSITE; PS00027; HOMEOBOX_1; 1... PROSITE; PS50071; HOMEOBOX_2; 1...
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J. Biol. Chem. 258:365-369(1983).
                                                                                                                                                        82988 MW;
                                                                                                                                                                                    Similarity 61.5%;
8; Conservative
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                                                                                                                                                                                         -:- TISSUE SPECIFICITY: COMPONENT OF BRUSH BORDER MICROVILLI.
-:- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
STRUCTURE BY NMR OF 792-826.

MEDLINE=97307248; PubMed=9164455,

McKnight C.J., Matsudalira P.T., Kim P.S.;

NMR structure of the 35-resdidue villin headpiece subdomain.";

Nat. Struct. Biol. 4:180-184(1997).

-! FUNCTION: YILLIN IS A CA(2+)-REGULATED ACTIN-BINDING PROTEIN. ITS

CAPPING FUNCTION IS LOCALIZED TO DOMAIN I; ITS SEVERING ACTION IS

A COOPERATION BETWEEN AN F-ACTIN BINDING SITE OF DOMAIN II AND THE

CAPPING ACTIVITY OF DOMAIN I.
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CRUCIAL FOR BINDING AN ACTIN FILAMENT.
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InterPro; IPR001974; -..
InterPro; PR00626; Gelsolin; 6.
PRINTS; PR00629; Gelsolin; 6.
PRINTS; PR00657; Gelsolin.
Calcium; Actin-binding; Capping protein; Repeat; 3D-structure.
Calcium; Actin-binding; Capping protein; Repeat; 3D-structure.
T34 CARE.
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PIR; A31822; A31822.
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2VIL; 01-APR-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequencing and characterization of the ntp gene cluster for vacuolar-type Na(+)-translocating ATPase of Enterococcus hirae."; J. Biol. Chem. 269:11037-11044(1994).
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Kakinuma Y.;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
V-TYPE SODIUM ATP SYNTHASE SUBGNIT I (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBGNIT I)
                                                                                                                                                                                                                                                             Length 826
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Pred. No. 14;
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MEDLINE-94209269; PubMed-8157629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTPI OR NTPM
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P43439;
                                                                                                                                    HELIX
TURN
STRAND
TURN
SEQUENCE
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TRANSMEM
TRANSMEM
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                                                STRAND
              STRAND
                                                                                     HELIX
                                                                                                                                                                                                                                                                               Best Loca
Matches
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NTPI_ENTHR
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                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- COFACTOR: CALCIUM IS REQUIRED FOR TRANSGLUTAMINASE ACTIVITY.
-:- SUBUNIT: MONOMER (BY SIMILARITY).
-:- TISSUE SPECIFICITY: HIGHEST LEVELS ARE DETECTED IN THE LUNG. LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND HEART, BUT NOT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 79-95; 157-166; 242-251 & 581-587.
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakanishi K., Nara K., Hagiwara H., Aoyama Y., Ueno H., Hirose S.; Cloning and sequence analysis of cDNA clones for bovine aortic-endothelial-cell transglutaminase.";

Eur. J. Bacchem. 202.15-21(1991).

-!- FUNCTION: CATALYZES THE CROSS-LINKING OF PROTEINS AND THE CONJUGATION OF POLYAMINES TO PROTEINS.

-!- CATALYTIC ACTIVITY: PROTEIN GLUTAMINE + ALKYLAMINE - PROTEIN N(5)-ALKYLGLUTAMINE + NH(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (EC 2.3.2.13) (TISSUE
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                             1; Length 664;
                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- INDUCTION: BY RETINOIC ACID.
                                                          POTENTIAL.
W -> G (IN REF. 2).
T -> I (IN REF. 2).
; 08CC146D6CB89AF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam: PF01841; Transglut_core; 1.
Pfam; PF01841; Transglutamin_C; 1.
Pfam; PF00927; Transglutamin_N; 1.
PROSITE; PS00547; TRANSGLUTAMINASES; 1.
Transferase; Acyltransferase; Calcium-binding.
ACT_SITE 277 277 BY SIMILARITY.
SEQUENCE 687 AA; 77112 MW; 7BBAOOF155779944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         687 AA
                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                             Score 41;
Pred. No.
                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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MEDLINE-92037637; PubMed-1682150;
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                                                                                                                                                                                                                             52.6%;
43.8%;
542
594
621
501
515
75620 M.
                                                                                                                                                                                                 Query Match
Best Local Similarity 43...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 ||||| : ::|: ||
205 RADESRMEEIASRYGF 220
                                                                                                                                                                                                                                                                                                                                  1 RADEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
                                                             601
501
515
664 AA;
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Halobacterium.
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   REDINING-20196067 Pubbmed=10731132;

RADAGINE-20196067 Pubbmed=10731132;

RADAGINE-20196067 Pubbmed=10731132;

RADAGINE-20196067 Pubbmed=10731132;

RADAGINE-20196067 Pubbmed=10731132;

RADAGINE M.D. Celliker S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.C., Wortern J.R., Tandell M.D., Zhang Q.C., Chan L.X.,

RADATIA J.F., Agbayania A., Baxendale G., Helf G., Nelson C.R., Ballew R.D.,

RADATIA J.F., Agbayania A., Baxendale J., Bayrakatrogol L., Beasley E.M.,

RADATIA J.F., Agbayania A., Baxendale J., Bayrakatrogol L., Beasley E.M.,

RADATIA J.F., Agbayania D.A., Burman B.P., Bhandari D., Bolshakov S.,

RADATIA J.F., Socker P. C., Baxen E.D.,

RADATIA J.F., Agbayania D.A., Burman B.P., Bhandari D., Bolshakov S.,

RADATIA J.F., Agbayania D.A., Burman B.P., Brottler P., Brottler P.,

RADATIA J.F., Socker B., Dend S., Burkaya A.D., Bovies P.,

RADATIA J.F., Socker B., Dend S., Burkov B.C., Dunn P.,

RADATIA J.F., Socker B., Dend S., Burkov B.C., Dunn P.,

RADATIA J.F., Socker B., Dend S., Dunkov B.C., Dunn P.,

RADATIA J.F., Baryandelista C.C., Ferraz C., Ferriera S., Eleischmann W.,

ROSIER C., Gabriellan A.E., Gang N.S., Dunkov B.C., Dunkov B.C.,

RADALI J.H., Harvey D., Helman T.J., Wel M. H., Thegwam C.,

RADALAI M., Ralush F., Karpen G.H., Ke.Z., Kennisson J.A., Ketchum K.A.,

RADALAI M., Ralush F., Karpen G.H., Ke.Z., Kennisson J.A., Ketchum K.A.,

RADALAI M., Ralush F., Karpen G.H., Ke.Z., Kennisson J.A., Ketchum K.A.,

RADALAI M., Murphy B., Murphy D.M., Nosheefi A.,

RADATIA S., Wow M., Murphy B., Murphy D.M., Nosheefi A.,

RADATIA S., Walkele B., Wollock M., Stungh R., Shen B.,

RADATA S., Woodage T., Saunders R.D.C., Scheeler F., Shen H.,

RADATA S., Woodage T., Wenter B., Wang A.H., Wang X.,

RADATA S., Walkel E.W., Wooday W., Stung S., Yoo O., Zheng C.,

RADATA S., Walkel B., Shooley W., Stung S., Sheng 
                                         ö
                                                                                                                                                                                                                P45890; 099X09;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
ACTIN-LIKE PROTEIN 13E.
PCT-YOPQUE, NEDADORAS ATTHOOPOGA; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TAXID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frankel S., Heintzelman M.B., Artavanis-Tsakonas S., Mooseker M.S.; "Identification of a divergent actin-related protein in Drosophila."; J. Mol. Biol. 235:1351-1356(1994).
                                         Gaps
                                         ;
0
   Length 687;
                                         Indels
   1;
                                                                                                                                                                                                            398 AA
   DB
                                       5; Mismatches
   Score 40;
                       Pred. No.
                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94141930; PubMed-8308899;
   51.3%;
                     46.78;
                                         Conservative
                                                                                              :|||:|: : : | ||
152 SDEERQEYVLTQQGF 166
                                                                                                                                                                                                            STANDARD;
                                                                            2 ADEEQQQALSSQMGF 16
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CANTON-S
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ACTU_DROME
                                     Matches
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MEDI.NE-20504483; PubMed-11016950;
MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Bebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                رم
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-91323116; PubMed-1864501;
Jones J.G., Young D.C., Dassarma S.;
Structure and organization of the gas vesicle gene cluster on the
Halobacterium halobium plasmid pNRC100.";
Gene 102:117-122(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Faust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NRC-1; PLASMID-pNRC100;
MEDLINE=99063795; PubMed=9847077;
NG W.V., Clufo S.A., Smith T.M., Bungarner R.E., Baskin D., Faus Hall B., Loretz C., Seto J., Slagel J., Hood L., DasSarma S.;
"Snapshot of a large dynamic replicon in a halophilic archaeon: megaplasmid or minichromosome?";
Genome Res. 8:1131-1141(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halobacterium sp. (strain NRC-1), and Halobacterium sp. (strain NRC-81), Plasmid pNRC100, Plasmid pNRC200, and Plasmid pHH1.
Archeea; Euryarchaeota, Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 1; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                            Interro, 178000279; -.
Pfam; PF00022; actin; 2.
Structural protein; Cytoskeleton.
SEQUENCE 398 AA; 45414 MW; 71905627B3F0FC05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GVPG11 OR GVPG OR VNG5026G) AND (GVPG12 OR VNG6025G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVG1_HALN1 STANDARD; PRT; 83 AA. P24371; 09H122; 01-MAR-1992 (Rel. 21, Created) 01-MAR-1992 (Rel. 21, Last sequence update) 01-0CT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                               EMBL; L25314; AAA17685.1; -.
EMBL; AE003500; AAF48499.1; -.
FlyBase; FBgn0011741; Actr13E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-NRC-1; PLASMID-PNRC100;
                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 REDEEQQQMVS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RADEEQQQALS 11
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haggaard-Ljungquist E., Halling C., Calendar R.; "DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizontal transfer of tail fiber genes among unrelated bacteriophages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 174:1462-1477(1992).
                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae; P2-like Viruses.
NCBL_TaxID=10679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 175;
Pred. No. 18;
2; Mismatches 2; Indels
  Length 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20287 MW; A2FFA76948260F17 CRC64;
  1;
                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
PROBABLE TAIL FIBER ASSEMBLY PROFEIN (GPC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                            175 AA
  DB
18;
                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SIMILARITY: BELONGS TO THE TFA FAMILY.
Score 38;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-92165720; Pubmed-1531648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF063097; AAD03287.1; -. PIR; C42291; C42291.
48.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 48.7%;
Best Local Similarity 66.7%;
Matches 8; Conservative
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                                          8; Conservative
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                                                                                                                       108 ADEQQQQAESQK 119
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                                                                               2 ADEEQQQALSSQ 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 AA;
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
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P32354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chaperone.
                                                                                                                                                                                                                            TFA_BPP2
P26699;
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                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. The Three are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                        Viruses; dsĎNA viruses, no RNA stage; Tailed phages; Myoviridae.
NCBI_TaxID=10677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 AA; 20310 MW; 71A0EBA3294FCCD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4FGDE7B4EF43C792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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01-OCT-2000 (Rel. 40, Last annotation update)
PROBABLE TAIL FIBER ASSEMBLY PROTEIN (GPU).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38.5; Di
Pred. No. 6.7;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                  STRAIN-NRC-817; PLASMID-PHH1; MEDLINE-92065812; PubMed-1956294;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL, M58557; AAA98192.1; -.
EMBL, AF016485; AAC82805.1; -.
EMBL, AE005141; AAG20722.1; -.
EMBL, X55648; CAA39174.1; -.
PIR; JQ1124; JQ1124.
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01-OCT-2000 (Rel. 40, Last seq
01-OCT-2000 (Rel. 40, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 AA; 10014 MW;
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58.8%;
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                                                                                                                                                                                 VESICLE SYNTHESIS
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nes 10; Conserv
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Matches 10)
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EMBL;
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EMBL;
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HSSP;
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                        Q -> H (IN REF. 1).
D -> H (IN REF. 1).
DSOVLKSSYGSGEPRINDLGKKKTVINDLLHYKKEKVILAP
SKNEWFKRREHREEVWQKHFGSKETKETSGSASDLEII
-> NFPKYSSLLYQGANLRTTYSVKKKLL (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMB3_HUMAN STANDARD; PRT; 1172 AA.
013751; 014733;
01-NOY-1997 (Rel. 35, Last sequence update)
01-NOY-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ILAMININ BETA-3 CHAIN PRECURSOR < TAMININ BIK CHAIN) (KALININ BI CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                      -1. FUNCTION: REQUIRED FOR DNA SYNTHESIS. REQUIRED FOR ENTRY INTO OR
                                                                           STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentles S., Hamly N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Whitchead S., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Solomon N.A., Wright M.B., Chang S., Buckley A.M., Dumas L.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
MEDLINE=95293372; PubMed=7774918;
Pulkkinen L., Gerecke D.R., Christiano A.M., Wagman D.W.,
Burgeson R.E., Uitto J.,
"Cloning of the beta 3 chain gene (LAMB3) of human laminin 5, candidate gene in junctional epidermolysis bullosa.";
Genomics 25:192-198(1995).
                    "Genetic and molecular analysis of DNA43 and DNA52: two new cell-cycle genes in Saccharomyces cerevisiae."; Yeast 8:273-289(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          D32CFF4A94FD9B2A CRC64;
                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB
Pred. No. 62;
                                                                                                                                                                                                        -!- SIMILARITY: TO S.POMBE CDC23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            571 AA; 65815 MW;
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                                                                                                                                                                                COMPLETION OF S PHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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18 SDEEDEQAIARELEF
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                                                                                                                                                                                                                                                                                                                                                        S48384; S48384
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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458
492
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Mellerio J.E., Eady R.A., Atherton D.J., Lake B.D., McGrath J.A.;

"E210K mutation in the gene encoding the beta3 chain of laminin-5
("LAMB3) is predictive of a phenotype of generalized atrophic benign

"E210K mutation in the gene encoding the beta3 chain of laminin-5
("LAMB3) is predictive of a phenotype of generalized atrophic benign

"E210K mutation in the gene encoding the beta3 chain of laminin-5
("LAMB3) is predictive of a phenotype of generalized atrophic benign

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"E210K mutation of laminin of ELMS 11998)

"E210K mit of mediate the matation of ELMS 11998

"E210K mutation of ELMS 11998

"E210K mutation of ELMS 11998

"E210K mutation of ENGRIFIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND

"E210K mutation one LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

"E210K mutation of ELMS 11998

"E210K muta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAINS THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

DOMAIN: DOMAIN VI IS GLOBULAR.

DISEASE: JUNCTIONAL EPIDERMOLYSIS BULLOSA GRAVIS (JEB) IS A
BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED
                                                                                                                                                                                                                                                                                                                                                                                            VARIANT JEB LEU-679.
MEDIINE-96055522; PubMed=7550237;
PulkKinen L., McGrath J.A., Christiano A.M., Uitto J.;
"Detection of sequence variants in the gene encoding the beta 3 chain of laminin 5 (LAMB3).";
Hum. Mutat. 6:77-84(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERMOLYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI). SIMILARITY: CONTAINS 6 LAMININ EGF-LIKE DOMAINS.
[2] SEQUENCE FROM N.A., AND SEQUENCE OF 172-190.
SEQUENCE 94209274; PubMed=7512558;
Gerecke D.R., Wagman D.W., Champliaud M.F., Burgeson R.E.;
"The complete primary structure for a novel laminin chain, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELÍULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
                                                                                                                                                                                                                                                   laminin Blk chain.";
J. Biol. Chem. 269:11073-11080(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT JEB LYS-210.
MEDLINE~99068967; Pubmed-9767254;
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U17749;
U17750;
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P02468;
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Gaps

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Length 1172;

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Score 38; DB 1; I
Pred. No. 1.3e+02;
3; Mismatches 4;
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COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
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58.3%;
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                                                 48.78;
                                                                                                                                                                                                     1064 AEGASEQALSAQEGF 1078
                                                    Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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Matches 7; Conserv
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                                                                                                                                                                                             PROSITE; PS00022; EGF_1; F. PROSITE; PS01186; EGF_2; 1. PROSITE; PS01148; LAMININ_TYPE_EGF; 5. Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
LAMININ BETA-3 CHAIN.
LAMININ A-TERMINAL (DOMAIN VI).

6 X LAMININ EGF-LIKE REPEATS (DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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41 RD -> E (IN REF. 2).

33 R -> P (IN REF. 2).

15 G -> A (IN REF. 2).

129572 MW; 61BCIA60BBD4FA05 CRC64;
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DOMAIN ALPHA.
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COILED COIL (POTENTIAL).
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LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5.
LAMININ EGF-LIKE 5.
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MISSING (IN REF. 2)
P -> A (IN REF. 2).
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                                          InterPro: IPR000561; -.
InterPro: IPR001886; -.
InterPro: IPR002049; -.
Pfam, PF00053; laminin_EGF; 6.
Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
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269 26
388 38
426 42
440 44
603 60
815 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 60:585-595(1990).
--- TISSUE SPECIFICITY: CNS STEM CELLS.
--- DEVELOPMENTAL STAGE: UPON TERMINAL NEURAL DIFFERENTIATION, NESTIN
--- IS DOWN REGULATED AND REPLACED BY NEUROFILAMENTS.
--- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                               Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_raxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Lendahl U., Zimmerman L.B., McKay R.D.G.; "CNS stem cells express a new class of intermediate filament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1; Length 1805;
Pred. No. 2.1e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001664; -. Parair Flamment; 2. PROSITE; PS00226; IF; Ilament; Colled coil; Heptad repeat pattern; Intermediate fillament; Colled coil; Heptad repeat pattern;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 COIL 2A.
LINKER 2.
14 COIL 24
198744 MW; B40EE14717E099BD CRC64;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NESTIN.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila;
                                                                                                                                                                                                                                                                                          -!- DOMAIN: THE MOLECULE IS IN A COLLED COIL STRUCTURE. THE SEQUENCE EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               functional aspects.";
Mol. Cell. Biol. 6:1965-1973(1986).
-!- ALTERNATIVE PRODUCTS: DRSOPHILA TROPOMYOSIN I GENE CAN PRODUCE
FOUR DIFFERENT ISOFORMS BY ALTERNATIVE SPLICING: A MUSCLE FORM,
A NON-MUSCLE FORM, AND TWO FUSION PROTEINS (33 AND 34).
-!- DOMAIN: THE MOLECULE IS IN A COLLED COIL STRUCTURE. THE SEQUENCE
EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
-!- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
-!- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
                                                                                                                                                                    MEDLINE-87106815; PubMed-3803921;
Hanke P.D., Storti R.V.;
Hauchetide sequence of a cDNA clone encoding a Drosophila muscle
tropomyosin II isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karlik C.C., Fyrberg E.A.;
"Two Drosophila melanogaster tropomyosin genes: structural and
                                                                      Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterrygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
Acridomorpha; Acridoidea; Acrididae; Locusta.
NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8C9E25EFEA664C0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01.JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
TROPOMYOSIN 1, MUSCLE ISOFORM (TROPOMYOSIN II)
01.JUL-1993 (Rel. 26, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
15.DUL-1999 (MSCLE.
Locusta migratoria (Migratory locust).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.4%; Score 37; DB 53.8%; Pred. No. 43; Live 3; Mismatches
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InterPro; IPR00053; -.
Pfam; PF00261; Tropomyosin; 1.
PRINTS; PR00194; TROPOMYOSIN;
PROSITE; PS000326; TROPOMYOSIN;
Muscle protein; Coiled coil; Repeat.
spoirNCE 283 AA; 32439 MW; 8C9E2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.0
Tr Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 ADEERMDALENQL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ADEEQQQALSSQM 14
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HSSP; P01100; 1FOS.
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                                                                                                                                                              SEQUENCE FROM N.A.
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P06754;
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                                                                                                                                                                                                                                                                                                             "Primary structure of the activation segment of procarboxypeptidase A
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92194312; PubMed-1548696;
Guasch A., Coll M., Aviles F.X., Huber R.;
Three-dimensional structure of porcine pancreatic
procarboxypeptidase A. A comparison of the A and B zymogens and their
determinants for inhibition and activation.";
J. Mol. Biol. 224:141-157(1992).
-!- CATALYTIC ACTIVITY: PEPTIDYL-L-AMINO ACID + H(2)O = PEPTIDE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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-1- SIMILARITY: BELONGS TO PEPTIBASE FAMILY M14; ALSO KNOWN AS THE ZINC CARBOXYPEPTIDASE FAMILY.
PIR; A25833; A25833.
PDB; 1PCA; 31-OCT-93.
                                                                                                                                         Sus scrofa (P1g).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                         Vendrell J., Aviles F.X., Genesca E., San Segundo B., Soriano F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000834; -. PROXYPEPT_ZN_1; PARTIAL.
PROSITE; PS00132; CARBOXYPEPT_ZN_2; PARTIAL.
PROSITE: PS001131; CARBOXYPEPT_ZN_2; PARTIAL.
Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Zymogen;
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                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 141:517-523(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION PEPTIDE.
                                                                    01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
CARBOXYPEPTIDASE A (EC 3.4.17.1) (FRAGMENT).
                                94 AA.
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                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS).
                                    PRT;
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                                                                                                                                                                                                                                                      MEDLINE=87100171; PubMed=3801014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
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Matches 7; Conservative
                                    STANDARD;
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82 DEEQEQMFASQ 92
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                                                                                                                                                                                                  NCBI_TaxID=9823;
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P31816;
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SEQUENCE
                                CBPA_PIG
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RESULT 13 TPMM\_LOCMI

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REPEAT
REPEAT
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                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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01-ocr-1996 (Rel. 34, Last sequence update)
01-ocr-2000 (Rel. 40, Last annotation update)
26S PROTEASOME REGULATORS SUBUNIT S5A (WULTIUBLOUITIN CHAIN BINDING
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Eukaryota; Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;

Bragnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van Nocker S., Deveraux Q., Rechsteiner M., Vierstra R.D.;
"Arabidopsis Map1 gene encodes a conserved ubiquitin recognition
component of the 26S proteasome.";
Proc. Natl. Acad. Sci. U.S.A. 93:856-860(1996).
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A -> S (IN REF. 2).
A -> AWYEADLERAEERA (IN REF. 2).
V -> L (IN REF. 2).
S -> A (IN REF. 2).
87AA353E34633901 CRC64;
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STRAIN-CV. COLUMBIA; TISSUE-Seedling;
MEDLINE-96149398; PubMed-8570648;
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STRAIN-CV. COLUMBIA;
MEDLINE-20083488; Pubmed-10617198;
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AAA28969.1; JOINED.
AAA28969.1; JOINED.
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Matches 7; Conserv
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M12840;
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SQ SEQUENCE 386 AA; 40757 MW; 2F5C89D9FACB4550 CRC64;
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ó; 0; Gaps Query Match
47.4%; Score 37; DB 1; Length 386;
Best Local Similarity 61.5%; Pred. No. 60;
Matches 8; Conservative 2; M.smatches 3; Indels

2 ADEEQQQALSSQM 14 |||:| ||: || 304 ADEDQDLALALQM 316 qq δλ

Search completed: July 5, 2001, 11:51:46 Job time: 505 sec

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046035 drosophila
099y31 drosophila
060518 homo sapien
021025 caenorhabdi
051025 caenorhabdi
051025 denorhabdi
051036 bacteriopha
0998b3 drosophila
0958b3 drosophila
0958b5 caenorhabdi
0958b5 caenorhabdi
0958b7 xylella fas
010610 helicoverpa
04088 phalaenopsi
0412D7 pseudomonas
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04130 caenorhabdi
0912D7 pseudomonas
0418B phalaenopsi
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04300 caenorhabdi
014977 homo sapien
09120 caenorhabdi
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 O65525 arabidopsis
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Medine 393:537-544(1998).

Medine S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglaneier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G.;

Taylor K., Whitchead S., Barrell B.G.;

Topichering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berthet F.-X., Birk Rasmussen P., Andersen P., Gicquel B.; Promoter analysis of the M. tuberculosis orfic gene encoding the early secreted antigenic target 6 kDa (ESAT-6)."; Submitted (MAX-1997) to the EMBL/GenBank/DDBJ databases. EMBL; ALC02120; CAA17966.1; -.. EMBL; ALC041213, AAC83445.1; -.. Tuberculist; RV3874; -..
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SEQUENCE 100 AA; 10794 MW; 285F4FC96F55D194 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
11-AUG-1900 (TrEMBLrel. 14, Last annotation update)
11-AUG-1900 (TrEMBLrel. 14, Last annotation update)
LHP OR RV3874 OR MTV027.09
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099482 drosophila
054414 acinetobact
05668 vibrio chol
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MEDILINE-91188700; PubMed-8446027;
MEDILINE-91188700; PubMed-8446027;
Eiglimeier K., Honoro M., Woods S.A., Caudron B., Cole S.T.;
"Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae.";
MOI. Microbiol. 7:197-206 (1993).
MOI. Microbiol. 7:197-206 (1993).
SEQUENCE 100 AA; 10964 MW; 460EE12F876EC383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Eiglmeier K., Garnier T., De Rossi E., Fsihi H., Cole S.T.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                            55.1%; Score 43; DB 14; Length 412; 57.1%; Pred. No. 9.9;
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                                                                                 Indels
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill j', Barrell B.G., Rajandream M.A.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                          100 AA
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                                                                              3; Mismatches
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MEDLINE-97000351; Pubmed-8843436;
                                                                                                                                                                                                                                                                                                                            033084;
01-JAN-1998 (TrEMBLrel. 05, Cr
01-JAN-1998 (TrEMBLrel. 05, La
01-NOV-1998 (TrEMBLrel. 08, La
SIMILARITY TO SMALL.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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256 RTDDEQQQRASSEL 269
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Best Local Similarity
Matches 8; Conserv
                                                    Best Local Similarity
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                               Query Match
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Length 100
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W; 1C17172C2B3D6EC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U95055; AAB5373.1; -
InterPro; IPR003124; -
Ffam; PF02205; WH2; 1.
SMART; SM02246; WH2; 1.
SEQUENCE 412 AA, 45652 MW; CA506F8893863386 CRC64;
                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 145.0 KDA PROTEIN C14F5.3 IN CHROMOSOME X.
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TaxID=51313;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
100.0%; Score 78; DB 2; I
100.0%; Pred. No. 1.1e-06;
ive 0; Mismatches 0;
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Pred. No. 2.6;
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POLY-GLU.
POLY-GLU.
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POLY - SER.
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                                                 16; Conservative
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28 SDEEEQYSSSSQLGF 42
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                       Best_Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE FROM N.A.
Query Match
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum (Wheat).
Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, Liliops1da, Poales, Poaceae, Pooideae, Triticeae,
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Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristlansen C.,
Sollid L.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Production of a panel of recombinant gliadins for the characterisation of T cell reactivity in coellac disease."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ133609; CAB76961.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 10; Length 270; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 902;
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PROSITE; PS00870; CLPAB_1; 1.
SROUENCE 902 AA; 98737 MW; DB45A33B091C0071 CRC64;
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Interpro; IPR003612; -.
PRINNS; PR00208; GLIADGLUTEN.
SEQUENCE 270 AA; 1.
SEQUENCE 270 AA; 31491 MW; 1DB4B6528EFADFF5 CRC64;
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Last annotation update)
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ed. No. 33;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               53.8%; Score 42; 57.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                          MEDLINE-20437337; PubMed-10984043;
                                                                                                                                                                                                                                                             EMBL; AE004447; AAG03480.1; -.
InterPro; IPR001270; -.
InterPro; IPR001939; -.
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.8
Best Local Similarity 57.1
Matches 8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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                                      SEQUENCE FROM N.A.
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NCBI_TaxID=287;
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ID Q2:
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                                        for
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugono S., Shiratori A., Sudo H., Wagatsuma M., Hosolif T., Kaku Y., Kodaira H., Kondo H., Sugawara M. Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S. Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
              Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map the B Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

-I. SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

EMBL, AL031031; CAA19850.1; -.

InterPro; IPR001789; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                          2; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK001353; BAA99644.1;
SEQUENCE 248 AA; 277462 WM; E9802B0415EDF62A CRC64;
                                                                                                                                                                                                                             Phosphorylation; Sensory transduction.
SEQUENCE 224 AA; 24101 MW; 2CD9EF5DC4A39B2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDNVV;
QDNVV;
01-0CT-2000 (TFEMBLrel. 15, Last sequence update)
01-0CT-2000 (TFEMBLrel. 15, Last sequence update)
01-0CT-2000 (TFEMBLrel. 15, Last annotation update)
CDNA FLJ10491 FIS, CLONE NT2RF2000239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91742 PRELIMINARY; PRT, 902 AA. 091742; U-1 MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                        Score 42; DB 2
Pred. No. 8;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB
Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                     Pfam; PF00072; response_reg; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE CLPA/B-TYPE CHAPERONE.
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                                                                                                                                                                                                                                                                                                        53.8%;
ilarity 64.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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| 170 AVEEQAEALSKQLG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11::1111 : 11
227 EERKQALSDRQGF 239
                                                                                                                                                                                                                                                                                                                                                                                    2 ADEEQQQALSSQMG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 EEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserva:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
''^a 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q9NVV1

RESULT **109NVV** 

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Best Loc Matches

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Gaps

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Gaps

RESULT Q91742

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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Madman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen IT., Relzer J., Saier M.H., Hanccok R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Redenbach, M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinsshi H., Hopwood D.A.;

Kinsshi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

-!- SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTIONAL EMBL; AL117387; CAB55719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.

Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saunders D.C., Harris D.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00345; HTH_GNTR; 1.
DNA-binding; Transcription regulation.
SEQUENCE 239 AA; 25886 MW; 21146B716B3097AE CRC64;
                                                                                                                                                                                                                                                                                                                          03AEF8670AEF3357 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 2;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 AA.
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 51.9%; Score 40.5; I Best Local Similarity 47.4%; Pred. No. 17; Matches 9; Conservative 4; Mismatches
                  MEDLINE-20437337; PubMed-10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2);
MEDLINE=97000351; Pubmed=8843436;
                                                                                                                                                                                 opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004799; AAG07203.1; -.
InterPro; IPR001451; -.
                                                                                                                                                                                                                                                                                                                      258 AA; 27891 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE GNTR-FAMILY REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 REDSEQQAKRQAMAEKLGF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RADEEQO---QALSSOMGF 16
                                                                                                                                                                                                                                                                           Pfam; PF00132; hexapep; 4. ProDom; PD001243; -; 1. SEQUENCE 258 AA; 27891 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000524; -. Pfam; PF00392; gntR; 1. PRINTS; PR00035; HTHGNTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                   IPR001537; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Saunders D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2);
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                                                                                                                                                                                                                                                                   InterPro;
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Q9RJV3
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                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
WIBDLINESTOL N2;
WIBDLINES-94150718; Pubmed-7906398;
WiBDLINE-94150718; Pubmed-7906398;
WiBOLN R., Ainscough R., Anderson R., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Caraton M., Dear S., Du Z., Durbin R., Favello A., Fullon L.,
Jones M., Kershaw J., Kirsten J., Laister L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle D.,
Lightning J., Lloyd C., Mcmurray A., Mortinor B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mig J., Thomas K., Vaudin M., Vaudin R., Waterston R.,
Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.;
Z. Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JUN-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databa EMBL; U29244; AAC71091.1; -. InterPro; IPR001095; -. InterPro; IPR001849; -. InterPro; IPR002106; -. Pfam: PP00169; PH; II. PR00166; TBC; I. PROSITE; PS00179; AA_TRNA_LIGASE_II_I; UNKNOWN_I.
              (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Pred. No. 48;
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, O-ACETYLSERINE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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              01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel.
                                                                                              ZK1248.10.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                           SIMILAR TO HUMAN.
                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=287;
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                                                    01-MAR-2001
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Q9HXI6;
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Length 239;

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Gaps

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Indels

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Length 258;

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"Isolation and characterization of drosocrystallin, a lens crystallin
gene of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRY OR DCY OR CG16963.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
   Gaps
                                                                                                                                                                                                                                                                               Perera J., Diaz E.;
the styrene catabolic cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 2; Length 437;
Pred. No. 36;
4; Mismatches 1; Indels
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                 437 AA; 49068 MW; 790263D88BDD4C56 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                437 AA.
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 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                              Velasco A., Alonso S., Garcia J.L., "Genetic and functional analysis of
                                                                                                                                          Created)
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                      Pseudomonas sp. strain Y2.";
Lacteriol. 180:1063-1071(1998).
EMBL; AJO00330; CAA33977.1;
InterPro. IPR000873;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-98155131; PubMed-9495743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00379; insect_cuticle; 1.
 3;
                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00501; AMP-binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00233; CUTICLE; 1.
472 AA; 55166 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                         033491;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TREMBLrel. 05,
01-MAY-2000 (TREMBLrel. 13,
PHENYLACETYL-COA-LIGASE.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 51.3
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                 Bacterla; Proteobacterla.
NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00947; CUTICLE.
8; Conservative
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                122 RIDEEQSAALSAKL 135
                          1 RADEEQQQALSSQM 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 EQQQQALCNELG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 EEQQQALSSQMG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                     RESULT 12
033491
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 Matches
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DB 5; Length 472;

51.3%; Score 40;

Query Match

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortnam J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Adaman J.R., Radiell M.D., Zhang O., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Man K.H., Doyle C. Baxter E.G., Helt G., Nollson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
Ballew R.M., Basus A., Baxendale J., Bayraktroglu L., Beasley E.M.,
Ballew R.M., Basus D.A., Butler H., Cadlew E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davids P.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davids P.,
RA GPADIOS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Cong F., Carrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Hetchum K.A.,
RA Hostin D., Houston K.A., Helman T.J., Wal M.-H., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Re Z., Kenniston J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Re Z., Kenniston J.A., Ketchum K.A.,
Alali M., Marlush R.A., Li J., Li Z., Liang Y., Lin X.,
Liako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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Relanct K., Renington K.A., Nobarry C., Morris J., Moshrefi A.,
Relanct K., Renington K.A., Nobarry C., Morris J., Wap Pacleb J.,
R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
R. Hilmans S.M., Woodage T., Wonley K., Whu D., Yang S., Yao Q.A.,
R. Spiers E., Spradling A.C., Stapleton M., Subsenber K., Shen W.,
R. Spiers E., Spradling A.C., Shangesen M., Stupski M.P., Shang S., Shen S.,
R. Spiers E., Spradling G.M., Welter S., Whu D.,
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                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                   Gaps
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                     Indels
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                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                     5
                                                                                                                                                                                                              486 AA.
  Pred. No. 39;
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0005664; Cry.
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000618; -.
                                                                                                     137 RLDEQQQQRLSA 148
                                                             1 RADEEQQQALSS 12
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                                                                                                                                                                                                                                                                                                                                           CRY OR CG16963.
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                                                                                                                                                                    RESULT 14
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                                                                                                             Gaps
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"Cloning and sequencing of genes encoding malonate decarboxylase in Acinetobacter calcoaceticus.";
Biochim. Biophys. Acta 1354:49-54(1997).

EMBL; AR121266; AAB97627.1; --
InterPro; IPR002086; --
InterPro; IPR002086; --
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.

PROSITE; PS00070; ALDBHYDE_DEHYDR_CYS; UNKNOWN_1.

SEQUENCE 548 AA; 60899 WW; C712AEC6CD8A52A4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acinetobacter calcoaceticus.
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
Acinetobacter.
NCBI_TaxID=471;
Score 40; DB 5; Length 486;
Pred. No. 41;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MALONATE DECARBOXYLASE ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=98041639; Pubmed=9375791;
    Query Match 51.3%;
Best Local Similarity 66.7%;
Matches 8; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                        | ||:||| ||:
| 146 RLDEQQQQRLSA 157
                                                                                                                                                                                         1 RADEEQQQALSS 12
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054414
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Search completed: July 5, 2001, 11:50:53 Job time: 476 sec

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Gaps

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 5, 2001, 11:45:44; Search time 130.35 Seconds (without alignments) 13.022 Million cell updates/sec

Run on:

US-09-462-480-12

Perfect score:

137 1 STNIRQAGVQYSRADEEQQQALSSQMGF 28 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

412676 seqs, 60623988 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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/SIDSB/gcgdata/geneseq/geneseqp/AA2000.DAT:\* A\_Geneseq\_0601:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		M. tuberculosis LH	M. tuberculosis LH	Mycobacterium tube	Mycobacterium tube	M. tuberculosis im	Mycobacterium tube	M. tuberculosis an	M. tuberculosis re	Mycobacterium tube	Mycobacterium tube	M. tuberculosis im
	qi		AAY08712	AAX-0-3707	AAW32454	AAW32386	AAW81707	AAW64340	AAY39137	AAY38994	AAW32444	AAW32376	AAW81747
	DB	1111	20	20	18	18	19	19	20	20	18	18	19
	Query Match Length DB ID		28	42	80	80	80	80	80	80	95	95	95
æ	Query Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score		137	137	137	137	137	137	137	137	137	137	137
	Result No.		г	7	m	4	S	9	7	80	თ	10	11

22 2	M. tuberculosis an M. tuberculosis re M. tuberculosis LH M tuberculosis Rv3 Mycobacterium tube M. tuberculosis fu	Mycobacterium anti Mycobacterium tube My tuberculosis fu My tuberculosis fus My tuberculosis fus My tuberculosis fus	Mycobacterium tub M. tuberculosis in M. tuberculosis an M. tuberculosis LH Mycobacterium tube M. tuberculosis im M. tuberculosis an Enterococcus faeca	Enterococcus faeca Male-enhanced anti Mouse male enhance Chlamydia pneumoni Bacillus agaradher Amino acid sequenc A 5' OT EST (oxyto Sequence of guinea
19 AAW64321 20 AAY32097 20 AAY39118 19 AAY38981 19 AAW64339	20 AAY39136 20 AAY38993 20 AAY03705 22 AAB35218 19 AAW19845			
1000 1000 1000 1000 1100 1000 1000 100				303 1325 1325 1325 431 2493 200 200 200 1
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137 137 137 137 137	137 137 137 137 137	137 137 137 137 137	122 122 78 78 64 64	46.5 46.5 46.5 466.5 466.5 466.5 466.5
112 114 116	22 22 23	22225 22225 22326	2 8 8 8 8 8 8 8 9 4 8 9 9 9 9 9 9 9 9 9 9	8 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

#### ALIGNMENTS

ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; M. tuberculosis LHP polypeptide antigenic fragment. Ŕ 28 AAY03712 ID AAY03712 standard; Protein; Mycobacterium tuberculosis. (first entry) immune response. WO9904005-A1. 07-JUN-1999 28-JAN-1999. AAY03712; \_ RESULT PART SERVICE S

97US-0052631 98WO-IB01091 16-JUL-1998; 16-JUL-1997; Rasmussen PB; Gicquel B, Berthet F, Andersen P,

(INSP ) INST PASTEUR. (STAT-) STATENS SERUM INST.

WPI; 1999-132249/11.

New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis - useful in vaccines, for diagnosis, and for expression of heterologous proteins

```
The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open regulatory expression signals of the ESAT-6 protein as well as an open cading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the M. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polynistidine. The two proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to be protein and the colonial and the colonial encoded by the polynucleotide as protective immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAY03706-713 represent antigenic fragments of the
                                  Claim 21; Page 65; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
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Gaps
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Length 28;
               Indels
100.0%; Score 137; DB 20; 100.0%; Pred. No. 5.8e-15;
                0
                Mismatches
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                Conservative
        Similarity
Query Match
Best Local Simi
Matches 28;
                                δ
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~ AAY03707

AAY03707 standard; Protein; 42 AA (first entry) 07-JUN-1999 AAY03707;

ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; M. tuberculosis LHP polypeptide antigenic fragment. response immune 

Mycobacterium tuberculosis.

WO9904005-A1

28-JAN-1999,

98WO-IB01091 16-JUL-1998; 97US-0052631 16-JUL-1997;

(STAT-) STATENS SERUM INST (INSP ) INST PASTEUR.

Rasmussen PB; Andersen P, Berthet F, Gicquel B,

WPI; 1999-132249/11

Mycobacterium for expression New nucleic acid containing regulator and LHP gene of l tuberculosis - useful in vaccines, for diagnosis, and of heterologous proteins

Claim 21; Page 64; 88pp; English.

The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigonic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the

recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the M. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein mycobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, HHP and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune presponse. Sequences AAX03706-713 represent antigenic fragments of the LHP polypeptide.

42 AA; Sequence

ö Length 42; Indels 100.0%; Score 137; DB 20; 100.0%; Pred. No. 9.3e-15; iive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 28; Conservative

28 1 STNIRQAGVQYSRADEEQQQALSSQMGF

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AAW32454 RESULT

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AAW32454 standard; Protein; 80

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AAW32454;

(first entry) 09-JAN-1998

Mycobacterium tuberculosis antigen Tb38-1F3.

Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;

skin testing; M.tuberculosis Mycobacterium tuberculosis.

WO9709428-A2

13-MAR-1997

96WO-US14674. 30-AUG-1996;

96US-0680574 12-JUL-1996;

95US-0523436. 95US-0533634. 01-SEP-1995; 22-SEP-1995;

96US-0620874 96US-0659683 22-MAR-1996 05-JUN-1996

(CORI-) CORIXA CORP

Skeiky YAW; Reed SG, Campos-neto A, Dillon DC, Houghton R, Twardzik DR, Vedvick TH; 

WPI; 1997-192903/17. N-PSDB; AAT91526.

New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis

Example 3; Page 149; 168pp; English.

A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TDS18-IES. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins blus ESAT-6, are useful in vaccines, preferably when formulated with a

· Sequence

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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;
vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis; infection; diagnosis; antigen; Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to A, Dillon DC, Houghton R, Lodes MJ;
Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 137; DB 19;
100.0%; Pred. No. 2e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                             M. tuberculosis immunogenic polypeptide Tb38-1F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3B; Page 139-140; 230pp; English
                       53 stnirqagvqysradeeqqqalssqmgf 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0818112.
96US-0730510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US18293
                                                                                                                              AAW81707 standard; Protein;
                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV64509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                           WO9816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                          27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-1998
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                                                                                                                                                                     AAW81707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW64340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                             5
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                                                                                                              AAW81707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TB38-IF3. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibendies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 80;
non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                            Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 137; DB 18; Best Local Similarity 100.0%; Pred. No. 2e-14; Matches 28; Conservative 0; Mismatches 0;
                                                                                                           Query Match 100.0%; Score 137; DB 18; Best Local Similarity 100.0%; Pred. No. 2e-14; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton R,
                                                                                                                                                                                                        1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 163; 190pp; English
                                                                                                                                                                                                                                                                                                                   AAW32386 standard; Protein; 80 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skin testing; M.tuberculosis.
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95US-0523435.
95US-0532136.
96US-0620280.
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Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                      80 AA;
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01-SEP-1995;
22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                           13-JAN-1998
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AAW32386;

SXE

AAW32386

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Gaps

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Sequence

Length 80; Indels Houghton R;

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments. can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. Bor natural killer cells and/or macrophages in tuberculosis-immune subjects. AA119249 to AA219460 and AAY39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                          New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen; diagnosis; detection; Infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis recombinant antigen protein Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 137; DB 20;
100.0%; Pred. No. 2e-14;
ive 0; Mismatches 0;
                                                                                                                  Campos-Neto A, Dillon DC, Hendrickson RC, Hor
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos-Neto A, Dillon DC, Hendrickson RC, Hot
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                         Example 3; Page 134-135; 299pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 stnirqagvqysradeeqqqalssqmgf 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 STNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY38994 standard; Protein; 80 AA.
                   98US-0072967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US03265.
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98US-0024753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                              WPI; 1999-527409/44.
N-PSDB; AAZ19310.
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                                                                               (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ19098
                   05-MAY-1998;
18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine;
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AAY38994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide comprises Mycobacterium tuberculosis antigen Tb38-1F3. A DNA molecule (see AAV44400) coding for Tb38-1F3 was isolated from a M. tuberculosis strain H37Ry genomic library. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M. tuberculosis antigen Tb38-1F3 amino acid sequence.
                                                                                                                                                                                                                                                                                     DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
                 Mycobacterium tuberculosis strain H37Rv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 146; 250pp; English.
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                                                                                                                                       97WO-US18214.
                                                                                                                                                                              97US-0818111
96US-0729622
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Reed SG, Skeiky YAW, Tward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Conservative
                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                               WPI; 1998-251292/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 AA;
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV44400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of tuberculosis
                                                       WO9816645-A2
                                                                                                                                       07-OCT-1997;
                                                                                                                                                                              13-MAR-1997;
                                                                                                                                                                                                   11-OCT-1996;
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                                                                                                23-APR-1998
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Sequence

Query Match

Matches

AAY39137;

RESULT AAY39137

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Gaps

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Indels

Houghton R; R, Vedvick TS;

Length 80;

Gaps

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Indels

Length 95;

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w immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                          vaccine; tuberculosis; non specific adjuvant;
                                                  Score 137; DB 10, No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed SG,
M.tuberculosis (for treatment or prevention).
                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen Tb38-1.
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                                                                                                                 1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
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                                                                                                                                                                                                       AAW32376 standard; Protein; 95
                                                               100.0%;
                                                                                                                                                                                                                                                                                                                       skin testing; M.tuberculosis.
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950S-0532136.
960S-0620280.
960S-0658800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon DC,
                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis
                                                                           Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-neto A, Dillon Do
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
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Best Local Similarity
Matches 28; Conserv
                          95 AA;
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22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
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                                                                                                                                                                                                                               AAW32376;
                           Sequence
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                                                                Query Match
                                                                                                                                                                              RESULT 10
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                                                This invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or anditications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                            nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in biologica as sample by detecting antibodies which bind with the polypeptides, and are useful as uncoines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky YAW;
                                                                                                                                                                                          Length 80;
                                                                                                                                                                               100.0%; Score 137; DB 20; Lengua. 100.0%; Pred. No. 2e-14; utsmatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis antigen Tb38-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houghton R,
                                                                                                                                                                                                                                           1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
                                                                                                                                                                                                                                                         53 stnirqagvqysradeeqqqalssqmgf 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 124; 168pp; English:
                         Example 3; Page 180; 323pp; English.
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                                                                                                                                                                                                                                                                                                                                 AAW32444 standard; Protein; 95
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95US-0533634.
96US-0620874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                  28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-neto A, Dillon Do
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-192903/17.
N-PSDB; AAT91509.
                                                                                                                                                                                                      Local Similarity
                                                                                                                                                    80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9709428-A2
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                                                                                                                                                                                         Query Match
Best Local Si
Matches 28;
                                                                                                                                                                                                                                                                                                                                                        AAW32444;
                                                                                                                                                     Sequence
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Skeiky YAW;

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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TD38-1. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 137; DB 18; ilarity 100.0%; Pred. No. 2.4e-14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
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RESULT

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This is an antigenic portion of Mycobacterium tuberculosis antigen Tb38-1. A DNA sequence (see AAV44384) coding for antigen Tb38-1 was isolated from a M. tuberculosis strain H37Rv expression library using sera from patients having pulmonary or pleural tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAM64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                                                                                                                                                                                                                                                                          New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis; antigen; fusion protein; Tb38-1; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                    rodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 137; DB 19; 100.0%; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                Dillon DC, Houghton R, Lodes M
/ YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis antigen Tb38-1.
 Mycobacterium tuberculosis strain H37Rv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 123; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY32097 standard; Protein; 95
                                                                                                                                         970S-0818111
960S-0729622
                                                                                                         97WO-US18214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 28; Conservative
                                                                                                                                                                                                                                                   Reed SG, Skeiky YAW,
                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                       WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 AA;
                                                                                                                                                                                                                                                                                                      N-PSDB; AAV44384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of tuberculosis
                                                                                                                                                                                                                                  Campos-Neto A,
                                   WO9816645-A2
                                                                                                       07-OCT-1997;
                                                                                                                                           13-MAR-1997;
                                                                                                                                                            11-OCT-1996;
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                                                                     23-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method
                                                                                                                                                                                                                                                 Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculosis; infection; diagnosis; antigen; Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           os-Neto A, Dillon DC, Houghton R, Lodes MJ; SG, Skeiky YAW, Twardzlk DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen Tb38-1 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 137; DB 19;
; Pred. No. 2.4e-14;
0; Mismatches 0;
                                                                                                                                                                                                               M. tuberculosis immunogenic polypeptide Tb38-1.
               95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3b; Page 117; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW81747 standard; Protein; 95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW64321 standard; Peptide; 95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US18293
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0818112.
96US-0730510.
                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                                           27-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV64491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                07-OCT-1997;
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11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                          WO9816646-A2
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                                                                                                                                                                                                                                                                                                                                                                              23-APR-1998
                                                                                                                                         AAW81747;
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               68
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                                                                                   AAW81747
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AAW64321

RESULT

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Gaps

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Gaps

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (A9). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. Bor natural killer cells and/or macrophages in tuberculosis-immune subjects. AAX19249 to AAX19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis; detection; infection; antibody; immunisation;
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                                                                                                                                                                                                                                                            Length 95;
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R, Vedvick TS;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis recombinant antigen protein Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                        100.0%; Score 137; DB 20;
11arity 100.0%; Pred. No. 2.4e-14;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A, Dillon DC, Hendrickson RC, Hc
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 137;
                                                                                                                                                                                                                                                                                                                           Example 3; Page 159; 323pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY38981 standard; Protein; 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-527416/44.
N-PSDB; AAZ19082.
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunity
                                                                                                                                                                                                               95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY38981;
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
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                                                                                                                                              New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                           This sequence represents the Mycobacterium tuberculosis antigen TD38-1. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens such as TD38-1, e.g. TDF-2 (see AAY32063) and a TDH9-TD38-1 fusion. The new fusion proteins are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
immunotherapy; diagnosis; immunisation; vaccine; infection;
Immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton R;
;, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. tuberculosis antigen Tb38-1 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 137; DB 20; 100.0%; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hendrickson RC, Ho
YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                Campos-Neto A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 113; 299pp; English.
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                                                                                                                                                                                            Claim 1; Fig 4D; 83pp; English.
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SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US03268.
98US-0056556.
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98US-0025197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                Skeiky YAW, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527409/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed SG,
                                                (CORI-) CORIXA CORP.
                                                                                                               WPI; 1999-601610/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A,
07-APR-1998;
30-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                components.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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0; Gaps Best Local Similarity 100.0%; Pred. No. 2.4e-14; Matches 28; Conservative 0; Mismatches 0; Indels

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Search completed: July 5, 2001, 11:45:44 Job time: 273 sec

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APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: PRETIY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower St. - Suite 1900
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                   Sequence 2, A
Sequence 2, A
Sequence 2, A
Sequence 2, A
Sequence 3, A
Sequence 23, A
Sequence 23, Sequence 24,
Sequence 24,
Sequence 26,
                                                                                                                                                                                                  Sequence 12,
                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: BOOVIL
COMPUTER: PLODDY disk
COMPUTER: TBM PC compatible
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
FILING DATE: 10-AUG-1993
PRIOR APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amazel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
THELECOMMUNICATION INFORMATION:
THELECOMMUNICATION INFORMATION:
THELECOMMUNICATION INFORMATION:
THELECOMMUNICATION INFORMATION:
                                                     US-08-467-8528-2
US-08-468-718-2
US-08-446-701-3
US-08-127-4918-2
US-08-127-4948-23
US-08-614-6868-1
US-08-644-6868-1
US-08-55-419-24
US-08-55-419-24
US-08-58-260-16
US-09-928-692-28
US-09-058-260-16
US-08-781-802-2
US-08-781-802-2
US-08-781-802-2
US-08-781-802-2
US-08-781-802-2
US-08-781-802-10
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                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08463081B Patent No. 5871960 Patent No. 5871960 Fatent No. 5871960 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.4%;
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; MOLECULE TYPE: protein
US-08-463-081B-4
amino acid
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Best Local Similarity
  ZIP: 90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, P
Sequence 36,
Sequence 36,
Sequence 2, P
Sequence 10,
Sequence 10,
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Sequence 1
Sequence 1
Sequence 1
Sequence 3
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-463-081B-4
US-08-461-379A-4
US-08-462-379A-4
US-08-465-585C-4
US-08-65-685C-4
US-08-65-646-4
US-08-145-101
US-08-73-893-10
US-08-73-893-10
US-08-144-121-3
US-08-144-121-3
US-08-144-121-2
US-08-144-121-3
US-08-144-121-3
US-08-144-121-3
US-08-144-121-2
US-08-144-121-3
US-08-144-121-3
US-08-146-148-3
US-08-148-36-10
US-08-452-106-148-3
US-08-452-106-148-3
US-08-452-106-148-3
US-08-452-106-148-3
US-08-227-536-2
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-247-491A-3
US-08-319-795-2
                                                                                                                                                  1 STNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                            193259 seqs, 20144635 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                            US-09-462-480-12
137
                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                      Perfect score:
                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
                                                         OM protein
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                                                                                                                                                                                                            Searched:
                                                                               Run on:
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No.
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60 amino acids
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US-08-462-390B-4
               CITY: Valley Forge
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserva
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                                                                                 19482
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  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
CORRESPONDENCE 35
CORRESPONDENCE ADDRESS:
  Gaps
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Patent No. 5871961
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
TITLE OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-UUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/330,108; 08/104,736
APPLICATION NUMBER: 6.07/796,066
APPLICATION NUMBER: 6.07/796,066
ATIONEY/AGENT INFORMATION:
NAME: V1'4 Ann A Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     (B) STREET: One Westlakes-Berwyn
8
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.4%; Score 43; Best Local Similarity 43.5%; Pred. No. Matches 10; Conservative 5; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, SOFTWARE: Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/461,37
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Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadli
                                                               5;
                                       5 RQAGVQYSRADEEQQQALSSQMG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 RKAGVILPKAEAEQQSSGVSCLG 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratner & Prestia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-461-379A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                         Valley Forge
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                                                                                                                                               RESULT 2
US-08-461-379A-4
10;
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Patent No. vosco...
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
APPLICANT: Smith, Nocleic Acids Encoding CRI Fusion Protein, Vector
NUMBER OF EXQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ANDRESSEE: (B) STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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(B) STREET: One Westlakes-Berwyn
                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
FRIOR APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-0C-1994
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY AGENT INFORMATION:
NAME: Viviana Anzel, Ph. D.
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Pred. No.
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APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: DART-040 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELGASE #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/08463074B
; Patent No. 6020155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 RKAGVILPKAEAEQQSSGVSCLG 45
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                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (610)407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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444 South Flower St. - Suite 1
                                                                                                                                                                                                                                                                        Kendall A. & Beadling, Carol
Nucleic Acids Encoding CR5
Polypeptide, Vector and Transformed Cell Thereof,
Expression Thereof
                                                                     Gaps
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                              DB 3; Length 60;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTATIONS: 38
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
(R) STREET:
(B) STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP App. # 96921319.8 FILING DATE: 5-JAN-1998 APPLICATION NUMBER: PCT/US/96/09194 FILING DATE: 5-JUN-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/330,108
                                                                     5; Mismatches
                            Score 43;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FP66 40035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 27-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, SOFTWARE: Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/652,446 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/462,390 FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/461,379 FILING DATE: 5-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: 08/739,523
29-OCT-1996
                                                                                                                                                                                                                                                    Sequence 4, Application US/08652446 Patent No. 6057427
                                                                                                                                            23 RKAGVTLPKAEAEQÓSSGVSCLG 45
                                                                                                            5 RQAGVQYSRADEEQQQALSSQMG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viviana Amzel, Ph. D. RATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (213) 622-7700
                            31.4%;
ilarity 43.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: 29-OCT
                                                                                                                                                                                                                                                                                                                 APPLICANT: Smith, Ke
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
                                               Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                   US-08-652-446-4
                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444South Flower St. - Suite 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & BeadTing, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETIY, SCHROEDER & POPLAWSKI
                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE PATENTIAN STATEM.
SOFTWARE PATENTIAN STATEM.
SOFTWARE PATENTIAN BATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                            NAME: VIVIANA AMZEL, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMUNICATION INFORMATION:
TELEPRONE: (213) 622-7700
TELEPRONE: (213) 489-4210
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Viviana Amzel, Ph. D.
REGISTRATION VONDER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB Pred. No. 3.1; 5; Mismatches
ALPLICATION NUMBER: US 07/796,066 FILING DATE: 20-NOV-91 ATTORNEY/ABOT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (B) STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 RQAGVQYSRADEEQQQALSSQMG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                Query Match 31.4%;
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                               LENGTH: 60 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-463-074B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-465-585C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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Californiaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-08-465-585C-4
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TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                   United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                              Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-735-893-10
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08144121
Patent No. 5610031
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wagnan, David W.
TITLE OF INVEWTION: Blk CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/144,121
FILING DATE: 27-0CT-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MGH-0780.0) MGP-021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                DB 3;
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Pred. No. 2.8;
5; Mismatches
                                                                                                                                                                                    Mismatches
                                                                                                                                            Query Match 31.4%; Score 43; Best Local Similarity 43.5%; Pred. No. Matches 10; Conservative 5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 ROAGVOYSRADE ---- EQQQALSSQMGF 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08735893; Patent No. 5914317; GENERAL INFORMATION:
                                                                                                                                                                                                                    5 RQAGVQYSRADEEQQQALSSQMG 27
                                                                                                                                                                                                                                                    23 RKAGVTLPKAEAEQOSSGVSCLG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MG
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 10
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.7%;
39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: BOSTON
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 39.37
Matches 11; Conservative
                  : 60 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 40 amino acids
SEQUENCE CHARACTERISTICS
                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                           US-08-144-121-10
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                                                                          ; MOLECULE TO
US-08-652-446-4
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Gaps
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Sequence 3, Application US/08144121
Sequence 3, Application US/08144121
Sequence 1. No Sel0031
Sequence 1. No Sel0031
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: GO State Street, suite 510
CITY: BOSTON
STATE: Massachusetts
TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                           COMPUTER: VALUE
COMPUTER: ELOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIAL
COMPUTER: TBM PC COMPATIAL
COMPUTER: TBM PC COMPATIAL
COMPUTER: PAPELICATION DATA:
APPLICATION NUMBER: US/08/735,893
FILING DATE: 18-OCT-1996
CLASSIEFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/144,121
FILING DATE: 27-OCT-1993
CLASSIECATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MYSTE, PAPELICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MYSTE, PAPELICATION: 435
REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV
TELECOMMUNICATION NUMBER: (MGH-0780.1) MGP-021DV
TELECOMMUNICATION INFORMATION:
ATTORNEY/AGENT NUMBER: (MGH-0780.1) MGP-021DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/144,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.7%; Score 42; 39.3%; Pred. No. 3
                                                                               ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510 CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 RQAGVQYSRADE----EQQQALSSQMGF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 ROOGAEAVOAQOLAEGASEQALSAQEGF 35
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FILING DATE: 27-OCT-1993

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Gaps
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Patent No. 5610031
GENERAL INFORMATION:
APPLICANT: Burgeson, Robert E.
APPLICANT: Wagman, David W.
TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 2; Length 114
Pred. No. 1.7e+02;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTERET: 60 State Street, suite 510
CITY: BOSTON
CITY: BOSTON
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/144,121
FILING DATE: 27-CT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MYGEN, Paul L.
REGISTRATION NUMBER: (MGH-0780.0) MGP-021
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1027 RQQGAEAVQAQQLAEGASEQALSAQEGF 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 ROAGVOYSRADE ---- EQQQALSSQMGF 28
        TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INPORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.7%;
Best Local Similarity 39.3%;
Matches 11; Conservative
                                                                                         LENGTH: 1147 amino acids
                                                                                                                                                  MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-144-121-2
                                                                                                                                                                                                                                                                                                                                                                                                                           766..1147
                                                                                                                                                                                                                                                                              Domain
232..411
                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                NAME/KEY: Domain
LOCATION: 1..231
FEATURE:
                                                                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-08-735-893-3
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Patent No. 5914317
GENERAL INFORMATION:
APPLICANT: Magman, David W.
TITLE OF INVENTION: Blk CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE S. 14
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 00 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
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ZUP: 02109

COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,893
FILING DATE: 18-OCT-1996
CLASSIFICATION 1435
PROOF APPLICATION NUMBER: US 08/144,121
FILING DATE: 27-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
FREFERENCE/DOCKET NUMBER: (MGH_D780.0) MGP-021
FELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
FELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1147 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MYSTS, Paul L.
NERGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.7%; Score 42; DB Best Local Similarity 39.3%; Pred. No. 1.7e Matches 11; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1027 RQQGAEAVQAQQLAEGASEQALSAQEGF 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 RQAGVQYSRADE ---- EQQQALSSQMGF 28
                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
766..1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
412..765
                                                                                                                                                                                                                                                                                                                                                                                                   Domain
232..411
                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: BOSTON STATE: Massac
                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-08-144-121-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-735-893-3
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APPLICANT: Joseph. Otsu, Masayuki; Panayotou, George; Volinia, APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
ADDRESSEE: Relfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/08780872;
Patent No. 5846624;
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
  POLYPEPTIDES HAVING KINASE ACTIVITY, THEIR PREPARATION AND USE
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.3%; Score 41.5; DB 2; 30.6%; Pred. No. 1.9e+02; iive 6; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|| || || 502 REAGESYSHAGLSNRLARDNELRENDKEQLKAISTR 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- DEEQQQALSSQ 25
                                                                                                                                                                                                                                                    MRELION ITEE: LEARCELCY COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordfeerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INNORMATION:
NAME: PASQUALINI, PATTICIA A.
REGISTRATION NUMBER: 34,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION: POLYPEPT
TITLE OF INVENTION: THEIR PR
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Felfe & Lynch
: 805 Third Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1080 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.3
Best Local Similarity 30.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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OPERATING SYSTEM: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                       New York
f: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
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                                                                                                                                                     STATE: New COUNTRY: US ZIP: 10022
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US-08-162-081B-36
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US-08-780-872-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
Bala; Waterfield, Michael Derek; Parker, Peter
                                                                                                                                                                                                                                  US-08-735-893-2

Sequence 2, Application US/08735893

Sequence 2, Application US/08735893

Parent No. 594317

SEMERAL INFORMATION:
APPLICANT: Burgeson, Robert E.
APPLICANT: Wagman, David W.
TITLE OF INVENTION: Blk CHAIN OF LAMININ AND METHODS OF USE NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                           Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.7%; Score 42; DB 2; Length 1165; 39.3%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 1.7e+02;
. . 8; Indels
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,893
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/144,121
FILING DATE: 27-OCT-1993
CLASSIFICATION: 435
                    Score 42; DB 1; Ler
Pred. No. 1.7e+02;
5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510
                                                                                                            5 ROAGVOYSRADE ---- EQUOALSSOMGF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 RQAGVQYSRADE----EQQQALSSQMGF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/08162081B Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, APPLICANT: Bala; Waterfield, Micha APPLICANT: Joseph; Otsu, Masayuki;
                      30.78;
39.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: United States
                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-735-893-2
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                                           Similarity
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
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                      Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                 Matches
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Gaps

15;

Indels

Length 1080;

DB 2;

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Gaps

19;

us-09-462-480-12.rai

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-----YSRAD---EEQ---QQALSSQMGF 28
                                                                                        Query Match
30.3%; Score 41.5; DB 5;
Best Local Similarity 32.6%; Pred. No. 2.6e+02;
Matches 15; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                              Search completed: July 5, 2001, 11:47:02 Job time: 316 sec
  ; MOLECULE TYPE: protein PCT-US95-10661A-2
                                                                                                                                                                                       2 TNIRQAGVQ---
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Sequence 2, Application PC/TUS9510661A

GENERAL INFORMATION:

APPLICANT: Washington University, et al.

TITLE OF INVENTION: Heemophilus Adherence and Penetration Protein
NUMBER OF SEQUENCES: 9

CORRESPONDENCES: 9

CORRESPONDENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ITP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: TBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: PCT/US95/10661A

FILING DATE: 16-AUG-1995

CLASSIFICATION STATES: PCT/US95/10661A

FILING DATE: 16-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41.5; DB 2;
Pred. No. 1.9e+02;
6; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|| || || || 502 REAGESYSHAGLSNRLARDNELRENDKEQLKAISTR 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DEEQQQALSSQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: FP-59941/RFT
TELECOMMUNICATION INFORMATION:
                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/162,081
FILING DATE: PEDFUARTY 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY,AGENT INFORMATION:
NAME: PASQUALINI, PARTICIO!
NAME: PASQUALINI, PARTICIO!
NAME: PASQUALINI, PARTICIO!
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9384
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
LENGTH 1080 manio acids
TYPE: amino acid
TYPE: amino acid
APPLICATION NUMBER: US/08/780,872
FILING DATE: 09-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08/296,791
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TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 25-AUG-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1394 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 30.6'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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PCT-US95-10661A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-780-872-36
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Thu Jul 5 13:58:47 2001

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 5, 2001, 11:48:36; Search time 79.63 Seconds (without alignments) 26.785 Million cell updates/sec

US-09-462-480-12

137 1 STNIRQAGVQYSRADEEQQQALSSQMGF 28 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	hypothetical prote	_	a)		ໝ	biphenyl-2,3-diol	citrate (pro-35)-1	male-enhanced anti	hypothetical prote	hy	conserved hypothet	CT632 hypothetical	probable multidrug	hypothetical prote	hypothetical prote	д	potassium transpor	hypothetical prote			ipaC protein - Shi	isocitrate dehydro	hypothetical prote		probable requlator	hypothetical 138.1	Ċ	myosin heavy chain	hypothetical prote
SUMMARIES	. QI	H70802	T10032	D82883	T15496	T08416	DAPSPC	4	T42722	T13235	F82151	H72040	G86583	н82171	T10623	S76513	S63249	T38083	A70689	T34333	A60112	S15578	I40382	G70803	S19680	H85839	E64979	A61231	S21801	T20241
	DB																		7											
	Length	100	100	743	1263	825	293	291	1325	198	224	531	531	343	416	441	576	880	108	381	382	382	423	460	687	1209	1210	1961	1999	2160
dР	Query Match	100.0	41.6	o.	38.3	ď.	34.3	33.9	33.9	33.6	33.6	33.6	33.6	32.8	32.8	32.8	32.8	32.8	32.5	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1
	Score	137	57	52	52.5	48	47	46.5	46.5	46	46	46	46	45	45	45	45	45	44.5	4.4	44	44	44	44	44	44	44	44	44	44
	Result No.	Н	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	. 18	19	20	21	22	23	24	25	26	27	28	29

phycocyanin linker	hypothetical prote	hypothetical prote	TSC-22 protein hom	hypothetical prote	hypothetical prote	hypothetical prote	alpha/beta-gliadin	hypothetical prote	lipoate-protein 11	probable threonine	oxidative cyclase	VP10' protein - Co	cell division prot	homeobox protein (	homeotic protein A
D29674	F84258	T09896	T29092	T32450	C71362	T20520	S07924	T04595	C83735	H71703	S17814	T02302	S75291	D96829	S71478
~	~	~	N	~	N	N	7	~	N	7	~	~	7	~	7
80	253	478	1040	118	291	297	313	322	330	333	575	602	665	745	747
31.8	31.8	31.8	31.8	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4
43.5	43.5	43.5	43.5	43	43	43	43	43	43	43	43	43	43	43	43
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT

H70802
hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C;Date: 17-Jul:1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C; Accession: H70802
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Aranthore, Garage D. Gileton J. D. Baylor V. Whitehead C. Barrell B.C.

A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987
A:Accession: H70802
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-100 <COL>
A:Cross-references: GB:AL022120; GB:AL123456; NID:93261558; PIDN:CAA17966.1; PID:9296
A:Cross-references: strain H37Rv
C:Genetics:
A:Genetics:

ö Length 100; Indels Query Match 100.0%; Score 137; DB 2; Best Local Similarity 100.0%; Pred. No. 9.8e-14; Matches 28; Conservative 0; Mismatches 0;

Gaps

1 STNIRQAGVQYSRADEEQQQALSSQMGF 28 δ g

hypothetical protein MLCB628.13c - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jul-2000
C;Accession: T10032
R;Edimeier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A;Title: Use of an ordered cosmid library to deduce the genomic organization of Mycob A;Reference number: 216917; MUID:93188700
A;Steference number: 216917; MUID:93188700
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA A;Residues: 1-100 <EIG> A;Cross-references: EMBL:Y14967; NID:92370268; PIDN:CAA75210.1; PID:92370280

ö 0; Gaps Score 57; DB 2; Length 100; Pred. No. 0.14; 7; Mismatches 8; Indels Query Match
Best Local Similarity 40.0%;
Matches 10; Conservative

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Diphenyl-2,3-diol 1,2-dioxygenase (EC 1.13.11.39) - Pseudomonas sp. (strain KKS102) N.Alternate names: 2,3-dihydroxybiphenyl dioxygenase C; Specdese: Pseudomonas sp. (strain KKS102) Cs Specias: Pseudomonas sp. (cjpate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jun-2000 C; Accession: A32312; PC2281; JU0085 R; Kimbara, K.; Hashimoto, T.; Fukuda, M.; Koana, T.; Takagl, M.; Oishl, M.; Yano, K. J. Bacteriol. 171, 2740-2747, 1989 A; Title: Cloning and sequencing of two tandem genes involved in degradation of 2,3-di $102.
  M.; Salan
                                                                     A Accession: T08416
A Molecule type: DNA
A Molecule type: DNA
A Molecule type: DNA
A Mesidues: 1-852 GQUE
A Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.230
A Cross-references: Cultivar Columbia; BAC clone F18B3
B; Rouse, D.T.; Heazlewood, J.L.
B; Rouse, D.T.; Heazlewood, J.L.
B; Rouse, D.T.; Heazlewood, J.L.
A; Description: Incomplete sequence of an Arabidopsis gene with similarities to myosin A; Reference number: S71195
A; Molecule type: DNA
A; Rocession: S71195
A; Molecule type: DNA
A; References: EMBL:U19616; NID:9699494; PID:9699495
C; Genetics:
                                                                                                                                                                                                                                                             to myosin
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C; Superfamily: biphenyl-2,3-diol 1,2-dioxyenase
C; Keywords: aromatic hydrocarbon catabolism; iron; oxidoreductase; PCB biodegradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein rep
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A, Molecule type: DNA
A, Residues: 1-293 <KIN>
A, Cross references: GB: M26433; NID: g151098; PIDN: AAA25750.1; PID: g151099
A, Experimental source: strain KKS102
A, Experimental source: Strain KKS103
A, Experimental source: Strain KKS103
A, Title: Identification of the bphA and bphB genes of Pseudomonas sp. strain
A, Reference number: JC2438; MUID: 94324977
  S.; Schaefer, M.; Zipp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: DDBJ:D17319; NID:g391831; PIDN:BAA04141.1; PID:g391837
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R;Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, 8 submitted to the Protein Sequence Database, May 1999
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Pred. No. 15;
3; Mismatches
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Pred. No. 36;
8; Mismatches
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52.9%;
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80 LRQAGVAFTRGDEALMQ
                                               A; Reference number: Z16409
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-16 <FUK>
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C;Superfamily: d
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A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-743 <GLA>
A;Residues: 1-743 <GLA>
A;Cross-references: GB:AE002148; GB:AF222894; NID:g6899495; PIDN:AAF30913.1; GSPDB:GN001
A;Experimental source: serovar 3; blovar 1
                                                                                                                                                                                                                                                                                                  Rigiass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
Submitted to GenBank, February 2000
A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A; Reference number: A82870
A; Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: CESP:C14F5.3
A;Introns: 21/3; 34/2; 740/2; 852/2; 881/2; 902/3; 970/3; 1005/2; 1041/3; 1093/3; 1125/3
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A; Cross-references: EMBL:U29082; NID:9861384; PID:9861386; PIDN:AAA68402.1; CESP:C14F5
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                                                                                                                                                                                                  DNA helicase II UU501 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug.2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: D82883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C14F5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15496
R;Minx, P.
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A;Description: The sequence of C. elegans cosmid C14F5.
A;Reference number: 218361
A;Accession: T15496
A;Status: preeliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Pred. No. 2.7;
9; Mismatches
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                                                  5 ROAGVOY-SRADEEQQQALSSQMGF 28
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C, Genetics:
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nes 8; Conservative
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C; Superfamily: helicase
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Best Local Similarity
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Best Local Si
Matches 8;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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ilarity 38.5%;
Conservative
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Best Local Similarity 34.0.
-haq 9; Conservative
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Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-531 <REA>
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630
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Gene 187, 45-53, 1997
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A;Reference number: 217631; MUID:97225795
A;Accession: T13215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T42722
R;Kondo, M.; Sutou, S.
DNA Seq. 7, 71-82, 1997
A;Title: Cloning and molecular characterization of cDNA encoding a mouse male-enhanced
A;Reference number: 222242; MUID:97217683
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:U32688; GB:L42023; NID:g1572966; PIDN:AAC21701.1; PID:g1572968; C;Superfamily: Yersinia pestis hypothetical 29.7K protein C;Keywords: carbon-carbon lyase; oxo-acid-lyase
                                                                citrate (pro-3S)-lyase (EC 4.1.3.6) beta chain - Haemophilus influenzae (strain Rd
C;Species: Haemophilus influenzae
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A;Residues: 1-1325 <KON>
A;Cross-references: EMBL:D78270; NID:d1096175; PID:d1020389; PIDN:BAA19612.1
                                                                                                                   C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Jul-2000
C;Accession: D64043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           male-enhanced antigen-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
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C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C;Accession: T13215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 291;
                                                                                                                                                                                                                                                                                                                                                           A:Status: nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Residues: 1-291 <TIGR>
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A;Description: supposed to play some role for spermatogenesis
C;Keywords: leucine zipper
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38.5%; Pred. No. 1e+02;
tive 10; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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39.4%;
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Best Local Similarity 38.5%
Matches 10; Conservative
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Best Local Similarity
Matches 13; Conserva
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A;Cross-references: GB:AE004260; GB:AE003852; NID:99656368; PIDN:AAF95001.1; GSPDB:GN
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
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A;Experimental Source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C. Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Reference number: A81500; MUID:20150255 A;Accession: A81501
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A;Residues: 1-531 <ARN>
A;Cross-references: GB:AE001656; GB:AE001363; NID:94377047; PIDN:AAD18885.1; PID:9437
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C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Accession: H72040; A81501
R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A; Reference number: A72000; MUID:99206606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein VC1853 [imported] - Vibrio cholerae (strain N16961
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A Molecule type: DNA
A, Residues: 1-198 <KOD>
A, Cross-teferences: EMBL:X98106, NID:g1926320; PIDN:CAA66744.1; PID:g1926359
C, Genetics:
A, Note: Rorf198
C, Superfamily: Lactobacillus phage phi-gle hypothetical protein R198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: F82150
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Pred. No. 14;
6; Mismatches
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Pred. No. 16;
7; Mismatches
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1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
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Job time: 376 sec
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A;Cross-references: GB:AE002268; GB:AE002161; NID:g7190029; PIDN:AAF38892.1; PID:g719003
A;Experimental source: strain AR39, HL cells
C;Genetics:
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A;Molecule type: DNA
A;Molecule 1-343 <HEL>
A;Cross-references: GB:AE004245; GB:AE003852; NID:99656183; PIDN:AAF94825.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
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A;Accession: H82171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A) Accession: G86583
A) Status: preliminary
A) Molecule type: DNA
A) Residues: 1-531 <STO>
A) CSTOS - References: GB:BA000008; NID:g8979118; PIDN:BAA98953.1; GSPDB:GN00142
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C;Genetics:
A;Gene: Cpj0746
C;Superfamily: conserved hypothetical protein TC0921
                                                                                                            A;Gene: CPn0746; CP1126
C;Superfamily: conserved hypothetical protein TC0921
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37;
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Pred. No. 43;
4; Mismatches
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Pred. No. 37;
5; Mismatches
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Pred. No. 4
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ilarity 47.8%;
Conservative
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ilarity 47.8%;
Conservative 4
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ilarity 35.7%;
Conservative
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Matches 11; Conserv
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Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
Matches 10; Conserv
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C; Genetics:
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Cypecies: Arabidopsis thaliana (mouse-ear cress)
Cypecies: Arabidopsis thaliana (mouse-ear cress)
Cypecies: Arabidopsis thaliana (mouse-ear cress)
Cyaccession: T10623
Cyaccession: T10623
Submitted to the Protein Sequence Database, June 1999
A)Reference number: 21693
A)Recession: T10623
A)Recession: T10633
A)Recession: T10633
A)Recession: T10633
A)Recession: T10633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803)
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 02-Sep-2000
C;Accession: S76513
R;Kanecko, T; Sato, S; Kotani, H; Tanaka, A; Asamizu, E; Nakamura, Y; Miyajima, O, K; Okumura, S; Shimpo, S; Takeuchi, C; Wada, T; Watanabe, A; Yamada, M; Yas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAA10359.1; Plb.g100 A;Cross-references: EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAA10359.1; Plb.g100 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: sensory transduction histidine kinase s110798; sensor histidine kinase F;172-435/Domain: sensor histidine kinase homology <SHK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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8
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Pred. No. 46;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB
Pred. No. 49;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 TNVQQA-LEYPEADPQQQRQQLQVIERLTQRLG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TNIRQAGVQYSRADEEQQ-----QALSSQMG 27
SANFQLADVQFQRAQRLRQDKVVSEQDF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S74322; MUID:97061201
A; Accession: S76513
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-441 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 SSSDRQVGMKSKREEEEEEA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.8%;
Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.8%;
Best Local Similarity 33.3%;
Matches 11; Conservative
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Thu Jul 5 13:58:48 2001

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 5, 2001, 11:51:45; Search time 41.8 Seconds (without alignments)
22.946 Million cell updates/sec Run on:

US-09-462-480-12 137 1 STNIRQAGVQYSRADEEQQQALSSQMGF 28 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 segs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	escript1	P17297 pseudomonas		_	Q9umn6 homo sapien		Q46455 moorella th	Q10065 schizosacch				P51176 bos taurus				-	triticum					0 gallus	-	Q03172 mus musculu	_	-		_	P08587 cavia cutle	Q13751 homo sapien	P11396 mastigoclad	_	2336	P45387 haemophilus
SUMMARIES	QI	BPHC_PSES1	CILB_HAEIN	G160_MOUSE	TRX2_HUMAN	YN15_YEAST	SELB_MOOTH	TRK2_SCHPO	IPAC_SHIDY	IPAC_SHIFL	IDH_BACSU	TGLC_BOVIN	MSH2_NEUCR	YEHI_ECOLI	MY SN_HUMAN	PYS1_ANASP	GDA7_WHEAT	BCHE_RHOCA	SELB_DESBA	FTH2_SYNY3	HGL2_ARATH	VILI_CHICK	ALS3_CANAL	ZEP1_MOUSE	YQC1_CAEEL	RPN2_YEAST	YQIX_BACSU	RP54_BACSU	TGLC_CAVCU	LMB3_HUMAN	PYS1_MASLA	CILB_ECOLI	P11A_HUMAN	HAP_HAEIN
	DB	-	7	-4	Н	-	Н	-	-	Н		Н	Н	7	-	-	7	-	-	-	Н	Н	-	-4	<del>, -1</del>	-	-	П	Н	٦	П	Н	Η,	1
	Query Match Length	292	291	1325	2715	576	634	880	382	382	423	687	937	1210	1960	80	313	575	634	99	745	826	1119	2688	468	945	255	436	689	1172	80	302	1068	1394
đ	Query Match	34.3	33.9	33.9	33.6	32.8	32.8	32.8	32.1	32.1	32.1	32.1	32.1	32.1	32.1	31.8	31.4	31.4	31.4	31,4	31.4	31.4	31.4	31.4	31.0	31.0	30.7	30.7	30.7	30.7	30.3	30.3	30.3	30.3
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P44596 haemophilus Q09472 homo sapien	P78024 mycoplasma Q10798 mycobacteri P00730 bos taurus	P23669 corynebacte P49643 homo sapien	P43439 enterococcu P34489 caenorhabdi p18106 drosophila	032483 rhodopseudo P34402 caenorhabdi
HAP1_HAEIN P300_HUMAN	IF3_MYCPN DXR_MYCTU CBPA BOVIN	THRC_CORGL PRI2_HUMAN	NTPI_ENTHR YMMI_CAEEL FDS DROWF	CAPP_RHOPA YLU8_CAEEL
пп				
1409	201 413 419	481 509	732	936 1207
30.3	20.00	29.9	0,000 0,000	2000
41.5	444	414	4 4 4	4 4 1
34 35	36 37 38	39	441	444

# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Relatschmann R.D., Addams M.D., White O., Clayton R.A., Kirkness E.F.,
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Soott J.D., Shirley R., Liu L.T., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Wenter J.C.,
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CITRATE LYASE BETA CHAIN (EC 4.1.3.6) (CITRASE) (CITRYL-COA LYASE
                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                               Length 292;
                                                                                                                                           Indels
           0
145
209 IRON.
260 IRON.
32113. MW; 5D D912F79EA8476 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 AA; 31854 MW; 9DB1B9D202CF221F CRC64;
                                                                                                             DB 1;
9;
                                                                                                                                                                                                                                                                      291 AA
                                                                                                                                            Mismatches
                                                                                                             Score 47;
Pred. No.
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-DEC-1998 (Rel. 37, Last ann
                                                                                                             34.3%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32688; AAC21701.1; -.
                                                                                                                                                                     4 IRQAGVQYSRADEEQQQ 20
                                                                                                                                                                                              79 LROAGVAFTRGDEALMQ 95
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                     SUBUNIT) (EC 4.1.3.34).
CITE OR H10023.
                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae
                          145
209
260
292 AA;
                                                                                                                           Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyase; Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=727;
3D-structure.
INIT_MET
METAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; HI0023
                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus
                                                                                                                                                                                                                                                                    CILB_HAEIN
                                                                                                             Query Match
Best Local S
Matches 9
                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                  P44460;
                                         METAL
                                                         METAL
                                                                                                                                                                                                                                                       CILB_HAEIN
                                                                                                                                                                                                                                          RESULT
KW
FT
FT
FT
SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTS CAN BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRX2_HUMAN STANDARD; PRT; 2715 AA.
Q9UMN6; Q9UK25; O95836; Q9Y669; Q9Y668; O15022;
01-0CT-2000 (Rel. 40, created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
TRTTHORAX HOWOLOG 2 (MTXED LINEAGE LEUKEMIA GENE HOWOLOG 2 PROTEIN).
TRX2 OR HRX2 OR MLL2 OR KIAA0340.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEVDIG CELLS, SPERMATOGONIA, OR SPERMATOCYTES.
-!- SIMILARITY: HIGH, TO HUMAN GOLGIN-160.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Seq. 7:71.82(1997).
-I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR TESTIED BEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLOGICALLY DETECTABLE MALE ANTIGEN (SDM).
-I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO EXPRESSION IN
                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CD-1; TISSUE-Testis;
MEDLINE-97217683; PubMed=9063644;
Kondo M., Sutou S.;
"Cloning and molecular characterization of cDNA encoding a mouse male-enhanced antigen-2 (Mea-2): a putative family of the Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3230636962C687B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GOLGIN-160 (MALE-ENHANCED ANTIGEN-2) (MEA-2).
                                                                                                                                    PRT; 1325 AA
                                     184 RAAGIQAFDTVYSNANNEEGFLKEAALIKQLGF 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 57;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.9%; Score 46.5; 38.5%; Pred. No. 57;
5 ROAGVQ----YSRADEEQ----QQALSSQMGF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatogenesis; Developmental protein.
DOMAIN 201 204 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 STRL-QAQVEHSHSSQQKQDSLSSEV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STNIRQAGVQYSRADEEQQQALSSQM 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1325 AA; 149880 MW;
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D78270; BAA19612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.5'
Matches 10; Conservative
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:96958; Golga3.
                                                                                                                                                                                                                                                                       (Monse)
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoantigen.";
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                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                  G160_MOUSE
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                                                                                               RESULT 3
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Gaps

6

Indels

9

Score 46.5; DE Pred. No. 11; 5; Mismatches

33.9%; 39.4%;

5

Conservative

Query Match Best Local Similarity Matches 13; Conserv

DB 1; Length 291;

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EMBL; AF105280; AAD26112.1;
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CONFLICT
SEQUENCE
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YN15_YEAST
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Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Testis, and Leukocyte;
MEDLINE-20105772; PubMed-10637508;
Huntsman D.G., Chin S.-F., Muleris M., Batley S.J., Collins V.P.,
Wiedemann L.M., Aparicio S., Caldas C.;
"MLL2, the second human homolog of the Drosophila trithorax gene,
to 19q13.1 and is amplified in solid tumor cell lines.";
                                                           SEQUENCE FROM N.A. (LONG ISOFORM).
Angrand D.O., Valvatne H., Jeanmougin F., Adamson A.,
van der Hoeven F., Olsen L., Tekotte H., Huang N., Poch O.,
Lamerdin J., Chambon P., Losson R., Stewart A., Aasland R.;
"Mammallan trithorax- and ASHI-like proteins: puttative chromatin
regulators which contain PHD fingers and SET domains.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE FROM N.A. (LONG AND TRUNCATED ISOFORMS).
                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of a 1 Mb region in human 19q13.1."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 BROMODOMAIN.
SIMILARITY: CONTAINS 1 SET DOMAIN.
SIMILARITY: CONTAINS 3 PHD ZINC-FINGER DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 816-2715 FROM N.A. (LONG ISOFORM).
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BAA20763.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Placenta, and Bone marrow;
MEDLINE-99339983; PubMed=10409430;
FitzGerald K.T., Diaz M.O.;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (LONG ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97349984; PubMed-9205841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ007041; CAB45385.1; -.
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                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                        Carrano A.V
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPQEPAPVPS -> PLSQSLLLPMTLQLSLSLGQWAAPTTS
ACLDSPLWSPLLLRPRCPLTGLQL (IN ISOFORM
                                                                                                                                     protein; Zinc-finger; Metal-binding;
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-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Funqi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Messenguy F., Dubois E., Vierendeels F., Scherens B., Pierard
Glansdorff N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN IN MET2-SEC2 INTERGENIC REGION.
YNL275W OR N0626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN ISOFORM TRUNCATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  > Q (IN REF. 5).

> Y (IN REF. 5).

> N (IN REF. 5).

> H (IN REF. 5).

C0615E981BBEB7BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                     Transcription regulation; Alternative splicing.

DNA_BIND 37 44 A.T HOOK (BY SIMILARITY).

DNA_BIND 110 117 A.T HOOK (BY SIMILARITY).

ZN_FING 1203 1252 PHD-TYPE 1.

ZN_FING 1253 1303 PHD-TYPE 2.

ZN_FING 1337 1396 PHD-TYPE 2.

DOMAIN 1449 1471 BROMODOMAIN (DIVERGENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.6%; Score 46; DB 1; Le 34.8%; Pred. No: 1.5e+02; tive 9; Mismatches 6;
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POLY-PRO.
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                                                      Pfam; PF00628; PHD; 3.
Pfam; PF00856; SET; 1.
Pfam; PF02008; Zf CXXC; 1.
PROSTIE; PS50280; SET; 1.
DNA-binding; Bromodomain; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 IRQAGVQYSRADEEQQQALSSQM 26
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834 834
941 941
1317 1317
1362 1362
1362 2622
2622 2622
2715 AA; 293511 M
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interpro; ipR001214; -.
interpro; ipR001965; -.
interpro; iPR002857; -.
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Best Local Similarity
Matches 8; Conserv
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CARBOHYD
CARBOHYD
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TRK2_SCHPO
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-I- PUOCITION: TRANSLATION FACTOR NECESSARY FOR THE INCORPORATION OF SELENCYSTEINE INTO POOTEINS. IT PROBABLY REPLACES E-TU FOR THE INSERTION OF SELENCOCYSTEINE DIRECTED BY THE UGA CODON. SELB BINDS
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
SELB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR (SELB TRANSLATION FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Moorella thermoacetica (Clostridium thermoaceticum).
Bacteria; Firmicutes; Bacillus/Clostridium group; Moorella group;
                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97049123; PubMed-8893853;
Kromayer M., Wilting R., Tormay P., Boeck A.;
"Domain structure of the prokaryotic selenocysteine-specific
elongation factor SelB.";
                                                                                                                                                                                                                                                 Length 576;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                   4EA3FFC89F66307A CRC64; '
                                                                                      exchange
                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                      634 AA
                                                                                    Hypothetical protein; Transmembrane; Anion
                                                                                                                                                                                                                                                                       Mismatches
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Pred. No.
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                                                                           _cotransp; 1.
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                                         EMBL, 271551; CAA96183.1; -. SGD, S005219; YNL275W. InterPro. PPR003020; -. Pfam; PP00955; HCO3_cotransp.
                                                                                                                                                                                                                                                 32.8%; 47.4%;
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                                                                                                                                                                                                                                                                                            RQAGVQYSRADEEQQQALS 23
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                                                                                                                                                                                                                    65027
                                                                                                                                                                                                                                                                       Conservative
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295
350
394
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Best Local Similarity
Matches 9; Conserv
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15-DEC-1998 (
15-DEC-1998 (
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Q46455;
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TRANSMEM
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                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gentles S., Odell C., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.,
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: TO OTHER FUNGAL TRK PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                           1; Length 634;
                                                                                                                                                                                                  7; Indels
sis; GTP-binding.

17 GTP (BY SIMILARITY).
64 GTP (BY SIMILARITY).
118 GTP (BY SIMILARITY).
118 GTP (BY SIMILARITY).
; 70666 MW; 626F9E8A693A8296 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                           880 AA
                                                                                                                                                           32.8%; Score 45; DB
38.1%; Pred. No. 42;
ive 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTASSIUM TRANSPORT PROTEIN 2. TRK2 OR SPACIF5.12.
                                                                                                                                                                                                                                        58
                                                                                                                                                                                                                                                              25 GVDTDRLKEEKERGISIELGF 45
                                                                                                                                                                                                                                        8 GVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport; Transmembrane;
                                                                                                                                                         Query Match 32.8
Best Local Similarity 38.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
    PROSITE; PS00301; EFACT
Protein biosynthesis; G
NP_BIND 10 17
NP_BIND 115 118
SEQUENCE 634 AA; 706
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591
645
704
776
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2283
2293
4244
603
603
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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571
625
684
787
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283
283
294
321
443
460
                                                                                                                                                                                                                                                                                                                                                                     TRK2_SCHPO
Q10065;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                     membrane proteins
                    NCBI_TaxID=623;
                                                                                                                                                                                                                                                  Toshikawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                                  Gaps
                                                                                                                                                                                                                                                                                                MEDLINE=92114800; PubMed=1766387;
Yao R., Palchaudhuri S.;
"Nucleotide sequence of the ipaBCD structural genes of Shigella dysenterlae.";
Mob. Microbiol. 5:2217-2221(1991).
-I-FUNCTION: ASSOCIATED WITH THE ENTRY OF THE BACTERIA INTO COLONIC BPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                 Fidesing invasion.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Plasmid 210 kb invasion pWR100, and Plasmid 230 kb pMYSH6000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 382;
                             Length 880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                   Indels
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2 KDA MEMBRANE ANTIGEN.
A22E1D6399EC90BF CRC64;
2CD17CF1FE24F128 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 9
                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S15578; S15578.
Antigen; Plasmid; Virulence; Membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.1%; Score 44; DB 1; 42.9%; Pred. No. 33;
                              1;
                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NoV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
42 KDA MEMBRANE ANTIGEN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 AA.
                             Score 45; DB 1
Pred. No. 60;
7; Mismatches
                                                                                                                                            382 AA
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                            PRT;
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                                                                                  210 AGVRNSQENEDRTEALSPALG 230
99848 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41098 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NIRQAGVQYSRADEEQQQALS 23
                                                                     7 AGVQYSRADEEQQQALSSQMG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X60777; CAA43191.1; -.
                             32.8%;
                  Ouery Match
Best Local Similarity 42.3.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                 Shigella dysenteriae.
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Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 AA;
880 AA;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                              Plasmid Invasion
                                                                                                                                                                                                                                                           NCBI_TaxID=622;
                                                                                                                                                                                                                                                                                         STRAIN-CG097
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ID IPAC_SHIFL
AC P18012;
                                                                                                                                           IPAC_SHIDY
Q03946;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE OF 20-64 AND 318-335.
MEDLINE-69307550; PubMed-2663721;
Sankaran K., Ramachandran V., Subrahmanyam Y.V.B.K., Rajarathnam S.,
Elango S., Roy R.K.;
"Congo red-mediated regulation of levels of Shigella flexneri 2a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Infect. Immun. 57:2364-2371(1989).
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                                                                                                                                                                                                                                                                                                   Baudry B., Kaczorek M., Sansonetti P.J.;
"Nucleotide sequence of the invasion plasmid antigen B and C genes (ipaB and ipaC) of Shigella flexneri.";
Microb. Pathog. 4:345-357(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional organization and nucleotide sequence of virulence Region-2 on the large virulence plasmid in Shigella flexneri 2a."; Mol. Microbiol. 3:1191-1201(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPITHELIAL CELLS.
-!- MISCELLANEOUS: SYNTHESIS OF THIS IMMUNOGEN IS REPRESSED AT 30 DEGREES CELSIUS AND RESTORED AT 37 DEGREES CELSIUS.
SEQUENCE FROM N.A.
SEROTYPE 5;
MEDLINE-89057927; PubMed-3057506;
WENGALESAN M.M., BUYSSE J.M., Kopecko D.J.;
"Characterization of invasion plasmid antigen genes (ipaBCD) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasakawa C., Adler B., Tobe T., Okada N., Nagai S., Komatsu K.,
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T -> I (IN REF. 3).
A -> T (IN REF. 3).
ED6481B161E58EB1 CRC64;
                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 85:9317-9321(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 33; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-2A; PLASMID-230 kb pMYSH6000;
MEDLINE-90014179; Pubmed-2552264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M34849; AAA98425.1; ALT_INIT.
EMBL; X15319; CAA33382.1; -.
PIR; A60112; A60112.
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                                                                                                                                                                                                                                                                               MEDLINE-89200844; PubMed-3071655;
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-M90T / SEROTYPE 5;
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Best Local Similarity 42.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
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                                                                                                                                              Shigella flexneri.
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                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 79-95; 157-166; 242-251 & 581-587
                                                                                                                                           Nakanishi K., Nara K., Hagiwara H., Aoyama Y., Ueno H., Hirose S.;
"Cloning and sequence analysis of cDNA clones for bovine aortic-
endothelial-cell transplutaminase.";
Eur. J. Blochem. 2021.5-21(1991).
-!- FUNCTION: CATALYZES THE CROSS-LINKING OF PROTEINS AND THE
CONJUGATION OF POLYAMINES TO PROTEINS.
-!- CATALYTIC ACTIVITY: PROTEIN GLUTAMINE + ALKYLAMINE = PROTEIN
N(5)-ALKYLGLUTAMINE + NH(3).
-!- COPACTOR: CALCIUM IS REQUIRED FOR TRANSGLUTAMINASE ACTIVITY.
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY HIGHEST LEVELS ARE DETECTED IN THE LUNG. LOW
-!- TISSUE SPECIFICITY: HIGHEST LEVELS ARE DETECTED IN THE LUNG. LOW
-!- TISSUE SARE FOUND IN THE LIVER, SPLEEN AND HEART, BUT NOT IN THE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huber D.H., Hausner G., Yamamoto K., Ishii C., Seidel-Rogol B.L., Bertrand H.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.1%; Score 44; DB 1; Length 687; 40.9%; Pred. No. 64; B; Indels iive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                              -!- INDUCTION: BY RETINOIC ACID.
-!- SIMILARITY: BELONGS TO THE TRANSGLUTAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hucerto, investor, 1.
Pfam: PF0081: Transglut core; 1.
Pfam: PF0086: Transglutamin_C: 1.
Pfam: PF0086: Transglutamin_N: 1.
PROSITE: PS000547; TRANSGLUTAMINASES; 1.
Transferase; Acyltransferase; Calcium-binding.
ACT_SITE 277 277 BY SIMILARITY.
SEQUENCE 687 AA; 77112 MW; 7BBA00F15E779944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSH2_NEUCR STANDARD; PRT; 937 AA. 013396.
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA MISMATCH REPAIR PROTEIN MSH2.
                                                                                                           TISSUE-Artery;
MEDLINE-92037637; PubMed-1682150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.1
Best Local Similarity 40.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001102; -. InterPro; IPR002931; -.
                                     Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=74-OR23-1VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurospora crassa
                                                        NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98048467; PubMed-9387221;
Lapldus A., Galleron N., Sorokin A., Ehrlich S.D.;
"Sequencing and functional annotation of the Bacillus subtilis genes
in the 200 kb rmB-dnaB region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase, NADP, Glyoxylate bypass; Tricarboxylic acid cycle. ACT_SITE 104 104 BINDING TO ISOCITRATE (BY SIMILARITY). SEQUENCE 423 AA; 46417 WW; CC69E694EB66D0D8 CRC64;
                                                                                                                                                                                                                                                                   Jin S., Sonenshein A.L., "Identification of two distinct Bacillus subtilis citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
PROTEIN-GLUTAMINE GAMMA-GLUTAMILIRANSFERASE (EC 2.3.2.13) (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
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               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
1SOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42) (OXALOSUCCINNATE DECARBOXXLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Microbiology 143:3431-3441(1997).
-!- CATALYTIC ACTIVITY: ISOCITRATE + NADP(+) = 2-OXOGLUTARATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; DB 1;
No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   687 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB
Pred No. 37;
6; -M.Smatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                          Bacteriol. 176:4669-4679(1994).
                                                                                                                                                                                                                                   STRAIN=168 / SMY;
MEDLINE=94321340; PubMed=8045898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0470; IDH_IMDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U05257; AAA96342.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.1%;
41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AGIEYAKGSEEVQKLIS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AGVQYSRADEEQQQALS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00180; isodh; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                  FROM N.A.
                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CO(2) + NADPH
                                                                                                           ICD OR CITC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGLC_BOVIN
P51176;
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                         genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTC_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGM2
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Gaps

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SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
MYSN_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    МУН9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMIS outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12.";
Sclence 277:1453-1474(1997).
--- SIMILARIYT TO E-COLI MOLYBDATE METABOLISM REGULATOR (MOLR).
--- CAUTION: REF. 1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
IN POSITIONS 349 TO 334.
  FUNCTION: INVOLVED IN POST-REPLICATIVE DNA-MISMATCH REPAIR, BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-K12 / BHB2600;
Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                     TO MISMATCH-CONTAINING DNA (BY SIMILARITY).
SUBUNIT: HETERODIMER OF MSH2 AND MSH6 (BY SIMILARITY).
SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P33346; P76430; Oleated) Created) 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) HYPOTHETICAL 138.1 KDA PROTEIN IN MOLR-BGLX INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL).
BC7AABE137423EB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 1;
Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1210 AA.
                                                                                                                                                                                                                                                                                                EMBL; AF030634; AAB84225.1; -.
InterPro; IPR000432; -.
InterPro; IPR02083; -.
Pfam; PF00488; Muts_C; 1.
Pfam; PF01624; Muts_N; 1.
PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
DNA repair; ATP-binding; DNA-binding.
NP_BIND 659 666 ATP (POTEMTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            937 AA; 105068 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0°
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875 GVQYSKQDVEEGSAL 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GVQYSRADEEQQQAL 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Church G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEHI_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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SO THE PART OF THE
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DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

MISCELLANDEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROWYOSIN (LAM) AND 1 HEAVY MEROWYOSIN (HAM). IT CAN LATER BE SPLIT EVETHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K.,
Gdula D., Adelstein R.S., Weir L.;
"Human nonmuscle myosin heavy chains are encoded by two genes located
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILNE=90138958; PubMed=1967836; Sacz C.G., Myers J.C., Shows T.B., Leinwand L.A.; Sacz C.G., Myers J.C., Shows T.B., Leinwand L.A.; Luman nonmuscle myosin heavy chain mRNA: generation of diversity through alternative polyadenylylation "; Proc. Natl. Acad. Sci. U.S.A. 87:1168(1990).

-1- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS, CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-1337 FROM N.A.
MEDLINE-92003925; PubMed-1912569;
MEDLINE-92003925; PubMed-1912569;
Toothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M.,
Arnaout M.A., Clayton L.K., Tenen D.G.;
"Cellular myosin heavy chain in human leukocytes: isolation of 5'
Colb. clones, characterization of the protein, chromosomal
localization, and upregulation during myeloid differentiation.";
Blood 78:1826-1833(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYSN_HUMAN STANDARD; PRT; 1960 AA.
P35579; 066805;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYOSIN HEAVY CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                             32.1%; Score 44; DB 1; Length 1210; 47.4%; Pred. No. 1.2e+02;
                                                                                                                                                  1210 AA; 138067 MW; 0C2D3412D3CD6574 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                        4; Mismatches
EMBL; U00007; AAA60478.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-715 FROM N.A.
MEDLINE-91316803; Pubmed-1860190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   952 NVRČKSVPRLRADDDQLKA 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Circ. Res. 69:530-539(1991).
           EMBL; AE000300; AAC75179.1;
EccGene; EG11995; yehr
Hypothetical protein.
SEQUENCE 1210 AA: 120067
                                                                                                                                                                                                                                                                                                                                                                                                                   3 NIROAGVOYSRADEEQQOA 21
                                                                                                                                                                                                                                                                                                     Best_Local Similarity 47.43
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on different chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBFRAGMENT (S2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYPE A) (NMMHC-A).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
PHYCOBILISOME 8.9 KDA LINKER POLYBEPTIDE, PHYCOCYANIN-ASSOCIATED, ROD
(L-8.9/R) (ROD CAPPING LINKER PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDIAGE 1109890; MEDIATE 110984650; MEDIATE 1109890; MEDIATE 1109890; MEDIATE 1109890; MELKARAP W.R., HASELKORN R.; "Cloning and light regulation of expression of the phycocyanin operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                             CALMODULIN-BINDING (BY SIMILARITY) CALMODULIN-BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                      GLOBULÁR HEAD (S1).
RODLIKE TAIL (S2 AND LMM DOMAINS).
COILED COIL (POTENTIAL).
ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                    ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
EAI -> RGH (IN REF. 3).
T -> S (IN REF. 3).
T -> M (IN REF. 4).
C -> Y (IN REF. 4).
KG -> GR (IN REF. 4).
E -> EE (IN REF. 2).
                                                                                                                                                                                                InterPro; IPR000048; -.
InterPro; IPR001609; -.
InterPro; IPR001269; -.
InterPro; IPR001269; -.
Pfam; PF00612; IQ; I.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF0063; myosin_head; 1.
PROSTES; PR00193; MYOSINHEAVY.
PROSTES; PS50096; IQ; 1.
Myosin; Colled coil; Actin binding; Alkylation; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anabaena sp. (strain PCC 7120)
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBL_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  588F84BB8C106E6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> EE (IN REF. 2)
-> A (IN REF. 2).
-> G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 1;
Pred. No. 2.1e+02
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 AA.
                                                                                                                                                                                                                                                                                                                                                                                   ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                   Multigene family; Calmodulin-binding
DOMAIN 1 836 GLOBULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1869 STRLKQLKRQLEEAEEEAQRANASR 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 STNIRQAGVQYSRADEEQQQALSSQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226531 MW;
TO OTHER NONMUSCLE MYOSINS
                                                                                                                       EMBL; Z82215; CAB05105.1; -.
EMBL; M81105; AAA5988.1; -.
EMBL; M69100; AAA61765.1; -.
EMBL; M31013; AAA36349.1; -.
HSSP; P08799; IMND.
MIM; 160775; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                  836
1960
1960
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYS1_ANASP
P07124;
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CONFLICT
CONFLICT
CONFLICT
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NP_BIND
DOMAIN
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MOD_RES
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RT of the cyanobacterium Anabaena.";

RL EMBO J 6.871-884(1987).

CC -1- SIMILARITY: TO OFFER PRYCOBILISOME LINKER PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration of the substance of the surplement by a collaboration of the surplement by non-profit institute. There are no restrictions on its counced by non-profit institutions as its content is in oway condified and this statement is not removed. Usage by and for commercial conditions and this statement is not removed. Usage by and for commercial conditions and this statement is not removed. Usage by and for commercial conditions and this statement is not removed. Usage by and for commercial conditions and this statement is not removed. Usage by and for commercial consequence and an enail to licensedisb-sib.ch).

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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 5, 2001, 11:50:52; Search time 123.78 Seconds (without alignments) 29.928 Million cell updates/sec Run on:

US-09-462-480-12 137 1 STNIRQAGVQYSRADEEQQQALSSQMGF 28 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

425026 Total number of hits satisfying chosen parameters:

425026 segs, 132305027 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_16:\* Database :

sp\_plant:\*
sp\_rodent:\*
sp\_urclassified:\*
sp\_vertebrate:\*
sp\_virus:\* 1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\* sp\_organelle:\* sp\_phage:\* 6: sp\_mammal 7: sp\_mhc:\*

Pred. No. is the number of resuffs predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	069739 mycobacteri	033084 mycobacteri	Q9ppy9 ureaplasma	Q09971 caenorhabdi	Q9svk4 arabidopsis	Q38834 arabidopsis	Q9vug3 drosophila	P97099 alcaligenes	Q9rbt1 pseudomonas	Q9vyt7 drosophila	Q9qyt3 mus musculu	Q9qyt2 mus musculu	003936 bacteriopha	Q9kqz4 vibrio chol	Q9ddj2 brachydanio	Q9z7f9 chlamydia p	Q9vwa0 drosophila	Q9epj3 rattus norv	Q9krg7 vibrio chol
	QI 1	069739	033084	Q9PPY9	009971	0 Q9SVK4	0 038834	Q9VUG3	P97099	Q9RBT1	Q9VYT7	1 Q9QYT3	1 Q9QYT2	003936	Q9KQ24	.3 Q9DDJ2	Q927F9	Q9VWA0	1 Q9EPJ3	Q9KRG7
	Query Match Length DB	100 2	100	.743 2	1263 5	852 1	904	210 5	293 2	293 2	1013 5	1447 1	1487 1	198 9	224 2	404	531 2	1543 5	200	343 2
æ	Query	100.0	41.6	40.1	38.3	35.0	35.0	34.3	34.3	34.3	34.3	33.9	33.9	33.6	33.6	33.6	33.6	33.6	33.2	32.8
	Score	137	57	55	52.5	48	48	47	47	47	47	46.5	46.5	46	46	46	46	46	45.5	45
	Result No.		7	e	4	2	9	7	<b>&amp;</b>	6	10	11	12	, 13	14	15	16	17	18	19

Q9svg6 arabidopsis Q55718 synechocyst Q9dxn0 human immun P71653 mycobacteri Q9nu84 homo sacien	,,,סיםט:	Vos.731 Fattus norv O17709 caenorhabdi Q9hqs9 halobacteri Q9hqf homo sapien	-0 -0 -1	083163 Treponema 080280 pseudomonas 062131 caenorhabdi 041529 triticum ae 041546 triticum ae 065517 arabidopsis 09Kf14 bacillus ha 092d93 rickettsia
10 09SVG6 2 055718 14 09DXN0 2 P71653 4 09N184	112001		11 6 2 4 6	2 083163 2 050280 5 050280 10 Q41529 10 Q41546 10 065517 2 Q9KF14 2 Q9KD93
44 44 1 6 9 1 0 8 8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	381 625 925 1961	2160 2160 253 434		
32.58	20000	322.1	31.8 31.8 31.8 31.4 31.4	331.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.
44 45 44 55 44 55	* * * * * * * * * * * * * * * * * * *	44 43 43 5 5 7	4 4 4 2 6 6 3 6 7 6 4 4 6 7 7 8 8 6	4 4 4 4 4 4 4 4 7 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
222 222 232 232 232 232 232 232 232 232	10000 10000 10000	330	2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	26 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

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Gaps

RESULT 033084

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Quetier F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1263;
                 Length 743;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U29082; AAA68402.1; -.
WormPep; C14F5.3; CE01782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-PRO.
W; 1C17172C2B3D6EC0 CRC64;
                                                                                                                                                                                                             01-NOV-1996 (TYEMBLRE1. 01, Created)
01-NOV-1996 (TYEMBLRE1. 01, Last sequence update)
01-JUN-2000 (TYEMBLRE1. 14, Last annotation update)
HYPOTHETICAL 145.0 KDA PROTEIN C14F5.3 IN CHROMOSOME X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MAY-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                Score 55; DB 2;
Pred. No. 3.1;
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Pred. No. 14;
8; Mismatches
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                                               Mismatches
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POLY-GLU.
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POLY-SER.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2000 (TrEMBLrel. 14, Last and
PUTATIVE DISEASE RESISTANCE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145003 MW;
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            40.1%;
40.0%;
                                                                                          4 GIDYSRLNQEQKEAVTADLG 23
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Hypothetical protein.
                                                                       GVQYSRADEEQQQALSSQMG
                                           Conservative
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
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                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
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258
987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001978; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1166
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         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salanoubat M.
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01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                     Minx P.;
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                                                                                                                                                                                                  126600
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                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-93188700; PubMed-8446027;
Eiglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
"Use of an ordered cosmid library to deduce the genomic organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria: Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
      Length 100;
                                                                                                                                                                                                                                                                                                                                                            Eiglmeier K., Garnier T., De Rossi E., Fsihi H., Cole S.T.; Suimitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.6%; Score 57; DB 2; Length 100; Best Local Similarity 40.0%; Pred. No. 0.17; Matches 10; Conservative 7: Mismatches 8: Indianal
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Mycobacterium leprae.";
Mol. Microbiol. 7:197-206(1993).
EMBL; Y14967; CAA75210.1;
SEQUENCE 100 AA; 10964 MW; 460EE12F876EC383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 407:57-762(2000).

Nature ABO2148; AAF30913.1; -
InterPro: IPRO00212; -
Pfam: PF00580; UvrD-helicase; 1.

SEQUENCE 743 AA; 86740 MW; 9D412574673D71E7 CRC64;
                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Last annotation update)
   Score 137; DB 2;
Pred. No. 5.4e-14;
0; Mismatches 0;
                                                                                                                                                                             100 AA.
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                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seque)
01-NOV-1998 (TREMBLrel. 08, Last annot:
SIMILARITY TO SMALL.
Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria;
                                                                             73 STNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                           1 STNIRQAGVQYSRADEEQQQALSSQMGF 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9PPY9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last anno
                                                                                                                                                                          PRT;
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MEDLINE=20500219; Pubmed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 IRQAGVQYSRADEEQQQALSSQMGF 28
100.0%;
                              28; Conservative
                                                                                                                                                                        PRELIMINARY;
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                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1769;
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 Query Match
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                              Matches
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Matches
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RESULT Q9PPY9

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Gaps

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5;
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Pred. No. 14;
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 MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 NQRRGGIDYSSSEDEEESMVVNKM 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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29.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 7; Conserv
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                       Gaps
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                                                                                                                            Length 852;
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EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALOGGG2: CAB42924.1;
InterPro; IPR000767;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-LANDSBERG ERECTA;
Rouse D.T., Heazlewood J.L.;
Submitted (1747.1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U19616; AAA63149.1;
Mendel, 13922; Arath;1426;13922.
InterPro; IPR000767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       904 AA; 103471 MW; 19699788D31F990E CRC64;
                                                 InterPro; IPR002182; -.
Pfam; PF00931; NB-ARC; 1.
PRINTS; PR0334; DISENSTIST.
SEQUENCE 852 AA; 97039 MW; 4Aldeoef39380186 CRC64;
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Last annotation update)
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Last annotation update)
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48;
                                                                                                                           Score 48; DB 10;
Pred. No. 45;
8; Mismatches 7;
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Pred. No. 48;
8; Mismatches
                                                                                                                                                                                                                                                                        904 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 AA
                                                                                                                                                                                                                                                                                   038834;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequenc
01-OCT-2000 (TrEMBLrel. 15, Last annotat
MYOSIN HEAVY CHAIN HOMOLOG (FRAGMENT).
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-KAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequ
01-WAY-2000 (TrEMBLrel. 13, Last anno
CG5048 PROTEIN.
                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                              736 INLRKLGLSLTRGDQIEEEELDS 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TNIRQAGVQYSRADEEQQQALSS 24
                                                                                                                                                                               2 TNIRQAGVQYSRADEEQQQALSS 24
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00364; DISEASERSIST.
                                                                                                                            35.0%;
34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 34.8%;
Matches 8; Conservative
                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00931; NB-ARC;
                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                          Brassicales; Bra
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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09VUG3;
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RESULT

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038834 9

RESULT

038834

Matches

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Adams M.D. Celniker S.E. Holt R.A. Evans C.A., Gocayne J.D., Andans M.D. Celniker S.E. Holt R.A. Hoskins R.A., Galle R.F., Andanstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Baradan R.G., Champe M., Pfeiffer B.D., Ra Ballew R.M., Basu A., Bared R.G., Champe M., Pfeiffer B.D., Ra Ballew R.M., Basu A., Barenan B.D., Bhandari D., Belshakov S., Ballew R.M., Basu A., Barenan B.D., Bhandari D., Belshakov S., Borthan M.R., Bouck J., Evoreport L.B., Davies P., Actoria D., Loughan D.A., Buttler H., Cadleu E., Center A., Chang C. Mays A.D., Davies P., Decthan M.R., Bouck J., Evoreport L.B., Davies P., Actoria D., Bolshakov S., Buttler H., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Bersin K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Bersin K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodoson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunkov B.C., Stale I. M. M., Glasser K., Glodek A., Gong F. Gorrell J.H., Gu Z., Genbart W.M., Glasser K., Glodek A., Gong F. Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A., Alali M., Kalush F., Karpen G.H., Kez J. Kennison J.A., Ketchum K.A., Marthel B.L., McIntosh T.C., McLeod M.P., McShefi A., Mount S.M., McIntosh T.C., McLeod M.P., Nebherson D., Merherle B., McIntosh T.C., McLeod M.P., Perlar M., Mush M. M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ratherle B.C., Stapleton M., Stupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O., Stuber E., Spradling A.C., Zhan M., Stupski M.P., Smith H.O., Kalber R., Rodong T., Wassarman D.A., Wootley K.C., Wu D., Yang G., Zhu X., Smith H.O., Kalber R., Zhong Y., Zhu X., Shu B., Zhong Y., Zhu X., Zhu X STRAIN=AS; TRANSPOSON=TN4371;
MEDLINE-97188526; PubMed-9037111;
Merlin C., Springeal D., Mergeay M., Toussaint A.;
Morganisation of the bhy gene cluster of transposon Tn4371, encoding enzymes for the degradation of biphenyl and 4-chlorobiphenyl Gaps ö Alcaligenes eutrophus (Ralstonia eutropha). Bacteria; Proteobacteria; beta subdivision; Ralstonia group; Length 210; Indels ggn0036437; CG5048. 210 AA; 24080 MW; EF9673135F670C4E CRC64; 01-MAY-1997 (TrEMBLrel. 03, Created) 01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

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Score 47;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                                 MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18/:Zio zio zio 2011.
103487; AAF48101.1; -
FBGN0030340; CG15740.
1013 AA; 111594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 RQAGVOYSRADEEQQQALSSQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.3
Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                             SEQUENCE FROM N.A.
                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003487
FlyBase; FBgn0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9QYT3;
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Pseudomonas sp. strain SY5, 2,3-dihydroxybiphenyl-1,2-dioxygenase,
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                           Pseudomonas sp. SY5.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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0
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                               Score 47; DB 2; Length 293;
Pred. No. 20;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                 bphC2.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF190706; AAF04140.1; -.
HSSP; P17297; IDHY.
                                                                                                293 AA; 32341 MW; 85D1A8702450D61F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3C194CE9DEEB8BD0 CRC64;
                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                         Fram: PF00903; Glyoxalase; 2.
ProDom; PD000977; -; 1.
PROSITE; PS00082; EXTRADIOL_DIOXYGENAS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfan, PF00903; Glyoxalase, 2.
ProDom; PD000977; -; 1.
PROSITE; PS00082; EXTRADIOL_DIOXYGENAS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 2;
Pred. No. 20;
                                                                                                                                                                                                                                         293 AA.
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                                                                                                                                                                                                                                                                                        2, 3-DIHYDROXYBIPHENYL-1, 2-DIOXYGENASE
                                                                                                                                                                                                                                                            Created)
compounds.";
Mol. Gen. Genet. 253:499-506(1997).
EMBL, x97984; CAA66622.1; -.
HSSP; P17297; lDHY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                               34.38;
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52.9%;
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(TrEMBLrel. 13, I
(TrEMBLrel. 13, I
                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                     4 IROAGVQYSRADEEQQQ 20
                                                                                                                                                                               Ouery Match 34.3
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 LRQAGVAFTRGDEALMQ 96
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                                                                                                                                                                                                                                        PRELIMINARY;
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                                       InterPro; IPR000325; -. InterPro; IPR000486; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000325; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                        MCBI_TaxID=106145;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG15740 PROTEIN.
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01-MAY-2000 (
01-MAY-2000 (
                                                                                                                                                                                                                                                                                                                               seudomonas.
                                                                                          Dioxygenase
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SY5;
                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                09RBT1;
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                                                                                                                                                                                                                                       Q9RBT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09VYT7;
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Q9VYT7
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RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Labang O., Chen L.X.,
RA Handon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayanl A., An H.-J., Andrews-Pfannkoch C., Baaldwin D.,
RA Beeson K.Y. Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
RA Butts K.C., Busam D.A., Buttler H., Cadleu E., Center A., Chandra I.,
RA Butts K.C., Busam D.A., Buttler H., Cadleu E., Center A., Chandra I.,
RA Butts K.C., Busam D.A., Daurler C., Perriss C., Ferriss S.M.,
RA Butts K.C., Cabrellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
RA Dodson K., Obup L.E., Downes M., Dugan-Rocha S., Pleisschmann W.,
RA Buttis N.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Bartis N.J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Allali M., Kalush F., Rarpen G. H., Kazvitz S., Kulp D. Lai Z.,
Allali M., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Marmel B.E., Kodirac C.D., Kraft C., Kravitz S., Kulp D. Lai Z.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murany D.M., Nelson D.L.,
RA Bazzolo M., Pittman G.S., Pan S., Pollard J., Wong X.,
Rabon D.R., Wassarmano I.A., Nixon K., Wusskern D.R., Pacle D.M.,
Rabon D.R., Wassarmano D.A., Weisheron D.R., Parle K., Wang X.,
Wang S.-Y., Wassarmano D.A., Weinstood R.M., Wangsenbach J.,
Rabon D.R., Wassarmano I.A., Strong R., Shen S., Shen K.,
Rabon S., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. Yeng S.M., Warer E.W., Rubin G.M., Yenges D.G., Shen R., Shen S., Shen S., Shen S., Shen S., Shen R., Shong S., Shen S., Shen R., Shen S., Shen R., Shen S., Shen R., She
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A,
MEA2/GOLGA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 1013; 78;
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SEQUENCE FROM N.A.

STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDLINE=20406833; PubMed=10952301;

MEDLINE=20406833; PubMed=10952301;

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Niermann W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                             MEDLINE=97225795; PubMed=9073065; Metanabe N., Hirakawa M., Kobine=97225795; PubMed=9073065; Medalia K.I., Oki M., Kakikawa M., Watanabe N., Hirakawa M., Yamada K., Taketo A.; "Genome structure of the Lactobacillus temperate phage phi gle: the whole genome sequence and the putative promoter/repressor system."; Gene 187:45-53(1997).

EMBL: X98106; CAA66744.1; -. SEQUENCE 198 AA: 22540 MW; E2509A66CA0DE4B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
 Length 1487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.6%; Score 46; DB 9; Length 198; 38.5%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                             Indels
                                                                                                                                                                                                                               DNA
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                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LACTOBRACILLUS BACTERIOPHAGE PHIGIE COMPLETE GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VC1853.
33.9%; Score 46.5; DB 11;
1larity 38.5%; Pred. No. 1.4e+02;
Conservative 10; Mismatches 5;
    рь
..4е+02;
5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                        1 STNIRQAGVQYSRADEEQQQALSSQM 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TNIRQAGVQYSRADEEQQQALSSQMG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:477-483(2000).
EMBL; AE004260; AAF95001.1;
TIGR; VC1853; -.
SEQUENCE 224 AA; 25135 MW
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                                                                                                                                                          PRELIMINARY;
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             Best Local Similarity
Matches 10; Conserv
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Matches 10; Conserv
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NCBI_TaxID=52979;
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Q9KQZ4;
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003936
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Wea2/Golga3 Gene Product is Indispensable for Spermatogenesis in the
                                                                                                                                                                                                                                                                                                                                                                         Gaps
       Mea2/Golga3 Gene Product is Indispensable for Spermatogenesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                           Length 1447;
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                                                                                                                                                                                                                                                                                                 MW; 53087BE7460B3E6F CRC64;
                                     ted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
AB029537; BAA86889.1; -.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                          Ouery Match 33.9%; Score 46.5; DB 11; Best Local Similarity 38.5%; Pred. No. 1.4e+02; Matches 10; Conservative 10; Mismatches 5;
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BAA86890.1; JOINED.
BAA86890.1; JOINED.
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AA; 162775
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BAA86890.1;
BAA86890.1;
BAA86890.1;
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BAA86890.1;
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SEQUENCE FROM N.A.
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AB029521; 1
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EMBL; AB029536;
SEQUENCE 1487
                                                                                   AB029522;
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Matsukuma S.;
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01-MAY-2000
01-MAY-2000
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SEQUENCE
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090YT2
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EMBL;
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MEDLINE-2073792; PubMed=10917738;
Inohara N., Nunez G.,
"Genes with homology to mammalian apoptosis regulators identified in zebrafish.",
Cell Death Differ. 7:509-510(2000).
EMBL, AR327410; AAG45230.1; -.
SEQUENCE 404 AA; 46077 MW; 629BECFFB4A87D3B CRC64;
                                          Gaps
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                                                                                                                                                                                                                                                                                                                              Brachydanlo rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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33.6%; Score 46; DB 13; Length 404;
Best Local Similarity 38.7%; Pred. No. 41;
Matches 12; Conservative 5; Mismatches 10; Indels
Query Match
33.6%; Score 46; DB 2; Length 224;
Best Local Similarity 34.6%; Pred. No. 22;
Matches 9; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                        404 AA.
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                                                                                              PRT;
                                                                       1 STNIRQAGVQYSRADEEQQQALSSQM 26
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Q9DDJ2;
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Q9DDJ2
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5, 2001, 11:50:52 Search completed: July Job time: 475 sec

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4.5	ompugen
version 4	- 2000
GenCore	(c) 1993
Ger	ပ္
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OM protein - protein search, using sw model

5, 2001, 11:45:44; Search time 130.35 Seconds (without alignments) 7.441 Million cell updates/sec July Run on:

Title:

US-09-462-480-13 78 Perfect score:

1 RADEEQOOALSSOMGF 16 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

412676 seqs, 60623988 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_0601:\* Database :

/gcgdata/geneseq/geneseqp/AA1989.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:\*/SIDS8/gcgdata/geneseq-geneseqp/AA1988.DAT:\*/SIDS8/gcgdata/geneseq-geneseqp/AA1988.DAT:\*/SIDS8/gcgdata/geneseq-gen /SIDS8/gcgdata/geneseq/genesegp/AA1998. /SIDS8/gcgdata/geneseg/genesegp/AA1995 /SIDS8/gcgdata/geneseg/genesegp/AA1996 /SIDS8/gcgdata/geneseg/genesegp/AA1990 /SIDS8/gcgdata/geneseg/genesegp/AA1991 /SIDS8/gcgdata/geneseq/geneseqp/AA1992 /SIDS8/gcgdata/geneseq/geneseqp/AA1993 /SIDS8/gcgdata/geneseq/geneseqp/AA1994 /SIDS8/gcgdata/geneseq/geneseqp/AA1980. /SIDS8/gcgdata/geneseq/geneseqp/AA1981. /SIDS8/gcgdata/geneseq/genesegp/AA1997 /SIDS8/gcgdata/geneseq/geneseqp/AA198

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.

# SUMMARIES

Description	M. tuberculosis LH	Mycobacterium tube	M. tuberculosis im	M. tuberculosis an	. M. tuberculosis LH	M. tuberculosis LH	Mycobacterium tube	Mycobacterium tube	M. tuberculosis im	Mycobacterium tube	M. tuberculosis an
Ω	AAY03713	AAW32460	AAW81698	AAY39128	AAY 08712	AA¥63707	AAW32454	AAW32386	AAW81707	AAW64340	AAY39137
BB	20	18	19	20	20	20	18	18	19	19	20
Query Match Length DB	16	28	58	28	28	42	80	80	80	80	80
Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	78	7.8	78	78	78	78	78	78	78	78	7.8
Result No.		~.	m	4	S	9	7	80	6	10	11

M. tuberculosis re Mycobacterium tube Mycobacterium tube M. tuberculosis im Mycobacterium tube	नेनन नेन	22 5 5	4484843	sis sis sis sis sis reri C-17 L-17
20 AAY38994 118 AAW32444 118 AAW32376 119 AAW81747 20 AAW4321		AAY0370 AAB3521 AAB1984 AAW8174 AAW6437		21 AAG1320 21 AAG1323 22 AAG4355 21 AAG4355 17 AAW04184 19 AAW01271 20 AAW92408 21 AAY99335 21 AAY99336
0 25 25 25 25 25 25 25 25 25 25 25 25 25	. 955 100 100 100 100	100 100 805 805	8005 8005 1005 1005 1005 1005 1005 1005	124 722 725 864 864 864 864
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### ALIGNMENTS

AAY03713 standard; Protein; 16 AA. AAY03713

AAY03713;

07-JUN-1999 (first entry) 

M. tuberculosis LHP polypeptide antigenic fragment.

ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; immune response.

Mycobacterium tuberculosis.

WO9904005-A1

28-JAN-1999.

98WO-IB01091. 16-JUL-1998;

97US-0052631. 16-JUL-1997;

Rasmussen PB; Andersen P, Berthet F, Gicquel B, (INSP ) INST PASTEUR. (STAT-) STATENS SERUM INST.

WPI; 1999-132249/11.

New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis - useful in vaccines, for diagnosis, and for expression of heterologous proteins

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Thu Jul

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The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the N. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune response. Sequences AAY03706-713 represent antigenic fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            new immunogenic polypeptide has been developed comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis antigen Tb38-1 Peptide 6.
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                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 78; DB 20; 100.0%; Pred. No. 5.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW32460 standard; Protein; 28 AA.
               Claim 21; Page 65; 88pp; English.
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95US-0523436.
95US-0533634.
96US-0620874.
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Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
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Best Local Similarity 100.
Matches 16; Conservative
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01-SEP-1995;
22-SEP-1995;
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05-JUN-1996;
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immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1 Peptide 6. The immunogenic protein, and fusion proteins antigen, Tb38-1 Peptide 6. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a methoc for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                      100.0%; Score 78; DB 18; Length 28; 100.0%; Pred. No. 1e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis immunogenic polypeptide TB38-1 peptide 6.
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Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 123; 230pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW81698 standard; Protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US18293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0818112
96US-0730510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                   1 RADEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                     13 radeeqqqalssqmgf 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-261042/23
                                                                                                                                                                               28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1997;
11-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1998
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW81698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAW81698
    252222255x8
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Gaps

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Length 16;

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Gaps

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100.0%; Score 78; DB 19; Length 28; ilarity 100.0%; Pred. No. 1e-06; Conservative 0; Mismatches 0; Indels

Similarity

Query Match Best Local Matches 1

tuberculosis tuberculosis,

Skeiky YAW;

16;

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M. tuberculosis LHP polypeptide antigenic fragment
                                                                                                                                                                  (INSP ) INST PASTEUR.
(STAT-) STATENS SERUM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RADEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 radeeqqqalssqmgf
                                                                                                                                                                                                                     WPI; 1999-132249/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1mmune response.
                                                                                                                                              16-JUL-1997;
                                                                                                                          16-JUL-1998;
                                                                                 WO9904005-A1
                                                                                                      28-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY03707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY03707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                              New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                           Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                        M. tuberculosis antigen Tb38-1 peptide 6 amino acid sequence.
                                                                                                                                                                                                                                                                                                                           Houghton R;
R, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 78; DB 20; Length 28; 100.0%; Pred. No. 1e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                          o A, Dillon DC, Hendrickson RC, Ho
Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 118; 299pp; English.
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                                                            AAY39128 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY03712 standard; Protein; 28
                                                                                                                                                                                                                                                    99WO-US03268
                                                                                                                                                                                                                                                                       98US-0072967
                                                                                                                                                                                       Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1999 (first entry)
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RADEEQQQALSSQMGF 16
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-527409/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 AA;
                                                                                                                                                                                                                                                                                                                            Campos-Neto A,
                                                                                                                                                                                                           W09942076-A2
                                                                                                                                                                                                                                                    17-FEB-1999;
                                                                                                                                                                                                                                                                        05-MAY-1998;
18-FEB-1998;
                                                                                                     05-NOV-1999
                                                                                                                                                                                                                                26-AUG-1999
                                                                                                                                                                                                                                                                                                                                       Lodes MJ,
                                                                                 AAY39128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY03712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                  AAY39128
                                         RESULT
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The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect gainst bacteria of the tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6; and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two provide a synergistic increase in ability to induce a protective immune response. Sequences AAV03706-713 represent antigenic fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis - useful in vaccines, for diagnosis, and for expression of heterologous proteins
ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 78; DB 20; Length 2 100.0%; Pred. No. 1e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. tuberculosis LHP polypeptide antigenic fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rasmussen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andersen P, Berthet F, Gicquel B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY03707 standard; Protein; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 21; Page 65; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-IB01091.
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                                                                                                                                                                                                  Mycobacterium tuberculosis
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New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (of sariant differing only in conservative substitutions and/or modifications). The present sequence represents a M tuberculosis antigen, Tb38-1F3. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                       Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                    Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-neto A, Dillon DC, Houghton R, Reed SG,
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78; DB 18;
Pred. No. 3.3e-06;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                 Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 149; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW32386 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.0%;
Matches 16; Conservative 0
                          95US-0533634.
96US-0620874.
96US-0659683.
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95US-0523435.
95US-0532136.
96US-0620280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             skin testing; M.tuberculosis
  95US-0523436
                                                                                                                                                                                                 Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US14675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RADEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Twardzik DR, Vedvick TH;
                                                                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                  WPI; 1997-192903/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 AA;
                                                                                                                                                                                                                                                                                                                N-PSDB; AAT91526
                                                                                                                                                                                                 Campos-neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                              for diagnosis
01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-1995;
22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW32386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW32386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACC NO SERVICE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention is directed to a polynuclectide carrying the regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynuclectide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the W. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or thair fragments, specifically ESAT-6; and (b) for diagnosing tuberculosis infection by catection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune commons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis - useful in vaccines, for diagnosis, and for expression of heterologous proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                     Rasmussen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0%; Score 78; DB 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                                                                                                                                               Berthet F, Gicquel B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW32454 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 64; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogen; vaccine;
Ling; M.tuberculosis.
                                                                                                                                   98WO-IB01091
                                                                                                                                                                                     97US-0052631
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                                                                                                                                                                                                                                           (INSP ) INST PASTEUR.
(STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0680574
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                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-132249/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 AA;
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                                                                                                                                                                                                                                                                                                                                  Andersen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JAN-1998
                 WO9904005-A1
                                                                                                                             16-JUL-1998;
                                                                                                                                                                                     L6-JUL-1997;
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                                                                       28-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW32454;
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AAW32454 RESULT

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80 AA;
                                       80 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                07-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                           WO9816645-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1998.
                                                                                                                                                                                                                                                        AAW64340;
                                         Sequence
                                                                                                                                                                                                                 AAW64340
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                                                                                                                                                                                                                                           SSXS
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                                                                                                    A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TD38-IF3. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibedies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (WT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                           Gaps
                                     New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                             100.0%; Score 78; DB 18; Length 80; 100.0%; Pred. No. 3.3e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;

    M. tuberculosis immunogenic polypeptide Tb38-1F3.

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                                                                           Example 3; Page 163; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW81707 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US18293,
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96US-0730510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                  1 RADEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-192904/17.
N-PSDB; AAT91460.
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                                                                                                                                                                                                                                                                                                          Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                        80 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1998
                                                                                                                                                                                                                                                                                             Query Match
Best Local S:
Matches 16;
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW81707;
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compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This polypeptide comprises Mycobacterium tuberculosis antigen Tb38-IF3. A DNA molecule (see AAV44400) coding for Tb38-IF3 was isolated from a M. tuberculosis strain H37Kv genomic library. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuberculosis; infection; diagnosis; antigen; Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dillon DC, Houghton R, Lodes MJ; YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 78; DB 19;
100.0%; Pred. No. 3.3e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                             100.0%; Score 78; DB 19; 100.0%; Pred. No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW64340 standard; Protein; 80 AA.
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96US-0729622.
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                         65 radeeqqqalssqmgf 80
                                                                                                                                                                                                                                                                                                                     1 RADEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
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AAY39137;

AAY39137 RESULT

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This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as
                                                                        Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                             Houghton R;
                                     M. tuberculosis recombinant antigen protein Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 78; DB 20;
100.0%; Pred. No. 3.3e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 180; 323pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW32444 standard; Protein;
                                                                                                                                                                                                                                  99WO-US03265
                                                                                                                                                                                                                                                                      98US-0072596
98US-0024753
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                                                                                                                             Mycobacterium tuberculosis.
05-NOV-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 16; Conservative
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N-PSDB; AAZ19098.
                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 AA;
                                                                                                                                                               WO9942118-A2
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18-FEB-1998;
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                                                                                                                                                                                                  26-AUG-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculogis antigen (Ag). Also described are vaccines and fusion protein—Containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                M. tuberculosis antigen Tb38-1F3 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 78; DB 20;
Pred. No. 3.3e-06;
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                                                                                                                         AAY39137 standard; Protein; 80 AA.
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16; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0025197
                                                                                                                                                                                                                                                                                                         immune response; skin test.
                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                (first entry)
                1 RADEEQQQALSSQMGF 16
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Best Local Similarity
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96US-0680574.

12-JUL-1996; 01-SEP-1995;

AAY38994;

12

RESULT 1

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Sequence

Matches

δ g

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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                            A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen. TD38-1. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                       New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection {\sf Trans}
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis immunogenic polypeptide Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3b; Page 117; 230pp; English.
                                                                                              Example 3; Page 136; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW81747 standard; Protein; 95 AA.
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96US-0730510.
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RADEEQQQALSSQMGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
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N-PSDB; AAV64491.
                                                                                                                                                                                                                                                                                                                                          95 AA;
   N-PSDB; AAT91445.
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11-OCT-1996;
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                                                                                                                                                                                                                        New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis
                                                                                                                                                                                                                                                                                                                                    A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a mon-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
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                                                                                                              Skeiky YAW;
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Pred. No. 4e-06;
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                                                                                                                Houghton R, Reed SG,
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                                                                                                                                                                                                                                                                                                   Example 3; Page 124; 168pp; English.
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100.0%;
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950S-0523435.
950S-0532136.
960S-0620280.
95US-0533634.
96US-0620874.
96US-0659683.
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Twardzik DR, Vedvick TH;
                                                                                                            Campos-neto A, Dillon DC,
Twardzik DR, Vedvick TH;
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N-PSDB; AAT91509.
                                                                          (CORI-) CORIXA CORP.
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Best Local Similarity
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22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
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Matches
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diagnosis of tuberculosis.
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0; Gaps Query Match

100.0%; Score 78; DB 19; Length 95;

Best Local Similarity 100.0%; Pred. No. 4e-06;

Matches 16; Conservative 0; Mismatches 0; Indels

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Search completed: July 5, 2001, 11:45:44 Job time: 273 sec

<sup>95</sup> AA; Sequence

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Type-6 M-protein. Porcine elstatin

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ALIGNMENTS
AAW64321
AAX33103
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AAP90955
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  07-JUN-1999
  AAY03711;
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  July 5, 2001, 11:45:43; Search time 130.35 Seconds (without alignments)
7.441 Million cell updates/sec
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/ SIDSB/gcgdata/geneseqp/Aa1981.DAT:*
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                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412676 seqs, 60623988 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                      - protein search,
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Perfect score:
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ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; M. tuberculosis LHP polypeptide antigenic fragment. Rasmussen PB Andersen P, Berthet F, Gicquel B, 97US-0052631. 98WO-IB01091 Mycobacterium tuberculosis. (INSP ) INST PASTEUR. (STAT-) STATENS SERUM INST immune response. WO9904005-A1 16-JUL-1998; 16-JUL-1997; 28-JAN-1999 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS8/gcgdata/geneseg/geneseqp/AA1997.DAT:\*/SIDS8/gcgdata/geneseg/geneseqp/AA1998.DAT:\*/SIDS8/gcgdata/geneseg/geneseqp/AA1999.DAT:\*/SIDS8/gcgdata/geneseg/geneseqp/AA2000.DAT:\*/SIDS8/gcgdata/geneseg/geneseqp/AA2001.DAT:\*

Mycobacterium for expression

New nucleic acid containing regulator and LHP gene of tuberculosis - useful in vaccines, for diagnosis, and of heterologous proteins

WPI; 1999-132249/11.

M. tuberculosis LH
M. tuberculosis LH
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AAW32386 AAW81707 AAW64340 AAY39137 AAY38994 AAW32444 AAW32376

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2 3 4 4 7 7 10 11 11

Description

AAY03711 AAY03707 AAW32454

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DB

Length

Query Match 1

Score

Result

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                                                      The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the M. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by captual ESAT-6; and (b) for diagnosing tuberculosis infection by colynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two provide a synergistic increase in ability to induce a protective immune control of the column and column
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    M. tuberculosis LHP polypeptide antigenic fragment.

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Pred. No. 8.4e-06;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY03707 standard; Protein; 42 AA.
                    Claim 21; Page 65; 88pp; English
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            polypeptide.
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The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the

Claim 21; Page 64; 88pp; English.

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recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the wit tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune response. Sequences AAY03706-713 represent antigenic fragments of the
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or modifications). The present sequence represents a M.tuberculosis antigen, DB38-IR3. The immunogenic protein, and fusion proteins containing one or more of the proteins or the proteins blus ESAT-6, are useful in vaccines, preferably when formulated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                   .;
0
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                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton R, Reed SG,
                                                                                                                                                                                                                                                                                             Score 77; DB 20;
Pred. No. 2.3e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 149; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW32454 standard; Protein; 80 AA.
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                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              960S-0680574.
950S-0523436.
950S-0533634.
960S-0620874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skin testing; M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US14674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                            1 QEAANKQKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-neto A, Dillon D
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-192903/17.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                           42 AA;
                                                                                                                                                                                                         polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT91526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-1998
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22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-1996
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW32454
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Sequence

SSXS

Query Match

Matches

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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunishing against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                   soluble; antigen; protective immunity; TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculosis; infection; diagnosis; antigen; Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                              M. tuberculosis immunogenic polypeptide Tb38-1F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 77; DB 19;
ilarity 100.0%; Pred. No. 4.6e-05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis antigen Tb38-1F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3B; Page 139-140; 230pp; English,
                                                                                                                               AAW81707 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW64340 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0818112.
96US-0730510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US18293
                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                     Tuberculosis; immunogenic;
                                                                                                                                                                                                           (first entry)
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   1 QEAANKQKQELDEIST 16
                         1 QEAANKQKQELDEIST 16
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N-PSDB; AAV64509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 AA;
                                                                                                                                                                                                                                                                                                                                                                            W09816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-1996;
                                                                                                                                                                                                           27-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                AAW81707
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/ormodifications). The present sequence represents a M.tuberculosis antigen, Tb38-IF3. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenic polypeptide(s) from soluble M. tuberculosis antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
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0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky YAW;
non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                            Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed SG,
                                                                                                          100.0%; Score 77; DB 18;
100.0%; Pred. No. 4.6e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 77; DB 18;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-neto A, Dillon DC, Houghton R,
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 163; 190pp; English.
                                                                                                                                                                                                                                                                                                                    AAW32386 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        skin testing; M.tuberculosis.
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950S-0523435.
950S-0532136.
960S-0620280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                 16; Conservative
                                                                                                                                                                                      1 QEAANKQKQELDEIST 16
                                                                                                                                                                                                           WPI; 1997-192904/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORI-) CORIXA CORP
                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥
                                                      80 AA;
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13-MAR-1997

AAW32386;

AAW32386

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12-JUL-1996 01-SEP-1995 22-SEP-1995 05-JUN-1996 22-MAR-1996

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Gaps

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Indels

Sequence

Houghton R; t, Vedvick TS;

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAI39249 to AAI39460 and AAY39083 to AAY39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                           New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon DC, Hendrickson RC, Houghton R;
SG, Skeiky YAW, Twardzik DR, Vedvick TS;

    M. tuberculosis recombinant antigen protein Tb38-1F3.

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100.0%; Pred. No. 4.6e-05;
ive 0; Mismatches 0;
                                                                                                          Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                      Example 3; Page 134-135; 299pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY38994 standard; Protein; 80 AA.
                98US-0072967
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                                98US-0025197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed SG,
                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                     WPI; 1999-527409/44.
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N-PSDB; AAZ19098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AA;
                                                                                                                                                                                       N-PSDB; AAZ19310
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              05-MAY-1998;
18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY38994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
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δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide comprises Mycobacterium tuberculosis antigen Tb38-1F3. A DNA molecule (see AAV44400) coding for Tb38-1F3 was isolated from a M. tuberculosis strain H37Rv genomic library. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                             New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
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    M. tuberculosis antigen Tb38-1F3-mmino acid sequence.

                                                                                                                                                                                                                                                              Houghton R, Lodes MJ;
dzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 77; DB 19; ilarity 100.0%; Pred. No. 4.6e-05; Conservative 0; Mismatches 0;
            Mycobacterium tuberculosis strain H37Rv.
                                                                                                                                                                                                                                                                                  Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 146; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY39137 standard; Protein; 80 AA.
                                                                                                                           97WO-US18214
                                                                                                                                                                 97US-0818111
96US-0729622
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                                                                                                                                                                                                                                                                Campos-Neto A, Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QEAANKOKOELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG, Skeiky YAW,
                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                        WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 AA;
                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV44400.
                                                WO9816645-A2
                                                                                                                           07-0CT-1997;
                                                                                                                                                                   13-MAR-1997;
                                                                                                                                                                                   11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-1999;
                                                                                      23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY39137;
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Matches

39

g Ω

AAY39137 RESULT

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Gaps

.; 0

Indels

Length 80;

Gaps

ö

Indels

Length 95;

New polypeptide comprising antigenic portions of M. tuberculosis

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vaccine; tuberculosis; non specific adjuvant;
                                                                                                 Score 77; DB 18;
Pred. No. 5.5e-05;
Mismatches 0;
  M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton R,
                                                                                                                                                                                                                                                                                                                            AAW32376 standard; Protein; 95 AA.
                                                                                                                                           .
0
                                                                                                 100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 950S-0523435.
950S-0532136.
960S-0620280.
960S-0658800.
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Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                 1 QEAANKQKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QEAANKQKQELDEIST 16
                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-192904/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                      Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 AA;
                                        95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT91445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9709429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-1997
                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                         AAW32376
                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
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                                                                            This invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TD38-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis - are
tuberculosis, also
                                                                                               nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW;
                                                                                                                                                                                                                                                                                                       Length 80;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunogenic polypeptide(s) from Mycobacterium useful in vaccines for prevention or treatment of
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                       100.0%; Score 77; DB 20; 100.0%; Pred. No. 4.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4ycobacterium tuberculosis antigen Tb38-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 124; 168pp; English.
                                        Example 3; Page 180; 323pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW32444 standard; Protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0680574.
95US-0523436.
95US-0533634.
96US-0620874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  skin testing; M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US14674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                               16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       1 QEAANKQKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                               Campos-neto A, Dillon D
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-192903/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                            80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT91509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9709428-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-1996,
05-JUN-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW32444;
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW32444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X D X X X X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X 
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Skeiky YAW;

Reed SG,

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                                                                                                                                                                                                A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or modifications). The present sequence represents a M.tuberculosis antigen antigen, TB38-1. The immunogenic polypeptide can be used to diagnose antigen, TB38-1. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 77; DB 18;
100.0%; Pred. No. 5.5e-05;
live 0; Mismatches 0;
                                                                                                                          Example 3; Page 136; 190pp; English.
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AAW81747;

AAW81747

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This is an antigenic portion of Mycobacterium tuberculosis antigen 1938-1. A DNA sequence (see AAV44384) coding for antigen Tb38-1 was isolated from a M. tuberculosis strain H37Rv expression library using sera from patients having pulmonary or pleural tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AMM4291-M64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, expression vectors and transformed or transfected host cells. Also tuberculosis and diagnostic kits for detecting M. tuberculosis antigen, captubered are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, cells tuberculosis.
                                                                                                                                                                                                                                                                                                                                              New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculosis; antigen; fusion protein; Tb38-1; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 77; DB 19;
100.0%; Pred. No. 5.5e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                     DC, Houghton R, Lodes M.
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen Tb38-1.
 Mycobacterium tuberculosis strain H37Rv.
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 123; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY32097 standard; Protein; 95 AA.
                                                                                                          97WO-US18214.
                                                                                                                                            97US-0818111.
96US-0729622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US07717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QEAANKQKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 qeaankqkqeldeist 69
                                                                                                                                                                                                                                    Dillon
                                                                                                                                                                                                                                     Campos-Neto A, Dillon
Reed SG, Skeiky YAW,
                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                       WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 AA;
                                                                                                                                                                                                                                                                                                            N-PSDB; AAV44384
                                    WO9816645-A2.
                                                                                                          07-OCT-1997;
                                                                                                                                              13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9951748-A2
                                                                        23-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY32097;
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 qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                     Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis; infection; diagnosis; antigen; Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton R, Lodes MJ;
zik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 77; DB 19; } 100.0%; Pred. No. 5.5e-05; waterhes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis antigen Tb38-1 peptide.
                                                                                                                                                                                                                 M. tuberculosis immunogenic polypeptide Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3b; Page 117; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campos-Neto A, Dillon DC, Houghto
Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                        AAW81747 standard; Protein; 95 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       970S-0818112.
960S-0730510.
                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US18293
                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis,
                                                                                                                                                                            27-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
               69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QEAANKQKQELDEIST 16
WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1997;
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11-OCT-1996;
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Sequence

Query Match

Matches

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RESULT 12

AAW64321

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Gaps

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Length 95; Indels

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAX19249 to AAX19460 and AAX39083 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                          AAY39225 are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis recombinant antigen protein Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 77; DB 20;
llarity 100.0%; Pred. No. 5.5e-05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campos-Neto A, Dillon DC, Hendrickson RC, Hc
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 159; 323pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY38981 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US03265
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98US-0024753.
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N-PSDB; AAZ19082.
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunity
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                                                                                                                                                                                                                                                                                                                                                                                95 AA;
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18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                     New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          TD38-1. The invention provides fusion proteins (see AAX32059771) containing at least 2 M. tuberculosis antigens such as TD38-1, e.g. TDF-2 (see AAX32063) and a TD49-TD38-1 fusion. The new fusion proteins are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the Mycobacterium tuberculosis antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. tuberculosis antigen Tb38-1 amino acid sequence.
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100.0%; Pred. No. 5.5e-05;
ive 0; Mismatches 0;
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YAW, Twardzik DR,
                                                                                                                                            Campos-Neto A;
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                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 4D; 83pp; English.
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SG, Skeiky
98US-0056556.
98US-0223040.
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                                                                                                                                         Skeiky YAW, Alderson M,
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nes 16; Conser
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Lodes MJ, Reed
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07-APR-1998;
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18-FEB-1998;
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Matches
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Best Local Similarity 100.0%; Pred. No. 5.5e-05; Matches 16; Conservative 0; Mismatches 0; Indels

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Sequence 3
Sequence 2
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Patent No.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-785-190-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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-105 - 710 - 9 -365 - 901 - 9 -246 - 517 - 21 -246 - 517 - 21 -463 - 772 - 21 -533 - 0500 - 4 -533 - 0500 - 4 -464 - 517 - 4 -464 - 517 - 4 -464 - 517 - 4 -247 - 908 - 2 -258 - 958 - 1 -760 - 797 - 3	ALIGNMENTS  119uhiko  1 SECIFICALLY  CATHEPSIN L  NN, MACPEAK &  enue, N.W.  0/1993  1/1993	α <del>ω</del> ν
US-08-105-710-9 US-08-46-517-21 US-08-46-517-21 US-08-463-772-21 US-08-24-3618-21 US-08-24-3618-2 US-08-24-3618-4 US-08-24-9618-4 US-08-24-9618-4 US-08-247-908A-2 US-08-247-908A-2 US-08-247-908A-2 US-08-247-908A-2 US-08-247-908A-2 US-08-247-908A-2 US-08-31-388B-18 US-08-708-708-708-708-708-708-708-708-708-	T. 1  1.478-520-1  1.478-520-1  1.478-520-1  1.478-520-1  1.478-520-1  1.478-520-1  1.478-520-1  1.478-520-1  1.478-520-1  1.478-520-1  1.458-519  1.588-519  1.5888-519  1.5888-519  1.5888-519  1.58	Score 39; D Pred. No. 9. ); Mismatche
	a, No. 56985. to POLYPEPTIDE FOLYPEPTIDE INITIBITING (1) 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
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500 1189 1189 1189 1189 1112 1112 1112 1112	A APPLICATION US/08478520 1. Application US/08478520 1. NFORMATION: 1. NFORMATION: 2. 5698519 2. ANT: Turk, Vito OF INVENTION: INHIBITING OF INVENTION: INHIBITING OF INVENTION: INHIBITING S. OF SEQUENCES: 1 SPONDENCES: 1 SPOND	pti 7at 13
$\alpha$	icatior 110. 110. atsunum urk, vi urk, vi urk, vi urk, vi urk, vi uri urk, vi urk, vi urk, vi urk, vi urk, vi urk	arit parit pose
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Applicatio  Applicatio  Ormalization  Turk, V  Turk, V  Turk, V  Turk, V  NUNENTION  SEQUENCES  TO Pen  Washington  DC  USA  10 VA  TYPE: Flo  READABLE F  TYPE: Flo  TYPE: Flo  TYPE: Flo  TYPE: Flo  TYPE: VI  TYPE: V	YP YP
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8 0 0 0 1 2 1 2 1 2 1 2 1 2 1 2 2 2 2 2 2	TESULT 1  US-08-478-520-1  Sequence 1, Applicati Patent No. 5698519  GENERAL INFORMATION: APPLICANT: Turk, TITLE OF INVENTION TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: SUGH STREET: 2100 Pe CITY: Washingto STATE: DC COUNTRY: USA ZIP: ZO037  COMPUTER READBLE MEDIUM TYPE: F1 COMPUTER: IBM POPERATION NUMB FILING DATE: 10 PRIOR APPLICATION NUMB FILING DATE: 11 APPLICATION NUMB FILING DATE: 11 APPLICATION NUMB FILING DATE: 12 APPLICATION NUMB FILING DATE: 11 APPLICATION	MOLECULE -08-478-520 Query Match Best Local Matches 1 QEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LeFebvre, Rance B.
APPLICANT: Perng, Guey-Chen
TITLE OF INVENTION: Methods and Compositions for Diagnosing
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              Score 38; DB 1; Length 700; Pred. No. 1.1e+02; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 700;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2307U-330/UC 90-017-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/720,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08785190 Patent No. 5977339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: James M. Heslin
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-326-2400
                                ; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids:
TYPE: AMINO ACID
TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-720-589-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.48;
58.38;
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58.38;
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amino acid
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Best Local Similarity 58.3.
                                                                                                                                                                                                                                              Query Match 49.4
Best Local Similarity 58.3
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-785-190-2
                                                                                                                                                                                                                                                                                                                                                        :| |||:|||:
286 DAKKKQKEELDK 297
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286 DAKKKOKEELDK 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-08-785-190-2
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Patent No. 5324630
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Perng, Guey-Chen
TITLE OF INVENTION: Lyme Disease
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: James M. Heslin
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 4; Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                            APPLICANT: Ruchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.0010S2
CURRENT APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER PILING DATE: 1990-01-2
EARLIER PILING DATE: 1990-12-2
EARLIER FILING DATE: 1980-12-2
EARLIER FILING DATE: 1980-12-2
EARLIER FILING DATE: 1990-06-13
NUMBER OF SEQ ID NOS: 16
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-330/UC 90-017-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 1e+02;
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APPLICATION NUMBER: US/07/720,589
FILING DATE: 19910628
                                      Sequence 5, Application US/09196293 Patent No. 6183755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Borrelia burgdorferi
US-09-196-293-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.48;
58.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 58.3
Matches 7; Conservative
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CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| |||:|||:
286 DAKKKQKEELDK 297
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                                                                               GENERAL INFORMATION:
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LENGTH: 663
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Gaps
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Pred. No. 1.2e+02;
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,431
FILING DATE: 17-JAN-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA A
COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Chalker, Alison
APPLICANT: Hodgson, John
TITLE OF INVENTION: No. 5891667el Spoilie
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
17-JAN-1997
17-JAN-1997
18: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P31349
FELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRICATION NUMBER: 9600955.0
FILING DATE: 17-JAN-1996
ATORNEY/AGENT INFORMATION:
NAME: Glimai, Edward R
RGIGSTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9600955.0
FILING DATE: 17-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08785431 Patent No. 5891667
                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.48;
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SEQUENCE CHARACTERISTICS:
LENGTH: 746 amino acids
TYPE: amino acids
STRANDEDNESS: single
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Best Local Similarity 66./۳
استاه 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gimmi, Edward R
REGISTRATION NUMBER: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                 APPLICATION NUMBER: FILING DATE: 17-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 ELIRKONOELDE 528
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                                                                                  Sequence 2, Application PC/TUS9205539
GENERAL INFORMATION:
APPLICANT: LeFebvre. Rance B.
APPLICANT: Dering, Guey-Chen
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: Lyme Disease
NUMBER OF SEQUENCES:
ADDRESSE: James M. Heslin
STREET: 2399 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.4%; Score 38; DB 5; Length 700; 58.3%; Pred. No. 1.1e+02; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE TO STATEM TO THE STATEM STATEM SOFTWARE STATEM STATEM SOFTWARE SOFTWARE PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06539 FILING DATE: 19920629 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M. REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 29,541

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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Patent No. 5891677

GENERAL INFORMATION:
APPLICANT: Chalker, Alison
APPLICANT: Hodgson, John
TITLE OF INVENTION: No. 5891667el Spoilie
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STARE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                  ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 700 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO;
SEQUENCE CHARACTERISTICS:
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PCT-US92-05539-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: California
COUNTRY: USA
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Best Local Similarity
Matches 7; Conserv
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                                                RESULT 5
PCT-US92-05539-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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APPLICANT: Greenwood, Rebecca C.
APPLICANT: Gentry, Daniel R.
TITLE OF INVENTION: NOVEL greA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SUSTWARRE: FastSED for Windows Version 2.0
SUSTEMIT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,804
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/917,456
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: DICKINSON, TOGG O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GMI0046
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GM10046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103-27.2
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 158 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 48.1
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OEAANKOKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 QESFEKLERELEELKT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLIL.
STATE: PA
COUNTRY: USA
TO: 19103-2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
Patent No. 6210674
                                                                                                                                                                                             a
                                                                                                                                                                         STATE: PA
COUNTRY: US
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-009-494-2
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                                                                                                                     Score 38; DB 2; Length 788;
Pred. No. 1.2e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 2;
Pred. No. 33;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESLSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/917,456
                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: DICKINSON, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/POCKET NUMBER: GM10046
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2225
                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08917456
Patent No. 5866368
GENERAL INFORMATION:
APPLICANT: Greenwood, Rebecca C.
APPLICANT: Gentry, Daniel R.
TITLE OF INVENTION: NOVEL greA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-229-804-2; Sequence 2, Application US/09229804
                                                                                                                     49.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QEAANKQKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-785-431-2
                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                 | || || || || || || || 559 ELIRKONQELDE 570
                                                                                                                                                                                           2 EAANKOKOELDE 13
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                      Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
COUNTRY: US
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
US-08-917-456-2
                                                                                                                                                                                                                                                                                            US-08-917-456-2
                                                                                                                       Query Match
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                                                Gaps
48.1%; Score 37; DB 4; Length 158; 43.8%; Pred. No. 33;
                                             Indels
                                                                                                                                                                                                                                Sequence 2, Application US/09009494
Patent No. 6150340
GENERAL INFORMATION MICHAEL T.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Lewlor, Elizabeth J.
TITLE OF INVENTION: No. 6150340el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STRRET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                           5; Mismatches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9510661A
GENERAL INFORMATION:
APPLICANT: Washington University, et al.
TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     ö
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Pred, No. 3.3e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                   Score 37; DB 4; Length 485;
Pred. No. 1.1e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10661A FILING DATE: 16-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16 AUG-1955
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,791
FILING DATE: 25-AUG-1994
CLASSIFICATION:
ATORNEY/GENT INCORNATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 18,801
REFERENCE/DOCKET NUMBER: FP-59941/RF
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (415) 781-1989
TELEX: (415) 398-3249
INFORMATION FOR SEQ 1D 00: 2:
REFERENCE/DOCKET NUMBER: GM50027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALILIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                        48.1%;
57.1%;
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Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 1394 amino acids amino acid
                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                        Query Match 48.1
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                           INFORMATION FOR SEQ ID NO:
                                                              TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein
PCT-US95-10661A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QEAANKQKQELDEIS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                             1 QEAANKQKQELDEI 14
                                                                                                                                                                                                                                                                                                                                                                                                                      :| | |: ||||:
48 KENAIKKAQELDEL 61
                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-09-010-233-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-10661A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Black, Michael T.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Lewis, Ceri J.
TITLE OF INVENTION: No. 6200774el Compounds
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 4; I
. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODFRATING SYSTEM: DOS
OOFRAARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 4
Pred. No. 1.1e+
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,857
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: 60/044,365
FILING DATE: 28-APR-1997
APPLICATION NUMBER: 60/044,366
FILING DATE: 28-APR-1997
ATTONREY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
                    us/09/009,494
                                                                              PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/037,857
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: 60/044,365
FILING DATE: 28-APR-1997
APPLICATION NUMBER: 60/044,366
FILING DATE: 28-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,795
REFERENCE/POCKET NUMBER: GM50028
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-010-233-8; Sequence 8, Application US/09010233; Patent No. 6200774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.18;
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215-994-2222
  CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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48 KENAIKKAQELDEL 61
                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Philadelphia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-09-009-494-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 19103-2793
                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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RESULT 13

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Length 584;
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/179,738
FILING DATE: 10-JAN-1994
CLASSIFICATION: 530
ATTONEY/AGENT TWO
               COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPEN LIBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,145
FILING DATE: UG-APR-1996
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/179,738
FILING DATE: 10-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08179738

Patent No. 5578462

GENERAL INFORMATION:
APPLICANT: Seizinger, Bernd R.
APPLICANT: Kley, Nikolai A.
APPLICANT: Bandth, Albert B.
TITLE OF INVENTION: No. 5578462el NF2 Isoforms
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 2;
Pred. No. 1.9e+02
4; Mismatches
                                                                                                                                                                                                                                                                                     NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REFRENCE/DOCKET NUMBER: 5998-0017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REGISTRACE/DOCKET WUMBER: 5998-0017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Reed & Robins
STREET: 635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NO. 557
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robins
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 584 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| : ||:| ||:|
462 REAERRAKOKLLEIAT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.8
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QEAANKQKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-179-738-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-628-145-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,738
FILING DATE: 10-JAN-1994
CLASSIFICATION: 530
                                                                                                                                                             APPLICANT: Seizinger, Bernd R.
APPLICANT: Kley, Nikolai A.
APPLICANT: Bianchi, Albert B.
TITLE OF INVENTION: No. 5578462el NF2 Isoforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 1; I
Pred. No. 1.9e+02;
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APPLICANT: Kley, Nikolai A.
APPLICANT: Blanchi, Albert B.
TITLE OF INVENTION: No. 5872214el NF2 Isoforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5998-0017
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REFRENCE/DOCKET NUMBER: 5998-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPACK: (415) 327-3231
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08628145
Patent No. 5872214
GENERAL INFORMATION:
                                                                                                     Sequence 7, Application US/08179738 Patent No. 5578462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...urkESSEE: Reed & Robins STREET: 635 Bryant Street CITY: Palo Alto STATE: Callfornia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                      STREE: 635 Bryant Street CITY: Palo Alto STATE: California CCUUNTY: U.S.A 2IP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         Reed & Robins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
1097 QEEAEKQRKQKDLIS 1111
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462 REAERRAKQKLLEIAT 477
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Best Local Similarity
Matches 8; Conservi
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                                                                                                                                             GENERAL INFORMATION:
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; ORGANISM: muri
US-08-179-738-7
                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                               US-08-179-738-7
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qq ŏ

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TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Innear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
ONCIGNAL SOURCE:
GREATH SOURCE:
GREATH MULINE
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Gaps ; Query Match

46.8%; Score 36; DB 1; Length 591;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 8; Conservative 4; Mismatches 4; Indels :|| : ||:| ||:| 462 REAERRAKOKLLEIAT 477 1 QEAANKQKQELDEIST 16 οy

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Search completed: July 5, 2001, 11:47:01 Job time: 315 sec

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4.5 Compugen	
version - 2000	
GenCore v c) 1993 -	
(c)	
Copyright	

OM protein - protein search, using sw model

July 5, 2001, 11:48:35; Search time 79.63 Seconds (without alignments) 15.306 Million cell updates/sec

16

US-09-462-480-11 77 1 QEAANKQKQELDEIST Title: Perfect score: Sedneuce:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	(+(+)+(+)+(+)+(+)+(+)+(+)+(+)+(+)+(+)+(	4 -	LICAL	eavy	poly(A)+ RNA trans	poly(A)+ RNA trans	ubiquinol cytochr	hypothetical prote	unknown protein, 4	hypothetical prote	dnaK-type molecula	myosin II heavy ch	myosin heavy chain	MG328 homolog P01_	early endosome ant	myosin heavy chain			al		tail	probable tail comp	IVY C	leukocyte cysteine		hypothetical prote			gag polyprotein -	
SUMMARIES	ID	170007	10000	27.77.T	A20020	T50344	T52000	RDBYUN	T47976	E96576	S67701	D71729	T47237	806117	S73693	A57013	B43402	T45782	A26297	T01029	T06694	T09202	T09271	A59252	S40455	S60838	S67189	T49044	B83947	3	T21259
	DB	; ,	4 (	<b>4</b> C	7 (	7										1		7	7	7	7	7	7	7	7	N	~	~	~	Н	7
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	Score	7.7		4 4 U u	0.4	43	43	42	41	41	41	41	41	41	41	41	41	40	40	40	40	40	40	40	39	39	39	39	39	39	36
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protein kinase SK2 serine/threonine p	hypothetical prote myosin heavy chain	conserved nypocnet promotes sex organ hypothetical prote	ABC transporter (A probable WRKY-type	hypothetical prote tola protein VC183	hypothetical prote exodeoxyribonuclea	hypothetical prote trans-cinnamate 4-	methionyl-tRNA syn
T34021 T14157	A64224 A46761	G65402 A44343 T16337	G84083 A84643	S77291 A82152	G84631 B82282	T39410 T06522	C82922
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1206	1853	239	263	305	440 446	449 503	521
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9.89 3.99	თ თ ი ო ო ი	8 8 8		388	3 8 3 3	38 38 8	38
30	33.2	3.5	37	39	<b>4</b> 1	4 4 4	45

## ALIGNMENTS

hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

Accession: H70802
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Perkhill, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Attile: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987
A; Reference number: A70500; MUID:98295987
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-100 <COL>
A; Residues: 1-100 <COL>
A; Residues: J-100 <C

A; Gene: Rv3874

Gaps ; 0 Length 100; Indels 100.0%; Score 77; DB 2; L Llarity 100.0%; Pred. No. 3.2e-05; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 16; Conserv

1 QEAANKQKQELDEIST 16 ŏ

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hypothetical protein T14G11.3 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C. Accession: T29795
R.Fulton, B.; Hawkins, J.
Submitted to the EMBL Data Library, November 1995
A. Description: The sequence of C. elegans cosmid T14G11.
A. Reference number: Z20687
A. Accession: T29795
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Residues: 1-727 <FUL>
A. Residues: 1-727 <FUL>
C. Genetics EMBL: U41024; PIDN:AAA82345.1; CESP:T14G11.3
A. Goodener: CESP:T14G11.3
A. Genetics: 39/3; 54/3; 84/2; 140/2; 210/1; 292/3; 332/3; 370/3; 445/3; 573/3; 662/3

Gaps

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C. Species: Schizosaccharomyces pombe)
C. Species: Schizosaccharomyces pombe
C. Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C. Accession: 1752000
R. Azad, A. K.; Tani, T.; Shiki, N.; Tsuneyoshi, S.; Urushiyama, S.; Ohshima, Y.
Mol. Biol. Cell 8, 825-841, 1997
A. Title: Isolabation and molecular characterization of mRNA transport mutants in Schizo
A. Accession: T52000
A. Accession: T52000
A. Accession: T52000
A. Accession: T52000
A. Molecule type: DNA
A. Residues: 1-1012 <AZA>
A. Residues: 1-1012 <AZA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, August 1995
A;Description: The sequence of S. cerevisiae cosmids 8166, 9787, 9717, and lambda 307
A;Reference number: S69553
                                                            A;Cross-references: EMBL:AL034433; PIDN:CAA22354.1; GSPDB:GN00066; SPDB:SPBC1604.21c
A;Experimental source: strain 972h-; cosmid c1604
C;Genetics: <WOO1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Rolecule type: DNA
A,Rossidues: 1-127 - ODIES-
A,Rossidues: 1-127 - ODIES-
A,Cross-references: EMBL.U33057; NID:g927764; PIDN:AAB64968.1; PID:g927796; GSPDB:GN
A,Cross-references: EMBL.U33057; NID:g927764; PIDN:AAB64968.1; PID:g927796; GSPDB:GN
B,Cross-references: EMBL.U33057; NID:grike, J.; Vaessen, R.T.M.J.; Grivell, L.A.
Eur. J. Biochem. 138, 169-177, 1984
A,Filtle: The biosynthesis of the ubiquinol-cytochrome c reductase complex in yeast.
A,Reference number: A00121; MUID:84108379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                poly(A)+ RNA transport protein Ptr3p - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1011;
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Pred. No. 72;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 2
Pred. No. 72;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:D87259; PIDN:BAA75198.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 2/3; 24/2
C;Superfamily: ubiquitin-activating enzyme El
                                                                                                                                                                                                                                                                                                                                         C; Superfamily: ubiquitin-activating enzyme El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%;
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ilarity 60.0%;
Conservative
                                                                                                                                                                   A;Gene: SPDB:SPBC211.09
A;Map position: 2
C;Genetics: <BEC1>
A;Gene: ptr3; SPDB:SPBC1604.21c
A;Map position: 1
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
                                   A; Molecule type: DNA A; Residues: 611-1011
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                                                                                                                                                                                                                                                                                                                                      myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum)
N.Contains: myosin APPase (EC 3.6.1.32)
C.Species: Dictyostelium discoideum
C.Species: Dictyostelium discoideum
C.Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Feb-2001
C.Accession: A26655; A47728; S00250
R.Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986
A.Fitle: Conserved protein domains in a myosin heavy chain gene from Dictyostelium discoint A26655, MUID:87092266
A.Accession: A26655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. Molecule type: DNA
A. Residues: 1734-1893 <WAG>
C. Comment: The root domain is highly periodic, containing a pattern of 7-residue repeats
C. Superfamily: myosin heavy chain; myosin motor domain homology
C. Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phos
F: 1819-700-main: globular head «THED»
F: 89-747/Domain: myosin motor domain homology <WMOT>
F: 89-747/Domain: myosin motor domain homology <WMOT>
F: 179-186/Region: nucleotide-binding motif A (P-loop)
F: 819-2116/Domain: alpha-helical rod <ROD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA

A; Mesidues: 203-2116 (DEL>

R; Wayle, G.; Moegel, A.; Scheel, J.; Gerisch, G.

FEBS Lett. 227, 71-75, 1988

A; Title: Phosphorylation of threonine residues on cloned fragments of the Dictyostelium

A; Reference number: S00250; MUID:88112226

A; Accession: S00250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Бod
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F; Wood, V.; Rajandreman, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M. submitted to the EMBL Data Library, February 2000 ***
A; Reference number: Z25063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-2116 cwRR>
A; Cross-references: GB:M14628; GB:M11938; NID:g167834; PIDN:AAA33227.1; PID:g167835
R; DeLozanne, A; Lewis, M; Spudich, J.A.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 6807-6810, 1985
A; Reference number: A24728; MUID:86016788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Cross-references: EMBL:AL139314; PIDN:CAB75417.1; GSPDB:GN00067; SPDB:SPBC211.09
A)Experimental source: strain 972h(-); cosmid c211
R;Beck, A.; Reinhardt, R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z21859
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      Length 727
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Pred. No. 74;
2; Mismatches
      2;
Score 45; DB 2
Pred. No. 25;
2; Mismatches
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58.4%;
60.0%;
                                                                Conservative
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                                                                                                                                                                313 QETANKLSHQLDEIN 327
                                                                                                                            1 QEAANKQKQELDEIS 15
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|1339 EAKNKKESELDEI 1351
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Ouery Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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A; Residues: 1-644 <WOO>
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GSPDB:GN0

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A:Description: involved in protein folding and assembling/disassembling of protein co
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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A;Residues: 1-610 <PER>
A;Cross-references: EMBL:274201; NID:91431239; PIDN:CAA98726.1; PID:91431240; MIPS:YD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dnaK-type molecular chaperone RP185 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: 12-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: D71729
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99033499
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A;Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14651.1; PID:g386
A;Experimental source: strain Madrid E
                           GB:AE005173; NID:g10645365; PIDN:AAG21485.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein YDL153c – yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                 Length 523
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R; Perrea, J.; Blugeon, C.; Delaveau, T.; Jacq, C.
submitted to the Protein Sequence Database, July 1996
A; Reference number: S67693
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89;
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Pred. No. 91;
2; Mismatches
                                                                                                                                                                                 Score 41; DB 2
Pred. No. 76;
2; Mismatches
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Pred. No. 89;
1; Mismatches
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56.2%;
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llarity 66.7%;
Conservative
                                                                                                                                                                                 53.2%;
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Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                     | | | :|| | | 463 AKKQNEELDRIAT 475
                                                                                                                                                                                                                                                                                            4 ANKOKOELDEIST 16
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
                     A.Cross-references: G.Genetics:
A.Gene: F22G10.8
A.Map position: 1
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A;Gene: SGD:SAS10
A;Cross-references:
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A;Gene: dnaK; RP185
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A; Residues: 1-523
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                                                                                                                                                                                                       A;Genome: nuclear
C;Superfamily: ubiquinol--cytochrome-c reductase 14K protein
C;Keywords: electron transfer; membrane protein; membrane-associated complex; mitochondr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F21F14.10 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000 C; Accession: T47976 C; Accession: T47976 C; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; submitted to the Protein Sequence Database, February 2000 A; Reference number: 224481
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                        A;Residues: 1-91,'Q',93-127 <DEH>
A;Cross-references: EMBL:X00256; NID:g3600; PIDN:CAA25064.1; PID:g3601
A;Experimental source: strain FL100
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A;Note: F21F14.10
C;Superfamily: Arabidopsis thaliana hypothetical protein F21F14.10
                                                                                                                                                                                                                                                                                                                                        1; Length 127;
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A;Experimental source: cultivar Columbia; BAC clone F21F14
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Pred. No. 30;
1; Mismatches
                                                                                                  C,Genetics:
A,Gene: SGD:OCR7; CR01; UCR7; COR4; MIPS:YDR529c
A,Cross-references: SGD:S0002937; MIPS:YDR529c
A;Map position: 4R
                                                                                                                                                                                                                                                                                                                                           Score 42; DB
Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                           54.5%;
69.2%;
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 69.2
Matches 9; Conservative
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28 NKQKQERDMVKT 39
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A; Status: preliminary
A; Molecule type: DNA
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A; Molecule type: DNA
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A; Reference number: S73327; MUID:97105885
A; Accession: S73693
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A;Accession: B43402
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64.3%;
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ilarity 53.3%;
Conservative
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Best Local Similarity 64.3
Matches 9; Conservative
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372 EATQKLKEELSEVET 386
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Best Local Similarity
Matches 8; Conserv
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C; Species: Gallus gallus (chicken)

C; Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Jun-2000

C; Accession: S06117

R; Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.

R; Katsuragawa, Y.; Vanagisawa, M.; Inoue, A.; Masaki, T.

Bir. J. Biochem. 184, 611-616, 1989

A; Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed in
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A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
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A; Cross-references: GB:X17590
A; Cross-references: GB:X17590
A; Note: this translation is not annotated in GenBank entry GGMHCFC, release 114
C; Superfamily: myosin heavy chain; myosin motor domain homology
F;1-303/Domain: myosin motor domain homology (fragment) < MMOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                        myosin II heavy chain [imported] - Naegleria fowler! (fragment)
C;Species: Naegleria fowler!
C;Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47237
R;Shaw, D.R.; Sullivan, P.K.; Marciano-Cabral, F.; Ennis, H.L.
R;Shaw, D.R.; Sullivan, P.K.; Marciano-Cabral, F.; Ennis, H.L.
A;Description: Codon usage in Naegleria fowler!
A;Reference number: 224413
A;Accession: T47237
A;Accession: T472413
A;Accession: T472413
A;Accession: T4724
A;Access
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873693
MG32B homolog P01_orf1033 - Mycoplasma pneumoniae (strain ATCC 29342)
C;Species: Mycoplasma pneumoniae
A;Variety: ArCC 29342
C;Date: 27-Reb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C;Accession: S73693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Le
Pred. No. 1.1e+02;
7; Mismatches 1;
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Pred. No. 1.3e+02;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: S06116; MUID:90032648
A;Accession: S06117
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.2%;
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                                                                                    :||| | |:|| || |257 KEAAEKAKKELSSTST 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.2
Best Local Similarity 42.9
Matches 6; Conservative
                                          16
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812 EKANKLQNELDNVSS 826
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575 EESATROKREIEEL 588
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                                          1 QEAANKQKQELDEIST
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Best Local Similarity
Matches 8; Conserv
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RESULT 14
A57013
early endosome antigen 1 - human
N;Alternate names: endosome-associated protein
C;Species: Homo sapiens (man)
C;Species: Totaliaghan J.M.; Steele-Mortimer, O.; Stenmark, H.; Parton, R.G.; Campbel
J; Biol. Chem. 270, 1353-13511, 1995
A;Title: ERAL, an early endosome-associated protein. EEAl is a conserved alpha-helica
A;Reference number: A57013
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1410 - REBS
A;Cross-references: GB:L440157; NID:g1016367; PIDN:AAA79121.1; PID:g1016368
A;Residues: 1-1410 - REBS
A;Residues: 1-254, C',256-257, LQ',260-276, A',278-283, A',285-519, D',521-574, EQ',5
A;Residues: ERBL:X789998; NID:g475933; PIDN:CAA55632.1; PID:g475934
A;Accession: S73693
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1033 <HIM>
A;Cross-references: EMBL:AE000035; GB:U00089; NID:g1674044; PIDN:AAB96015.1; PID:g167
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myosin heavy chain-B, neuronal - chicken
N;Contains: myosin Afrease (EC 3.6.1.32)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: B43402; A43402
B;Takahashi, M.; Kawamnto, S.; Adelstein, R.S.
J. Biol. Chem. 267, 17864-17871, 1992
A;Title: Evidence for inserted sequences in the head region of nonmuscle myosin speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Cross-references: GDB:1369996
C;Superfamily: human early endosome antigen 1
C;Keywords: calmodulin binding; endocytosis; metal binding; peripheral membrane
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                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 2; Pred. No. 1.5e+02; 2; Mismatches 3;
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A; Molecule type: mRNA
A; Residues: 1-2007 cTAK.
A; Residues: 1-2007 cTAK.
A; Residues: 1-2007 cTAK.
A; Cross-references: GB:M93676; NID:g212448; PIDN:AAA48988.1; PID:g212452
A; Notecule type: mRNA
A; Rocession: A43402
A; Molecule type: mRNA
A; Residues: 1-211;222-631;653-2007 cTA2>
A; Cross-references: GB:M93676; NID:g212448; PIDN:AAA48985.1; PID:g212449
A; Rosidues: 1-211;222-631;653-2007 cTA2>
A; Cross-references: GB:M93676; NID:g212448; PIDN:AAA48985.1; PID:g212449
A; Note: sequence extracted from NCBI backbone (NCBIN:112864)
C; Comment: Alternatively spliced sequence (NCBIN:112864)
C; Comment: Alternatively spliced sequence (NCBIN:112864)
C; Comment: Alternatively spliced sequence (NCBIN:112864)
C; Superfamily: myosin heavy chain: B, neuronal #status predicted coil; hydrolase; methylated
F; 1-211, 222-631, 653-2007/Product: myosin heavy chain: B, nonmuscle #status predicted
F; 88-802/Domain: myosin motor domain homology cMMOT>
F; 11-211, 222-631, 653-2007/Product: myosin heavy chain: B, nonmuscle #status predicted
F; 88-802/Domain: actin binding #status predicted
F; 632-652/Region: actin binding #status predicted
F; 632-652/Region: actin binding #status predicted
F; 802-114/Region: actin binding #status predicted
F; 875-2007/Pomain: coiled coil #status predicted
F; 875-2107/Rogion: actin binding #status predicted
F; 875-2107/Rogion: actin bind
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F;129/Modified site: N6.N6.N6-trimethyllysine (Lys) #status predicted
F;184/Binding site: ATP (Lys) #status predicted
F;132,742/Active site: Cys #status predicted
F;1354/Binding site: phosphate (Pir) (covalent) #status predicted
F;1987/Binding site: phosphate (Ser) (covalent) #status predicted
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Pred. No. 3+02;
3; Mismatches 4; Indels
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Best Local Similarity 53.3%;
Matches 8; Conservative
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2 EAANKQKQELDEIST 16 | ||| :||| :|| 1311 EKANKLQNELDNVSS 1325

6 G

Search completed: July 5, 2001, 11:48:36 Job time: 375 sec THIS PAGE BLANK (USPTO)

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 5, 2001, 11:51:44; Search time 41.8 Seconds (without alignments) 13.112 Million cell updates/sec

US-09-462-480-11 77 1 QEAANKQKQELDEIST 16 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 segs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	p08799 distance		P00128 saccharomyc	P33319 proteus vul		P75310 mycoplasma	P08089 streptococc	homo	s sns	P35479 sus scrofa	Q28986 sus scrofa	Q28987 sus scrofa	P27400 simian foam	P47460 mycoplasma	_			Q43067 pisum sativ		_		P01039 rattus norv	_	-	026762 methanobact		P47297 mycoplasma	_	Q10419 leuconostoc	Q02916 coturnix co	_	5	P94545 bacillus su
SUMMARIES	MYS2 DICDI	UBA1_SCHPO	UCR7_YEAST	IF3_PROVU	DNAK_RICPR	Y328_MYCPN	M6_STRPY	MYSO_HUMAN	CPI2_PIG	CPI1_PIG	CYT5_PIG	CYT8_PIG	GAG_SFV3L	HMW2_MYCGE	MY5A_MOUSE	Y861_SYNY3	YBB9_SCHPO	TCMO_PEA	VIE3_MCMVS	CLPB_MYCPN	CHDM_DROME	CYTA_RAT	YCX6_PORPU	YOY8_CAEEL	Y666_METTH	L.A_HUMAN	TYPH_MYCGE	U2R1_MOUSE	MESE_LEUME	NFL_CDTJA	Y397 WYCGE	RF2P_DROME	MUS2_BACSU
DB	-	ı ,-	Н	-		Н	-	-	Н	-	Н	,	Н	7	ч	٦	-	Н	-	-	-	-	Н	-	-	Н	~	Н	-	-	Н	-	٦
% Query Match Length	2116	1012	127	179	627	1033	483	1976	35	103	103	103	643	1805	1853	302	449	503	611	715	1982	103	121	194	293	408	421	428	457	555	266	299	785
% Query Match	58.4	S	54.5	53.2	53.2	53.2	51.9	51.9	50.6	50.6	50.6	50.6	50.6	50.6	50.6	49.4	49.4	49.4	49.4	49.4	49.4	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1
Score	•	43	42	41	41	41		40	39	39	39	39	39	39	39	38	38	38	38	38	38	37	37	37	37	37	. 37	37	37	37	37	37	37
Result No.		7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

Q9u3v9 drosophila P45387 haemophilus	P25386 saccharomyc P12270 homo sapien	P09940 pichia jadi	Qypq1/ ureaplasma P09413 anabaena fl	O66612 aquifex aeo P08672 plasmodium	P08675 plasmodium	P08673 plasmodium
XMS2_DROME HAP_HAEIN	USO1_YEAST TPR_HUMAN	IATP_PICJA	GREA_UREPA GVPC_ANAFL	OGG1_AQUAE CSP_PLACB	CSP_PLACL	CSP_PLACC
		٠,			Н	-
1184	1790 2349	100	156 193	226 378	378	398
48.1	48.1 48.1	46.8	46.8 8.8	46.8 46.8	46.8	46.8
37	37	36	36 36	36	36	36
34	37	96.	41	4 4 3 8	44	45

## ALIGNMENTS

RA WARILCK H.W., de Lozanne A., Leinwand L.A., Spudich J.A.;  RA WARILCK H.W., de Lozanne A., Leinwand L.A., Spudich J.A.;  R. Conserved protein domains in a myosin heavy chain gene from Dictyostellum discoldeum.";  R. Dictyostellum discoldeum.";  R. POC. Natl. Acad. Sci. U.S.A. 83:9433-9437(1986).  RA BUCHNE-40353583; PubMed-2387408;  RA BUCK-Velemeter D., Schleicher M., Grabatin B., Wippler J., Gerisch G.;  REPLACEMENT OF THE SCHLESS CHARCOLLE Explain B., Wippler J., Gerisch G.;  REPLACEMENT OF CHARCOLLE RESIDENCE CHARCOLLE EXPLAINTED BRY CHAIN FROM THE CHARCOLLE Explainted To The Charcolle Heavy Chain fragment of Dictyostellum myosin II.";  RA BUCK NEWSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762.  RESE Lett. 227:71-75(1988).  RA PHOSPHORYLARE-55345066; PubMed-7619795;  RA REDILNE-95345066; PubMed-7619795;  RA REDILNE-95345067; PubMed-7619795;  RA REDILNE-95345067; PubMed-7619795;  RA SAMENT I.:  RA RAMENT RAMENT I.:  RA RAMENT I.:  RA RAMENT RAMENT RAMENT RAMENT R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFRAGENT ($2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUR REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA HELICAL COLLED COLLS.

CHARACTERISTIC FOR ALPHA HELICAL COLLED COLLS.

PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES THE ACTIN ACTIVATY OF ACTIVITY.

MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ATPASE ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT THE SH-1 POSITION (688).

SIMILARITY: THE GLOBULAR HEAD AS SEQUENCE SHOWS A HIGH DEGREE OF SIMILARITY WITH THE GLOBULAR HEAD SEQUENCES OF MUSCLE & NONMUSCLE SIMILARITY WITH THE GLOBULAR HEAD SEQUENCES OF MUSCLE & NONMUSCLE HEAVY CHAINS. BY COWTRAST THE ROD SEQUENCE IS LESS CONSERVED, BUT THE PERIODICTITIES OF HYDROPHOBIC & CHARGED RESIDUES, WHICH DICTATE
                                                                                                                                                                                                                       MEDLINE-98070605 PUBMed-9405148;
Bauer C.B., Kuhlman D.A., Bagshaw C.R., Rayment I.;
Rauer C.B., Kuhlman D.A., Bagshaw C.R., Rayment I.;
Rauer C.B., Kuhlman D.A., Bagshaw C.R., Rayment I.;
Bauer C.B., Kuhlman D.A., Bagshaw C.R., Rayment I.;
Band C.B., Garden E.B., Bagshaw C.R., Rayment I.;
Discription of Mg.24 (37) -0-(N-methylanthraniloyl) nucleotides bound to the Dictyostellum discoideum myosin motor domain.";
J. Mol. Biol. 274:394-407(1997).
J. MOL. Biol. 274:394-407(1997).
ACTIVITY FRAT IS ACTIVATED BY ACTIN.
ACTIVITY FRAT IS ACTIVATED BY ACTIN.
ACTIVITY PRAFIN MYOSIN IN HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE POSTERIOR CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN BE FURTHER
SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                  Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.; x-ray structures of the MaADP, MgATPganmaS, and MgAMPPNP complexes of the Dictyostelium discoideum mycsin motor domain."; Biochemistry 36:11619-11628(1997).
Dictyostellum discoideum myosin motor domain to 1.9-A resolution."; Biochemistry 35:5404-5417(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin; Coiled coil; Actin-binding; ATP-binding; 3D-structure; Heptad repeat pattern; Methylation; Akylation; Phosphorylation. DOMAIN 1 1 2116 RODLIKE TAIL (S1 AND LMM DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE ALPHA-HELICAL COILED-COIL STRUCTURE, ARE CONSERVED.
                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
                                                            X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 1-762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 10 DOMAIN.
                                                                                 MEDLINE=97452580; PubMed=9305951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, M14628; AAA3327.1; -. PIR, A26655; A26655. PIR, S00250; S00250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DictyDb; DD01008; mhcA.
InterPro; IPR000048; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001609; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-96
03-DEC-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1MMA; 03-DEC-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1MMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1MND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1VOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1LVK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORTEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1MMN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMMG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1MNE;
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PDB;
PDB;
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PDB;
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                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation and molecular characterization of mRNA transport mutants in
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                           U1-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
UBIQUITIN-ACTIVATING ENZYME E1 1 (POLY(A)+ RNA TRANSPORT PROTEIN 3).
PTR3 OR SPECIEO 4.21C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BECK A., Reinhardt R., Lyne M., Rajandream M.A., Barrell B.G.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTIVATES UBIQUITIN BY FTRST ADENTAATING WITH ATP ITS
CARBOXY-TERMINAL GLYCINE RESIDUE AND THEREAFTER LINKING THIS
RESIDUE TO THE SIDE CHAIN OF A CYSTEINE RESIDUE IN E1, YIELDING
AN UBIQUITIN-E1 THIOLESTER AND FREE AMP.
-!- SATHWAY: FIRST STEP IN UBIQUITIN CONJUGATION.
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBUNIT: TO E1 IN OTHER SPECIES.
                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                     Score 45; DB 1; Length 2116;
Pred. No. 35;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Azad A.K., Tani T., Shiki N., Tsuneyoshi S., Urushiyama S.,
Ohshima Y.;
                                               ACTIN-BINDING.
METHYLATION (DI-) (POTENTIAL).
ALKILATION (SH-1).
PHOSPHORYLATION (BY MHCK).
                                                                                                           (BY MHCK).
                                                                                                                           PHOSPHORYLATION (BY MHCK).
W; 2FC3770BB1EE56A1 CRC64;
   COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfan; PF00899; Thir family; 2.
Pfan; PF02134; UBACT_repeat; 1.
PROSITE; PS00536; UBIQUITIN_ACTIVAT_1; FALSE_NEG.
                                                                                                              PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                              PRT; 1012 AA.
                                  ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION. MEDLINE-97311754; PubMed-9168469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe."; Mol. Biol. Cell 8:825-841(1997).
                                                                                                                                                                                                                                                                                                                                                          UBA1_SCHPO STANDARD; F C094609; 090879; 01-007-2000 (Rel. 40, Created) 01-007-2000 (Rel. 40, Last seque) 01-007-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 611-1012 FROM N.A.
                                                                                                                                                                                        58.48;
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                                                                                                                                           243871
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                                                                                                                                                                                                                       9; Conservative
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|1339 EAKNKKESELDEI 1351
 2116
186
660
752
130
678
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1833
2029
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InterPro; IPR000127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
NCBL_TaxID=4896;
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                          1823
1833
2029
2116
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SEQUENCE
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UBA1_SCHPO
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-> Q (IN REF. 1). 1F1BA3DB6C4067B4 CRC64;

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14565 MW;

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Mitochondrion; Inner membrane; Electron transport; Respiratory chain;
                                                   92
127 AA;
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                                Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                      IF3_PROVU P33319;
                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Dietrich F.S., Mulligan J., Allen E., Cherry J.M., Ching E.,
Berno A., Carpenter J., Chen E., Cherry J.M., Ching E., Duncan M.,
Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
Mosedale D., Nakahara K., Namath M., Oefner P., Oh C., Petel F.X.,
Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
Winant A., Yelton M., Botstein D., Davis R.W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME
-!- FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME
IS PART OF THE MITCCHOURIAL RESPIRATORY CHAIN. THIS COMPONENT
IS PART OF THE MITCCHOURIAL PROPOUND FUMPING.
-- INVOLVED IN REDOX-LINKED PROTON PUMPING.
-- O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
(COMPLEX III SUBUNIT VII)
0CR7 OR CR01 OR UCR7 OR YDR529C OR D9719.32.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The biosynthesis of the ubiquinol-cytochrome c reductase complex in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: FUNCI BC1 COMPLEX CONTAINS 10 SUBUNITS; 3 RESPIRATORY SUBUNITS, 2 CORE PROTEINS AND 5 LOW-MOLECULAR WEIGHT PROTEINS. SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE. SIMILARITY: BELONGS TO THE UGCRB/OCR7 FAMILY. CAUTION: WAS ORIGINALLY THOUGHT TO BE THE UBIQUINONE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yeast. DNA sequence analysis of the nuclear gene coding for the 14-kDa subunit.";
Eur. J. Biochem. 138:169-177(1984).
                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de Haan M., van Loon A.P.G.M., Kreike J., Vaessen R.T.M.J.,
Grivell L.A.;
                                                                                                                                                 Length 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: QH(2)+2 FERRICYTOCHROME C=Q+2 FERROCYTOCHROME C.
                                                                                                                                                                                              4; Indels
                                                                       AB5207808ACC6C2D CRC64;
PS00865; UBIQUITIN_ACTIVAT_2; 1. conjugation; Ligase; Nuclear protein.
                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                         127 AA.
                                                                                                                                                                                            2; Mismatches
                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                 Score 43;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 28583 / FL100;
MEDLINE-84108379; PubMed-6319130;
    PROSITE; PS00865; UBIQUITIN_ACT Ubiquitin conjugation; Ligase; ACT_SITE 593 BY SEQUENCE 1012 AA; 112948 MW;
                                                                                                                                             55.8%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X00256; CAA25064.1; -. EMBL; U33057; AAB64968.1; -. PIR; A00121; RDBYUN. SGD; S0002937; QCR7.
                                                                                                                         Ouery Match
Best Local Similarity 60.v.
9; Conservative
                                                                                                                                                                                                                                                                      : |||| |||| ||
777 ETAANKDKQELKSIA 791
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                           UCR7_YEAST
P00128;
                                                                                                                                                                                                                                                                                                                                                                                UCR7_YEAST
                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FERST MICROBIOL. Lett. 112:211-216(1993).

-!- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE EQUILIBRUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABLIITY OF 30S SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liveris D., Schwartz J.J., Geertman R., Schwartz I.; "Molecular cloning and sequencing of infC, the gene encoding translation initiation factor IF3, from four enterobacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 179;
                       Score 42; DB 1; Length 127;
Pred. No. 5.5;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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IMPORTANT FOR 30S BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA0650013E76D71D CRC64;
                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TRANSLATION INITIATION FACTOR IF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBUNIT: MONOMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO THE IF-3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
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Pred. No. 11;
5; Mismatches
                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intervio, ...
Pfam; PF00707; IF3; 1.
PROSITE; PS00938; IF3; 1.
factor; Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 13315;
MEDLINE=94010248; PubMed=8405963;
                                                                                                                                                                                                                                                                                                                                                       (Rel. 28, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L11257; AAC36812.1; -.
                       54.5%;
Query Match
Best Local Similarity 69.2
Loc 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
'.'... 7; Conserve
                                                                                                                          2 EAANKQKQELDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P02999; 2IFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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:6XDZ60 DNAK\_RICPR

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                                                             "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-86111835; PubMed-3511046;
Hollingshead S.K., Fischetti V.F., Scott J.R.;
"Complete nucleotide sequence of type 6 M protein of the group
Streptococcus. Repetitive structure and membrane anchor.";
J. Biol. Chem. 261:1677-1686(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 43-122 FROM N.A.
MEDIINE-83166224; PubMed=3885219;
Scott J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
"Relationship of M protein genes in group A streptococci.";
Proc. Natl. Acad. Sci. U.S.A. 82:1822-1826(1985).
                   Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 1033;
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 1033 AA; 118078 MW; B32A330BEA4869BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
M PROYPEIN, SEROTYPE 6 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                    Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91126460; PubMed=1846974; Fischetti V.A.;
PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                               EMBL; AE000035; AAB96015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 53.2
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           832 QESYNKVKAELNEI 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QEAANKQKQELDEI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=97105885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHAGOCYTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                           Herrmann R.;
                                                                                  pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M6_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
M6_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Öλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 396:133-140(1998).
--- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
--- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99039499, PubMed=9823893; Andersson J.O., Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A638A0A5A5C8ACC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN MG328 HOMOLOG (P01_ORF1033).
MPN474 OR MP367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DNAK PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1033 AA.
                                                                                627 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                   Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41;
Pred. No. 4
                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Chaperone; AIP-binding; Heat sho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ235270; CAA14651.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.2%;
56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||| | |:|| || || 257 KEAAEKAKKELSSTST 272
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STRAIN=ATCC 29342 / M129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pneumoniae.
                                                                                                                                                                                                                                Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                          STRAIN-MADRID E;
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                                                                                                                                                                                                          DNAK OR RP185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondria.
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P75310;
                                                                                  DNAK_RICPR
                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE :
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Best Loca Matches

οy g RESULT 6 Y328\_MYCPN

AC OC OC OC OX REP REP RC AC

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Gaps

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3; Indels

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                                             SCI. Am. 264:32-39(1991).
-1- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SEROTYPES
OF PROTEIN M. PROTEIN M. IS CLOSELY ASSOCIATED WITH VIRULENCE OF
THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
"Neural vector. Herpes may open the way to gene therapy in neurons.";
                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: TO OTHER M PROTEINS. SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
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-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-1- MISCELLANEOUS: EACH MYOSIN HEAVY CAMIN CAM BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01576; Myosin_tail; 1.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                       EMBL; M69181; AAA99177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.9
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000048; -. InterPro; IPR001609; -. InterPro; IPR002928; -. Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EAANKQKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    844
1976
1976
                                                                                                                                                                                                                                                                                                                                                                               PIR; B61231; B61231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1976 AA;
                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P08799; 1MND.
MIM; 160776; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene family.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT).
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SEQUENCE
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P80736;
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NP_BIND
MOD_RES
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      SO DE REPETE E EL PERE E EL PETETE EL PETETE E EL PETE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-96025307; PubMed=7499478;
Phillips C.L., Yamakawa K., Adelstein R.S.;
"Cloning of the cDNA encoding human nonmuscle myosin heavy chain-B and analysis of human tissues with isoform-specific antibodies.";
J. Muscle Res. Cell Motil. 16:379-389(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 63-722 FROM N.A. MEDLINE-91316803; PubMed-1860190; MEDLINE-91316803; PubMed-1860190; Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K., Gdula D., Adelstein R.S., Weir L.; "Human nonmuscle myosin heavy chains are encoded by two genes located
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLY/PRO-RICH (CELL WALL-SPANNING),
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. Res. 69:530-539(1991).
FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS, CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAPPING. SUBUNIT: MYOSIN IS A HEXAMBRIC PROTEIN THAT CONSISTS OF 2 HEAVY SUBUNITS. (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN,
    institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                      Virulence; Phagocytosis; Cell wall; Duplication; Repeat; Antigen;
                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
10.27 AA TANDEM REPEATS.
4.5 X 25 AA TANDEM REPEATS.
TWO DIRECTLY REPEATED 27 AMINO ACID BLOCKS SEPARATED BY 15 AMINO ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 483;
                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68F87F28DB53A448 CRC64;
                                                                                                                                                                                                                                                                             M PROTEIN, SEROTYPE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 45;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROPHILIC.
                                                                                                                                    InterPro; IPR001899; -
Pram: PF00746; Gram_pos_anchor; 1.
PRINTS; PR00115; GPOSANCHOR:
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEINS
                                                                                                                                                                                                                                    Coiled coil; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.9%;
                                                                                                EMBL; M11338; AAA26920.1; -. PIR; A26297; A26297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 EEAANKERENKEAIGT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OEAANKOKOELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                           483
477
477
483
138
347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE B) (NMMHC-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                  43
458
478
69
157
279
                                                                                                                                                                                                                                                                                                                                                                                                                                     348
412
449
                                                                                                                                                                                                                                           ransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYSO_HUMAN
P35580;
                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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"Differences in specificity for the interactions of stefins A, B and
D with cysteine proteinases.";
FEBS Lett. 395:113-118(1996).
-!- FUNCTION: POTENT INHIBITOR OF CATHEPSINS L AND S, AND PAPAIN.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBCELLULAR BELONGS TO THE. TYPE I CYSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
SUBFRAGMENT (S2).
SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST
TO OTHER NONMUSCLE MYOSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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RODLIKE TAIL (S2 AND LAM DOMAINS).
COILED COIL (POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LEUKOCYTE CYSTEINE PROTEINASE INHIBITOR 2 (PLCPII) (STEFIN D2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myosin; Coiled coil; Actin-binding; Alkylation; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
4W, B2BB87FF35EA124F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 1;
Pred. No. 2e+02;
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22 QEIANKVKPQLEE
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                 NCBI_TaxID=9823;
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                                          CYT5_PIG
Q28986;
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"Differences in specificity for the interactions of stefins A, B and D with cysteine proteinases.";

FEBS Lett. 395:113-118(1996).

"I FEBS Lett. 395:113-118(1996).

"I FUNCTION: POTENT INHIBITOR OF CATHEPSINS L AND PAPAIN.

"I SUBCELLULAR LOCATION: CYTOPLASMIC.

"I SUBCELLULAR LY: BELONGS TO THE TYPE I CYSTATIN FAMILY.

R PIRS 740455; 340455.

"R HSSP, PO1040; 1CYU.

"R InterPro: IPR000010; "

"R InterPro: IPR00031; cystatin; I.

"PROSITE; PR000295; STEFINA."

"R PROSITE; PS00287; CYSTATIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Leukocyte;
MEDIINE-94086524; PubMed-8262248;
Lenarcic B., Ritonja A., Dolenc I., Stoka V., Berbic S., Pungercar J.,
Strukelj B., Turk V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Pig leukocyte cysteine proteinase inhibitor (PLCPI), a new member of
the stefin family.";
FEBS Lett. 336:289-292(1993).
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-WOV-1997 (Rel. 35, Last annotation update)
LEUKOCYTE CYSTEINE PROTEINASE INHIBITOR 1 (PLCPI) (STEFIN D1).
                                                                                  REACTIVE SITE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOCKED (PARTIAL).
REACTIVE SITE (BY SIMILARITY)
SECONDARY AREA OF CONTACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.6%; Score 39; DB 1; Length 103; llarity 61.5%; Pred. No. 13; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                         Length 35;
                                                                                                                                                                                                                                   3; Indels
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                                                                                                                          6A3A4167907D9B94 CRC64;
                                                                                                                                                                                         DB 1;
                                                                                                                                                                                    Score 39; DB 1;
Pred. No. 4.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          103 AA.
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MEDLINE-97053662; PubMed=8898076;
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61.5%;
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3925 MW;
                 Pfam; PF00031; cystatin; 1. Thiol protease inhibitor.
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Best Local Similarity
'.hog 8; Conserv?
HSSP; P01040; 1CYU
                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                        35 AA;
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ACT_SITE
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SEQUENCE
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P35479;
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22 QEIANKVKPQLEE 34

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                                                                                                                                                                                                                                                                                                         TISSUE-Bone marrow;
Pungercar J., Strukelj B.;
Submitted (DEC-1955) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS AN INTROFLELLULAR THIOL PROTEINASE INHIBITOR.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE TYPE I CYSTATIN FAMILY.
                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: THIS IS AN INTRACELLULAR THIOL PROTEINASE INHIBITOR.
---- SUBCELLULAR LOCATION: CYTOPLASMIC.
---- SIMILARITY: BELONGS TO THE TYPE I CYSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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SECONDARY AREA OF CONTACT.
9F4FDE8580AAEB44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%; Score 39; DB 1; Length 103; 61.5%; Pred. No. 13; 1.1ve 2; Mismatches 3; Indels
                                             01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYSTATIN AS (STEFIN AS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYSTATIN A8 (STEFIN A8).
103 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00031; cystatin; 1.
PRINTS; PR00295; STEFINA.
PROSITE; PS00287; CYSTATIN; 1.
Thiol protease inhibitor.
ACT_SITE 10 10 REA
SITE 51 55 SEC
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SEQUENCE 103 AA; 11743 MW;
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Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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1805 AA

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sequencing.";
J. Bacteriol. 175:7918-7930(1993).

J. Bacteriol. TOMPONENT OF THE CYTOSKELETON-LIKE STRUCTURE WHICH
-!- FUNCTION: COMPONENT OF THE WALL-LESS MYCOPLASMA. THIS
STABILIZES THE STAPE OF THE WALL-LESS MYCOPLASMA. THIS
CYTOSKELETON-LIKE NETWORK OF ACCESSORY PROTEINS CONTAINING HWM
PROTEINS 1 TO 5 ALLOWS THE PROPER ANCHORING OF CYTADHESIN PROTEINS
IN THE MYCOPLASMAL MEMBRANE AT THE ATTACHMENT ORGANELLE (BY
                                                                                                                                                                                                                                                                                                            Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult G.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.E., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium.";
                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-94075230; Pubmed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                 Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 557-659 FROM N.A.
                                                                                                                                                                                                                  Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                           Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 33530 / G-37;
                                                    STANDARD;
                                                                                                                                                                                                                                NCBI_TaxID=2097;
                                                                                                                                                                HMW2 OR MG218.
                                                    HMW2_MYCGE
                                                                                                                                                  PROTEIN 2)
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SEQUENCE
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                    RESULT 14
HMW2_MYCGE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic organization and expression of simian foamy virus type 3
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                                                                                                                                                                                                                                             REACTIVE SITE (BY SIMILARITY).
SECONDARY AREA OF CONTACT.
9F521E8580AAEB44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1; Length 643;
Pred. No. 87;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                             Length 103;
                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92124734; PubMed-1310187;
Renne R., Friedl E., Schweizer M., Fleps U., Turek R.,
Neumann-Haefelin D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C53A0575BA9B5949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simian foamy virus (type 3 / strain LK3) (SFV-3). Viruses; Retroid viruses; Retroviridae; Spumavirus
                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-UUL-1993 (Rel. 26, Last annotation update)
GAG POLYPROTEIN (CORE POLYPROTEIN).
                                                                                                                                                                                                                                                                                                                             Score 39; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M74895; AAA47795.1; ALT_INIT.
                                                                                                                                                           InterPro; IPR001713; -.
Pfam; PF00031; cystatin; 1.
PRINTS; PR00295; STEFINA.
PROSITE: PS00287; CYSTATIN; 1.
Thiol protease inhibitor.
ACT_SITE 10 10 10 REA
SITE 51 55 SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Polyprotein.
INCE 643 AA; 69785 MW;
                                                                                                                                                                                                                                                                               103 AA; 11713 MW;
                                                                                                                                                                                                                                                                                                                             50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.6%;
                                                                                                               EMBL; U41733; AAB03262.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186:597-608(1992)
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 61...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                 InterPro; IPR000010; -. InterPro; IPR001713; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 QEIAQMQRDELEEI 140
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                                                                                                                                                                                                                                                                                                                                                                                           1 QEAANKQKQELDE 13
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22 QEIANKVKPOLEE 34
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Best Local Similarity
8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11644;
                                                                                                                                 HSSP; P01040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAG_SFV3L
P27400;
                                                                                                                                                                                                                                                                              SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. Tractitute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercion and this statement is not removed. Usage by and for commercion entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                      MW; 11D093AF173284FD CRC64;
                                                                                                                                                                                                                                                                                                                                                         COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                 COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39, DB 1; Le
Pred. No. 2.6e+02;
5; Mismatches 1;
                                                                                                                                                                                                                                                                                          Cytadherence; Structural protein; Coiled coil.
DOMAIN 28 838 COILED COIL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1853 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.68;
                                                                                                                                                                                                                        EMBL; U39701; AAC71437.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                         216252
                                                                                                                                                                                                                                         ; U02165; AAD12447.1;
; MG218; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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1512 DSTNKQRKELNEL 1524
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                                                                                                                                                                                                                                                                                                                                                                                                      1805 AA;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                         1632
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MY5A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MY5A_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - FUNCTION: MAY BE INVOLVED IN MELANOSOME TRANSPORT, OR ALTERNATIVELY, IT MAY BE REQUIRED FOR SOME POLARIZATION PROCESS INVOLVED IN DENDRITE FORMATION.
-! - SUBDINI: MAY BE A HOMODIMER, WHICH ASSOCIATES WITH MULTIPLE CALMODULIN OR MYOSIN LIGHT CHAINS.
                                                                                                                     MYO5A OR DILUTE.
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY, CLASS-5 MYOSIN SUBPAMILY.
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PROSITE; PS50096; IQ; 5.
Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN VA) (MYOSIN 5A).
                                                                                                                                                                                                                                                                                                                                                                                                  Novel myosin heavy chain encoded by murine dilute coat colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAIL.
ACTIN-BINDING (POTENTIAL).
5 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-91141583; PubMed-1996138;
Mercer J.A., Seperack P.K., Strobel M.C., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALMODULIN-BINDING (BY SIMII
CALMODULIN-BINDING (BY SIMII
ATP (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mercer J.A., Seperack P.K., Strobel M.C., Copeland N.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL.
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MGD; MGI:105976; Myo5a.
InterPro; IPR000048; ...
InterPro; IPR001609; ...
InterPro; IPR002710; ...
Pfam; PF01843; DIL; 1...
Pfam; PF00612; 10; 6...
Pfam; PF00663; myosin_head; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coiled coil; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X57377; CAA40651.1; -. PIR; A46761; A46761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 349:709-712(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jenkins N.A.;
Nature 352:547-547(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jenkins N.A.
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NP_BIND
MOD_RES
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REPEAT
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                                                          Gaps
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0
                               Score 39; DB 1; Length 1853;
Pred. No. 2.6e+02;
i: Mismatches 3; Indels
503E93D48CA6B766 CRC64;
                                                                                                                                                   5, 2001, 11:51:45
1853 AA; 215594 MW;
                                 50.6%;
                    Ouery Match
Best Local Similarity 50.0
                                                                                            :| |:| ||| |::
1010 EERADKYKQETDQL 1023
                                                                               1 QEAANKQKQELDEI 14
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Job time: 504 sec
SEQUENCE
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 5, 2001, 11:50:51; Search time 123.78 Seconds (without alignments) 17.102 Million cell updates/sec

US-09-462-480-11 77 1 QEAANKQKQELDEIST 16 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

425026 seqs, 132305027 residues Searched:

425026 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp\_rodent:\*
sp\_unclassified:\*
sp\_vertebrate:\*
sp\_virus:\* sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_organelle:\*
sp\_phage:\* SPTREMBL\_16:\*
:: sp\_archea:\*
:: sp\_bacteria:\* sp\_plant:\* sp\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Score	% Query Match	% Duery Match Length DB	DB	ID	Description
77	100.0	100	7	069739	069739 mycobacteri
45	58.4	727	Ŋ	Q22505	Q22505 caenorhabdi
45	58.4	1581	4	092614	092614 homo sapien
45	58.4	1976	ဖ	027991	. Q27991 bos taurus
45	58.4	1976	11	Q9JLT0	Q9jlt0 rattus norv
43	55.8	681	ນ	Q9VDE0	Q9vde0 drosophila
43	55.8	1339	വ	90MA60	09vw06 drosophila
42	54.5	275	14	Q9DIE2	Q9die2 iridovirus
42	54.5	1273	14	Q9QSK2	Q9qsk2 chilo iride
42	54.5	2035	11	61МС60	Q9jmh9 mus musculu
41	53.2	176	œ	Q9TL15	Q9tl15 nephroselmi
41	53.2	211	10	Q9M279	Q9m279 arabidopsis
41	53.2	545	٣	005842	Q05842 saccharomyc
41	53.2	610	ო	Q12136	Q12136 saccharomyc
41	53.2	746	ស	025561	025561 naeqleria f
41	53.2	829	10	Q9LPI3	O9lpi3 arabidopsis
41	53.2	1410	4	014221	Q14221 homo sapien
41	53.2	1411	4	Q15075	Q15075 homo sapien
41	53.2	2007	13	002015	002015 gallus gall

09scz8 arabidopsis 064525 arabidopsis 095x38 streptococc 09su52 arabidopsis 064293 streptococc 064293 streptococc 064293 streptococc 064293 streptococc 092576 homo sapien 09u145 homo sapien 09u145 homo sapien 09x010 drosophila 09x487 streptococc 012481 saccharomyc 09u45 arabidopsis 09x82 arabidopsis 09x82 arabidopsis 09x82 arabidopsis 09x82 drosophila 09x83 drosophila 09x83 drosophila 09x83 drosophila 09x83 schistosoma 01977 caenorhabdi 01203 chimpanzee	092603 homo sapien 09nq10 homo sapien 09nq11 homo sapien 09wu41 mus musculu
10 095C28 5 09N8A0 10 064525 10 064525 10 095U52 9 064282 9 064282 9 064282 9 064282 10 095U65 4 09U016 5 09W0L0 5 09W0L0 10 09WC2 10 09WC2 2 09EF2 2 09EF2 2 09EF2 3 012481 0 01E27 10 09B86 5 045038 5 045038	000
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2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	444 122 1244 124

# ALIGNMENTS

RESULT

RESULT Q22505

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Itoh K., Adelstein R.S.;
"Neuronal cell expression of inserted isoforms of vertebrate nonmuscle myosin heavy chain II-B.";
myosin heavy chain II-B.";
BJ. iol. Chem. 270:14533-14540(1995).
EMBL; AB022023; BAA36494.1;
EMBL; U15716; AAA87715.1;
                                   MEDLINE-97191544; PubMed-9039502;
Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of CDNA clones from cell line KG-1 and brain.";
EMBL: D86970: BAA13206.1; -.
HSSP; P08799; IMMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohara M., ishiguro N., Shinagawa M.;
"Bos taurus nonmuscle myosin heavy chain B mRNA, complete cds.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

S8.4%; Score 45; DB 4; Length 1581;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1976;
                                                                                                                                                                                                                                                         InterPro; IPR001609; -.
Pfam: PF00063; myosin_head; 1.
Pfam: PF000635; myosin_head; 1.
Probom: PF000135; 10; 1.
SWART; SW00015; 10; 1.
SEQUENCE 1581 AA; 180549 MW; FFA85576ABFC56B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6144354451C0F790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 11, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NONMUSCLE MYOSIN HEAVY CHAIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 6; 1
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1976 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=CEREBRAL CORTEX;
MEDLINE=95301542; PubMed=7782316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229097 MW;
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Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 204-302 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000048; -.
InterPro; IPR001609; -.
InterPro; IPR002017; -.
                                                                                                                                                                                                                          InterPro; IPR000048; -.
                                                                                                                                                                                                                                               InterPro; IPR001553; -.
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| 1326 EEANKEKQELQE 1337
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
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Q27991;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Dullin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Bightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieq J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
Waterston A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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100.0%; Score 77; DB 2; Length 100; 100.0%; Pred. No. 0.0001; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U41024; AAA82345.1; -. SEQUENCE 727 AA; 81325 MW; 42581312925DF1F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fulton B., Hawkins J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45;
Pred. No.
                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-94150718; Pubmed-7906398;
                                                                                                                                                                                                                   Q22505
Q22505;
Q1-NOV-1996 (TrEMBLrel, 01, C.
01-NOV-1996 (TrEMBLrel, 01, L.
01-NOV-1998 (TrEMBLrel, 08, L.
SIMILAR TO L96 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               092614;
01-FEB-1997 (TrEMBLrel. 02, C.
01-FEB-1997 (TrEMBLrel. 02, L.
01-MAR-2001 (TrEMBLrel. 16, L.
MYELOBLAST KIAA0216.
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60.0%;
                                         16; Conservative
                                                                             1 QEAANKQKQELDEIST 16
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                                                                                                      313 QETANKLSHQLDEIN 327
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                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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                Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
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  Query Match
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RESULT 092614

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RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Burkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gong F., Gornell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Harris M.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,
RA Martei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho O., Zhon W., Zhou X., Zho S., Zho X., Zhon M., Zhou X., Zho X., Zho X., Zhon 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. (CBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Wan R.H., Doyle C., Baxter E.G., Hellt G., Nelson C.K., Miklos G.L.G., Warl K.H., Doyle C., Baxter E.G., Hellt G., Nelson C.K., Miklos G.L.G., Abril J.F., Agbayani A. An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78529 MW; FF140F97D5252699 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB
Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003733; AAF55856.1; -.
FlyBase; FBgn0038860; CG10825.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
CG9279 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 55.8%;
Best Local Similarity 64.3%;
Matches 9; Conservative
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667 AANKEKIELEKIMT 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00252;
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SEQUENCE
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01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-MAY-2000 (TEMBLrel. 16, Last annotation update)
02010825 PROTEIN.
CG10825 PROTEIN.
CG10825 PROTEIN.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., in P. W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SPREAGE-DAMLEY, TISSUE-BRAIN;
STRAIN-SPREAGE-DAMLEY, TISSUE-BRAIN;
Yam J.W.P., Chan K.W., Hislao W.L.W.;
"Suppression of transformed phenotype by overexpression of nonmuscle myosin heavy chain-B in p53val135-transformed rat fibroblast.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AF139055; AAF61445.1; -.
               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQ; 1.
AA; 228963 MW; E32708BF9BF2B470 CRC64;
                                                                                                                                                                                                                                                           Last sequence update)
               4:
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2; Mismatches 4
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                                                                                                                                                                                               PRT; 1976 AA.
               Mismatches
                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                   NONMUSCLE MYOSIN HEAVY CHAIN-B.
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InterPro; IPR002928; -.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00612; IQ; 1.
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PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLEL. 15, 01-OCT-2000 (TrEMBLEL. 15, 01-MAR-2001 (TrEMBLEL. 16,
                                                                        1280 EKANKLONELDNVST 1294
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Matches 9, Conservative
            Conservative
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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                                                     EAANKQKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR00048; -
InterPro; IPR001609; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00015; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
            6
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                                                                                                                                                                                          Q9JLTO
Q9JLTO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VDE0
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                                                     ~
            Matches
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Gaps

Gaps

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Indels

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Darai G.;

SEQUENCE FROM N.A.

Muller K., Tidona C.A., Bahr U., Darai G.;

"The DNA sequence of Chilo iridescent virus between the genome coordinates 0.974 and 0.101";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

-! CATALYTIC ACTIVITY: N DECXYNUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + DNAM(N) (BY SIMILARITY).

-! SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.

EMBL; AF083915; AAD48150.1; -.

EINTERPRO: JPR002064; -.

FILESPRO: JPR0021064; -.

Pfam: PPODLBS DNA POLYMERASE TYPE-B FAMILY.

EMBL; AF083915; DNA_POL_BS 5.
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Furusawa T., Ikawa S., Yanai N., Obinata M.;
"Isolation of a novel PDZ-containing Myosin from hematopoietic supportive bone marrow stromal cell lines.";
Biochem. Biophys. Res. Commun. 270:67-75(2000).
EMBL: AB026497; BAA93660.1;
InterPro; IPR001478;
InterPro; IPR001409;
InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                             (CIV) (Insect iridescent virus type 6). no RNA stage; Iridoviridae; Iridovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 14; Length 1273;
Pred. No. 2.4e+02;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA replication; DNA-binding; DNA-directed DNA polymerase.
SEQUENCE 1273 AA; 147662 MW; CC514AD83F7299A3 CRC64;
                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2035 AA.
       d. No. 58;
Mismatches
          Pred. No.
                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20200096; PubMed-10733906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYOSIN CONTAINING PDZ DOMAIN. MYSPDZ.
     46.78;
                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16, DNA POLYMERASE.
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Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00106; DNAPOLB.
SMART; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                 191 EKENKSKEDIDEITS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | || || |:::|||::
| 826 EKENKSKEDIDEITS 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        Chilo iridescent virus (Viruses, dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EAANKQKQELDEIST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel.
                                                                               EAANKOKOELDEIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10488;
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01-OCT-2000
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                                                                                                                                                                                                                               090SK2
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       Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
NCBI_TaxID=113375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 5; Length 133
Pred. No. 1.8e+02;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01302; CAP_GLY; 1.
PROSITE; PS00845; CAP_GLY; 1.
SEQUENCE 1339 AA; 152535 MW; 3BB624E7EBC7C0B6 CRC64;
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31746 MW; 0AB60A2FD34131F5 CRC64;
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Last annotation update)
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       Beeson K.Y., Benos P.V., Berman B.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
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FlyBase; FBgn0036882; CG9279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%;
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01-MAR-2001 (TrEMBLrel, 16,
01-MAR-2001 (TrEMBLrel, 16,
01-WAR-2001 (TrEMBLrel, 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.5%;
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 QDVSSKLKRELDEIA 449
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275 AA;
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Query Match

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EDGGKQKQEIDE 288
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NKQKQERDMVKT 39
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
                                          SEQUENCE FROM N.A.
                                                                                                                                                         SEQUENCE FROM N.A.
        NCBI_TaxID=3702;
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ID Q12136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II;
Brassicales, Brasslcaceae, Arabidopsis.
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                                                                                                                                       Length 2035;
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                                                                                                                                   Score 42; DB 11; Length 20
Pred. No. 3.7e+02;
2; Mismatches 2; Indels
                                                                               C5CE4BB053475119 CRC64;
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Turmel M., Otis C., Lemieux C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR137379; ARD54801.1; -.
InterPro; IPR001302; -.
InterPro; IPR00146; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast.
Bukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
NCBL_TaxID=31312;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 24.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999)
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Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                        176 AA
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                                                                                                                                                                                                                                                                                                                                                        PRT;
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Pfam; PF00595; PDZ; 1.
Pfam; PF00612; IQ; 1.
PRINTS: PR00193; MYOSINHEAVY.
SMART: SMO0015; IQ; 1.
SEQUENCE 2035 AA; 230905 MW;
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                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| |: || |: |
68 QDAVNQLKQALQELET 83
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1780 EESNKEKQELQE 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nephroselmis olivacea.
                                                                                                                                                                                                                  2 EAANKQKQELDE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast
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Q9M279;
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Q9TL15
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MEDLINE-97127830; PubMed-8972581;
Delaveau T., Blugeon C., Jacq C., Perea J.;
"Analysis of a 23 kb region on the left arm of yeast chromosome IV.";
Yeast 12:1587-1592(1996):
EMBL; X97751; CAA66339.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Choisne N., Robert C., Brottier P., Wincker P., Cattolico L., Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Salanoubat Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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64;
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SEQUENCE FROM N.A.
Perea J., Blugeon C., Delaveau T., Jacq C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 3; Length 54:
Pred. No. 1.5e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL138642; CAB71891.1; ...
Hypothetical protein.
SEQUENCE 211 AA; 24684 MW; 77688F50645CC43F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; CAA66339.1; -.
545 AA; 63003 MW; 51455448475962B4 CRC64;
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01, Last sequence update)
08, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAV-2001 (TrEMBLrel. 16, Last annotation update)
ORF YDL153C.
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Pred. No.
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ilarity 66.7%;
Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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01-NOV-1998 (TrEMBLrel.
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025561;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN II HERVY CHAIN (FRAGMENT).
MAGGLETIA fowler1.
BUKARYOCA: Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
NCBL_TAXID-5763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SARAIN=LEE MP;
SARAIN=LEE MP;
Shaw D.R., Sullivan P.K., Marciano-Cabral F., Ennis H.L.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U43192; AAB01786.1; -
InterPro; IPR02017; -
NON TER
SEQUENCE 746 AA; 87781 MW; 3771A80AAFC2FF43 CRC64;
                                                                 MIPS;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            SEQUENCE FROM N.A.

Rine J.D., Kamakaka R.T.;

Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; 274201; 27498726.1; -.

EMBL; U63063; AAB05801.1; -.

SGD; SO002312; SAS10.

SEQUENCE 610 AA; 70259 MW; 9278BF873834FC7E CRC64;
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Best Local Similarity 42.9
Matches 6; Conservative
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342 EDGGKQKQEIDE 353
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[2]
SEQUENCE FROM N.A.
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025561
LD 025561.
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Search completed: July 5, 2001, 11:50:52 Job time: 475 sec

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M. tuberculosis LHP polypeptide antigenic fragment.
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                               AAY32097
AAY32097
AAY38981
AAW81706
AAW84339
AAY39136
                                                                                                      AAY38993
AAY03705
AAB35218
AAB19845
AAW81746
AAW64379
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AAY39224
AAY39176
AAY39081
AAY39033
AAY03706
AAW32456
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AAB35234
AAB43002
AAY59109
AAW06201
AAY33400
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AAR99052
AAW32376
AAW81747
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                      AAW6432]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
07-JUN-1999
 AAY03710;
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 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5, 2001, 11:45:43; Search time 130.35 Seconds (without alignments) 7.441 Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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83
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## SUMMARIES

	Description	M. tuberculosis LH	Mycobacterium tube	M. tuberculosis im	M. tuberculosis an	Mycobacterium tube	Mycobacterium tube	M. tuberculosis im	Mycobacterium tube	M. tuberculosis an	M. tuberculosis re	Mycobacterium tube
	Q	AAY03710	AAW32457	AAW81695	AAY39125	AAW32454	AAW32386	AAW81707	AAW64340	AAY39137	AAY38994	AAW32444
	E .	20	18	19	50	18	18	19	19	20	20	18
	Query Match Length DB ID	16	27	27	27	80	80	80	80	80	80	95
<b>P</b>	Query Match I	100.0	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2
	Score	83	79	79	79	79	79	79	79	79	79	79
	Result No.		7	e	4	2	9	7	80	6	10	11

SSAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; Immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; Immune response.
4ycobacterium tuberculosis.
WO9904005-A1.
28-JAN-1999.
16-JUL-1998; 98WO-IB01091.
16-JUL-1997; 97US-0052631.
(INSP.) INST PASTEUR. (STAT-) STATENS SERUM INST.
Andersen P, Berthet F, Gicquel B, Rasmussen PB;
API; 1999-132249/11.
New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis - useful in vaccines, for diagnosis, and for expression of heterologous proteins

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The present invention is directed to a polynucleotide carrying the regulatory expressions signals of the ESAT-6 protein as well as an open regulatory expression signals of the ESAT-6 protein as well as an open cading fram ecoding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the M. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two provide a synergistic increase in ability to induce a protective immune the polynucleotide. LHP and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune the polynucleotide may be used to express almost and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune the polynucleotide may be used to expense and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune the polynucleotide may be used to expense the polynucleotide may be used to expense the polynucleotide may be used to expense the polynucleotide with the polynucleotide may be used to expense the polynucleotide may be used to expen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogen; vaccine; tuberculosis; non specific adjuvant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon DC, Houghton R, Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 83; DB 20; 100.0%; Pred. No. 8.6e-07;
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                    Claim 21; Page 65; 88pp; English.
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Conservative
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95US-0533634
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96US-0659683
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Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AA;
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22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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AAW32457
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immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1 Peptide 3. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins proteins pare. SSAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
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                                                                                                                                                                                                     Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 27;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. tuberculosis immunogenic polypeptide TB38-1 peptide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.2%; Score 79; DB 19; L
100.0%; Pred. No. 6.3e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                   Score 79; DB 18; 1
Pred. No. 6.3e-06;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 122; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       AAW81695 standard; Protein; 27 AA.
                                                                                                                                                                                       95.2%; Scc.
100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0730510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.2
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                     Query Match 95.2
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                     1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                                   7 gslqgqwrgaagtaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 AA;
                                                                                                                                                    27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAW81695;
                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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Gaps

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Gaps

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Indels

1 GSLQGQWRGAAGTAA 15

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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TD38-IP3. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                   Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                              Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                              Houghton R, Reed SG,
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95.2%; Score 79; DB 18;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis antigen Tb38-1F3.
Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 149; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW32386 standard; Protein; 80 AA.
                                                    skin testing; M.tuberculosis
                                                                                                                                                                                                                               96US-0680574.
95US-0523436.
95US-0533634.
96US-0620874.
                                                                                                                                                                                               96WO-US14674
                                                                                                                                                                                                                                                                                                         96US-0659683
                                                                                                                                                                                                                                                                                                                                                                              Dillon DC,
                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Campos-neto A, Dillon D
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-192903/17.
N-PSDB; AAT91526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in vacc
for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9709429-A2
                                                                                                                          WO9709428-A2
                                                                                                                                                                                               30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JAN-1998
                                                                                                                                                                                                                                                      01-SEP-1995;
22-SEP-1995;
                                                                                                                                                                                                                                                                                                         05-JUN-1996;
                                                                                                                                                              13-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAX19249 to AAX19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                  Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                              M. tuberculosis antigen Tb38-1 peptide 3 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79; DB 20; Length 27; Pred. No. 6.3e-06; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon DC, Hendrickson RC, Ho
SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 117; 299pp; English.
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100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW32454 standard; Protein; 80
                                                                                                       AAY39125 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US03268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0072967
98US-0025197
                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                7 gslqgqwrgaagtaa 21
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A,
Lodes MJ, Reed
                                                                                                                                                                                                                                                                                                                                                             WO9942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1998;
18-FEB-1998;
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                                                                                                                                           AAY39125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                      AAY39125
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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                         Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide comprises Mycobacterium tuberculosis antigen 1878-187. A DNA molecule (see AAV4400) coding for Tb33-1F3 was isolated from a M. tuberculosis strain H37Rv genomic library. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAM64291-R664379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis; infection; diagnosis; antigen; Tb38-1F3
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Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                             95.2%; Score 79; DB 19;
100.0%; Pred. No. 2e-05;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis antigen Tb38-1F3
                                                                                                                    Example 3B; Page 139-140; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 146; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW64340 standard; Protein; 80 AA
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96US-0729622
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                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     31
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Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                    17 gslqgqwrgaagtaa
             WPI; 1998-261042/23.
N-PSDB; AAV64509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-251292/22
                                                                                                                                                                                                                                                     80 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1998.
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                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                Query Match
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AAW64340
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                                                                                                                                                                                                                                                                                                                                                                 modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1F3. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;
                                                                                                                                                                                                                                                 New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                          A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                               Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; Length 80;
2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                            Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;

    M. tuberculosis immunogenic polypeptide Tb38-1F3.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                               Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                              Example 3; Page 163; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW81707 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.2%; Scor.
100.0%; Pre
0;
                                                       95US-0523435.
95US-0532136.
96US-0620280.
96US-0658800.
             96WO-US14675
                                         96US-0680573
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960S-0730510.
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                                                                                                                                                            Dillon DC,
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                                                                                                                                                                            Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-192904/17.
N-PSDB; AAT91460.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                  (CORI-) CORIXA
                                                                                                                                                               Campos-neto A,
            30-AUG-1996;
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                                                         01-SEP-1995;
                                                                     22-SEP-1995;
22-MAR-1996;
                                                                                                   05-JUN-1996;
                                         12-JUL-1996;
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AAW81707
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Length 80 0; Indels 100.08;

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Best Local Similarity 100.
Matches 15; Conservative
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18-FEB-1998;
                                                                                                                                                                                                                                                                   05-NOV-1999
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                                                                                                                                                                                                                               AAY38994;
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                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNas encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to
                                                                                                                                                                                                                               Gaps
             expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
DNA sequences encoding such polypeptides, recombinant
                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                         Length 80;
                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis antigen Tb38-1F3 amino acid sequence.
                                                                                                                                                                                       Query Match 95.2%; Score 79; DB 19; Best Local Similarity 100.0%; Pred. No. 2e-05; Matches 15; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 134-135; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   AAY39137 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US03268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0025197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                 1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ19310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                               80 AA;
                                                                                             of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-1999
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY39137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY39225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                 AAY39137
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DB 20; Length 80;

95.2%; Score 79;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel recombinant antigens and their encodin nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                     detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton R;
;, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                      Indels
                                                                                                                                                                                                                                                                                                                                           M. tuberculosis recombinant antigen protein Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
Pred. No. 2e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.2%; Score 79; DB 20;
100.0%; Pred, No. 2e-05;
ive 0; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 180; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 AA
                                                                                                                                                                                                              AAY38994 standard; Protein; 80 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW32444 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0072596
98US-0024753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US03265
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.2
Best Local Similarity 100.
Matches 15; Conservative
                                                              1 GSLOGOWRGAAGTAA 15
                                                                                    1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
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N-PSDB; AAZ19098.
                                                                                                                                                                                                                                                                                                                                                                                     Antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-1998
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Skeiky YAW;

Reed SG,

Antigen;

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immunogenic part of a folule Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents an tuberculosis antigen, TD38-1. The immunogenic polypeptide can be used to diagnose antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                 New immunogenic polypeptide(s) from soluble M. tuberculosis antigens
                                                                                                                                                                                                                                                                                                                                                                       A new immunogenic polypeptide has been developed comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.2%; Score 79; DB 18; Length 95; 100.0%; Pred. No. 2.3e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     useful for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculosis immunogenic polypeptide Tb38-1.
                                                                                                                                                                       Campos-neto A, Dillon DC, Houghton R,
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                    Example 3; Page 136; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW81747 standard; Protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.2°,
100.0%; Pre
0;
                              96US-0680573.
95US-0523435.
95US-0532136.
96US-0620280.
96US-0658800.
96WO-US14675
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96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-192904/17.
N-PSDB; AAT91445...
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                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 AA;
 30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9816646-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1997;
                                                                     22-SEP-1995;
22-MAR-1996;
                                                                                                       05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW81747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32
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   δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                  immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogen; vaccine; tuberculosis; non specific adjuvant;
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                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 79; DB 18; Length 95;
Pred. No. 2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                    Houghton R, Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 124; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW32376 standard; Protein; 95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%; : 100.0%;
                                                                                                                                                                                                        96US-0680574.
95US-0523436.
95US-0533634.
96US-0620874.
                                  skin testing; M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  skin testing; M.tuberculosis
                                                                                                                                                                         96WO-US14674
                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                 Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                 Campos-neto A, Dillon D
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 gslqgqwrgaagtaa 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-192903/17.
                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT91509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for diagnosis
                                                                                                                                                                                                                                           22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
                                                                                                  WO9709428-A2
                                                                                                                                                                         30-AUG-1996;
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                                                                                                                                                                                                          12-JUL-1996;
01-SEP-1995;
                                                                                                                                      13-MAR-1997
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Sequence

Query Match

ò Op AAW32376;

RESULT

Antigen;

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Gaps

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New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis \cdot
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the Mycobacterium tuberculosis antigen Tb38-1. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens such as Tb38-1, e.g. TbF-2 (see AAY32063) and a Tb99-Tb38-1 fusion. The new fusion proteins are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculosis; antigen; fusion protein; Tb38-1; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                           Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                         DB 19; Le
2.3e-05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.2%; Score 79; DB 20; 100.0%; Pred. No. 2.3e-05; ive 0; Mismatches 0;
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A;
                                                                                                                                                                                           Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                       AAY32097 standard; Protein; 95 AA.
                                                                                                                                                                                         95.2%; Scilarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 4D; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US07717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alderson M,
                                                                                                                                                                                                                                                                    1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                              1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Lhaq 15; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-601610/51
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 AA;
                                                                                                                                     95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09951748-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-APR-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY32097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                         AAY32097
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                                                                                                                                                                                                                                                                                                                                                                                                                             δ
    8
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                                                                                                                                                                   This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is an antigenic portion of Mycobacterium tuberculosis antigen TD38-1. A DNA sequence (see AAV44384) coding for antigen TD38-1 was isolated from a M. tuberculosis strain H37Rv expression library using sera from patients having pulmonary or pleural tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen,
                                                      Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB 19; Length 95;
Pred. No. 2.3e-05;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection; diagnosis; antigen; Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen Tb38-1 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DC, Houghton R, Lodes M
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis strain H37Rv
                                                                                                                                 Example 3b; Page 117; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 123; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW64321 standard; Peptide; 95 AA.
                                                                                                                                                                                                                                                                                                                                                  95.2%; Sc...
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US18214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0818111
96US-0729622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
Les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 gslqgqwrgaagtaa 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed SG, Skeiky YAW,
WPI; 1998-261042/23.
N-PSDB; AAV64491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-251292/22
                                                                                                                                                                                                                                                                                                          95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9816645-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                          Sequence
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Search completed: July 5, 2001, 11:45:43 Job time: 272 sec

2, App Appli

sednence Sed

132,

4, Appli

Sequence 139,

Sequence Sequence

Appli

Sequence Sequence

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GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V.
APPLICANT: Lewis, Randolph V.
APPLICANT: A., Mind A.
APPLICANT: A., Mind A.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: OWTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSONDENCE ADDRESS:
ADDRESSONDENCE ADDRESS:
CITY: Falls Church
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STREET: Usginla
STREET: Usginla
STREET: Usginla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
US-08-425-069-52
US-08-317-844B-52
US-07-857-224B-58
US-08-589-028-6
US-08-784-582-6
US-08-785-271-6
US-09-031-898-2
US-08-31-818-2
US-08-31-615-5
US-08-31-615-5
US-08-31-615-5
US-08-31-615-5
                                                                                                                                                                       US-08-906-769-139
US-08-906-616-139
US-08-639-075A-139
US-09-012-431-139
                                                                                                                                                              PCT-US96-11445-4
                                                                                                                                    US-08-659-251-4
US-09-256-490-4
                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/425,069
FILING DATE: 19-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REDECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 US-08-425-069-46; Sequence 46, Application US/08425069; Patent No. 5728810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: nephila clavipes FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
  NAME/KEY: Peptide LOCATION: 1..31
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                                                                                  July 5, 2001, 11:47:00 ; Search time 61.79 Seconds (without alignments) 5.216 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46,
Sequence 42,
Sequence 54,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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Sequence 4
Sequence 4
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Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6G_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-317-844B-46
US-08-425-069-42
US-08-317-844B-42
US-08-317-844B-42
US-08-317-844B-42
US-08-515-251A-4
US-08-317-844B-2
US-08-317-844B-2
US-08-317-844B-2
US-08-348-006B-5
US-09-348-006B-5
US-09-348-006B-5
US-08-348-006B-5
US-08-348-006B-5
US-08-348-0166-5
US-08-413-118-5
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US-08-317-844B-58
                                                                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-00685-4
                                                                                                                                                                                                                         193259 seqs, 20144635 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                           1 GSLOGOWRGAAGTAAA 16
                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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19111
19111
19111
19111
759
759
980
980
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303
303
3441
4441
4441
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308
308
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38
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                                                             OM protein
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4 GGLGGQGAGAAAAAA 19

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APPLICANT: Lewis, Randolph V.
APPLICANT: Lewis, Randolph V.
APPLICANT: Liminar, Ming
APPLICANT: Hinmar, Ming
APPLICANT: Hinmar, Ming
APPLICANT: Hinmar, Ming
TITLE OF INVENTION: ISOLATED BNA CODING FOR SPIDER SILK
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
FILING DATE: 19-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-106P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 105-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                            ; Sequence 42, Application US/08425069; Patent No. 5728810; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-425-069-54; Sequence 54, Application US/08425069; Patent No. 5728810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS: not relevant not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 50.6
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GGLGGGGAGAAAAA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22046
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: INC. ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                       RESULT 3
US-08-425-069-42
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                                                                                                                                                                                                                                                                                                          Sequence 46, Application US/08317844B
Patent No. 5989894
GENERAL INFORMATION:
APPLICANT: Lewis, Ming
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: RSOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                        Length 31;
                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2;
Pred. No. 2.2;
0; Mismatches
                                                                                      Score 42; DB 1;
Pred. No. 2.2;
0; Mismatches
; OTHER INFORMATION: /label= silkl_repeat US-08-425-069-46
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CTHER INFORMATION: /label= silkl_repeat
US-08-317-8448-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 1447-105P
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELERAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: not relevant MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: nephila clavipes
                                                                                        50.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.6%;
Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                      Ouery Match 50.6
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                      4 GGLGGQGAGAAAAAA 19
                                                                                                                                                                          1 GSLQGQWRGAAGTAAA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U C ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
FRAGMENT TYPE: in
ORIGINAL SOURCE:
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US-08-317-844B-46
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US-08-317-8448-54

US-08-317-8448-54

Sequence 54, Application US/083178448

Patent No. 598984

Patent No. 598984

Patent No. 5989894

APPLICANT: Lewis, Randolph V.

APPLICANT: Lewis, Randolph V.

APPLICANT: Ku, Ming

APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK

TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL

TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch

CREEPENT OF ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CREEPENT OF ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5989894th Washington Street CIIX: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%; Score 42; DB 2; 62.5%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: /label- silkl_repeat
US-08-317-844B-42
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUTTR: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: MUTPHY Jr., Gerald M
REGIETRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEX: 248345
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: nephila clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GSLQGQWRGAAGTAAA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N<sub>O</sub>
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: no
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                    TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
STREET: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFORMED CELL
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Fatent No. 5989894
GRHERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Au, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
ITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
CORRESPONDENCES:
ADDRESSEE: BLICH, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
FILING DATE: 19-APR-1995
CLASIFFCATION: 435
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 24,977
RECISTRATION NUMBER: 1447-106P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 1;
Pred. No. 2.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , LUCATION: 1.34 orHER INFORMATION: /label= silkl_repeat
US-08-425-069-54
Hinman, Michael B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: nephila clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 205-8050
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.6
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GSLQGQWRGAAGTAAA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                  22046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-317-844B-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: E
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Sequence 2, Application US/08425069
Sequence 2, Application US/08425069
Fatent No. 5728810
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Human, Michael B.
TITLE OF INVENTION: FOOTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSES: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
STREET: Virginia
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                            ;
0
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0
                                                                                                                                                                                                     Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 718;
                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRI: 2.2046

ZIP: 22046

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
FTIING DATE: 19-APR-1995
                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 1
Pred. No..67;
0; Mismatches
                                                                                                                                                                                                     Score 42; DB Pred. No. 32; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1447-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULPHY JT., GERLIG M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                     50.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.6%;
ilarity 62.5%;
Conservative
                                                LENGTH: 367 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 718 amino acids
amino acid
(650) 325-7823
                                                                                                                                                                                  Ouery Match
Best Local Similarity 42.9'
                  INFORMATION FOR SEÓ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 GGLGGGGAGAAAAA 115
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                                                                                                                     ; MOLECULE TYPE: protein US-08-515-251A-4
                                                                                                                                                                                                                                                                                                                      347 SIKGEWQGVIGATA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-425-069-2
                                                                                                                                                                                                                                                                                2 SLQGQWRGAAGTAA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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US-08-425-069-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GERLACH, GERALD F.
APPLICANT: WILLSON, PHILIP J.
APPLICANT: WILLSON, PHILIP J.
APPLICANT: ROSSI-CAMPOS, AMALIA
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: ACTINOBACILLUS PLEUROPNEUMONIAE OUTER
TITLE OF INVENTION: MEMBRANE LIPOPROTEIN A AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 2; Length 34;
Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/515,251A
FILING DATE: 15-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/971,558
FILING DATE: 05-NOV-1992
ATIONE DATE: 05-NOV-1992
ATIONEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /label= silkl_repeat
US-08-317-8448-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, STITE 200
CITY: MENLO PARK
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0027.10
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
                                                                     REFERENCE/DOCKET NUMBER: 1447-105P
REPERENCE/DOCKET NUMBER: 1447-105P
TELEPHONE: (703) 241-1300
TELEPAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/08515251A; Patent No. 5891677; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 JAKANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL:
                                     NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: nephila clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.6%;
62.5%;
                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GSLQGQWRGAAGTAAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GGLGGGGAGAAAAA 19
                                                                                                                                                                                                                                        amino acid
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANGE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
                                              SOFERATION SIGNATION OF STATEMENT OF STATEMENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,177
FILING DATE: US/09/034,177
FILING DATE: WERWITH
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BILLINGS, LUCY J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0486 US
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FLING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 18992IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08348006B Patent No. 5658756 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: HAND, J., MARK
REGISTRATION NUMBER: 36,545
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 GGLGGQGAGAAAAA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LIBRARY: GenBank
; CLONE: GI 1174414
US-09-034-177-3
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STATE: NEW JERSEY
COUNTRY: USA
21P: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-348-006B-5
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                              Sequence 2, Application US/08317844B

Sequence 2, Application US/08317844B

Patent No. 598984

GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: AU, Ming
APPLICANT: AU, SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSES:
ATTORNEY/ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ATTORNEY/ADDRESSES:
ADDRESSES:
ADDRESSES:
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ADDRESSES:
ATTORNEY/ADDRESSES:
ADDRESSES:
ADDRE
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Pred. No. 67;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KESULT 10
US-09-034-177-3
Sequence 3, Application US/09034177
Patent No. 612746
GENERAL INFORMATION:
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharman CITY:
STREET: 3174 P.
CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MULPHY Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/COCKET UNMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 718 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62.53
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GSLQGQWRGAAGTAAA 16
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-317-844B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                     US-08-317-844B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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TELECOMMUNICATION INFORMATION:

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Sequence 5, Application US/09158657
Patent No. 6214564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GSLQGQWRGAAGTA 14
                                                                                                                                                                                                                                                                 CITY: RAHWAY
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-10166-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1911;
                                                                                                                                                                                                                              Pred. No. 3.9e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 2; Length 191
Pred. No. 3.9e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NEW JERSEY
COUNTRY: USA
ZITE: 07055-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: HAND, J. MARE
REGISTRATION NUMBER: 36,545
REFERENCE/COCKET NUMBER: 18992DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08800825AP Patent No. 5866397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
         TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           48.28;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 732-594-4720 INFORMATION FOR SEQ ID NO: 5:
                                                                  LENGTH: 1911 amino acids
                                                                                                                                                                                       Query Match
Best Local Similarity 57.10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
908-594-3905
908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-348-0068-5
                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-800-825A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GSLOGOWRGAAGTA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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US-08-800-825A-5
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Gaps
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APPLICANT: RODAN, GIDGON A
APPLICANT: ROTAL AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSE
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: ROLAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: WUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SECRENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: J. MARK HAND - MERCK & CO., INC
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36,545
ER: 18992DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1911 amino acids
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Gaps

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Length 759; 5; Indels

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Score 39; DB 2;
Pred. No. 2e+02;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: July 5, 2001, 11:47:01 Job time: 315 sec
| TELEPHONE: (512) 418-3000
| TELEFAX: (512) 474-7577
| INFORMATION FOR SEQ ID NO: 2:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 759 amino acids
| TYPE: amino acid
| STRANDEDNESS:
| TOPOLOGY: linear
| US-08-450-351-2
                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                   1 GSLOGOWRGAAGTA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08450351
Fatent No. 5981213
GENERAL INFORMATION:
APPLICANT: Hannen, Merja E.
APPLICANT: Helminen, Merja E.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO
TITLE OF INVENTION: USFPUL ANTIGENS OF MORAXELLA CATARRHALIS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 5; Length 1911;
Pred. No. 3.9e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10166
FILING DATE: 09-SEPT-1994
                                                                                                                                                                          FILING DATE: 09-SEPT-1994
CLASSIFICATION UNDEER: FULLOS94/10100
CLASSIFICATION 18
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35403
REFERENCE/DCCKET NUMBER: 18992
TELEPHONE: 908-594-4720
TELEPKX: 908-594-4720
TELEFX: 138825
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DGOKET NUMBER: AMCY:019
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/450,351
FILING DATE: 25-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| :| ||||
825 GSLLARWEPPAGTA 838
                       ZIP: 07065
COMPUTER READABLE FORM:
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77210
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                     07065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US94-10166-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-450-351-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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Thu Jul 5 13:58:38 2001

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July 5, 2001, 11:48:35; Search time 79.63 Seconds (without alignments) 15:306 Million cell updates/sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                 219241 seqs, 76174552 residues
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                           US-09-462-480-10
83
1 GSLQGQWRGAAGTAAA 16
                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                 Run on:
                                                                                                                                                                                               Title:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries pirl:\* pir2:\* pir3:\* pir4:\* PIR\_68:\* Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ľď			U	3C3.10 protein - S	melanocyte-specifi	probable ABC-type	hypothetical prote	adenylosuccinate l	probable adenylosu	probable fadE8 pro	hypothetical prote	11		transcription enha	transcription enha	probable ammonium	major ampullate fi	lactococcin Al pre	probable beta-1 -	methionyl-tRNA for	hypothetical prote	hypothetical prote	Ω	probable tryptopha	probable membrane	endo-1,4-beta-xyla	macrolide 3-0-acyl	hypothetical prote
SUMMARIES																														
SUM	T es	H70802	B70600	G70695	T35661	T10919	JC6113	D64833	F85619	C75033	H71135	A70826	A85217	T04441	139649	A40679	B40679	T03441	A36068	D49786	D70525	S23108	E85933	T30743	B83450	E72488	T02863	JC7578	40	G75393
	DB	7	7	7	7	~	7	~	7	~	7	7	7	7	7	7	~	7	~	~	7	~	~	~	~	~	~	٣	~	~
	Query Match Length	100	103	999	1186	124	203	255	255	450	450	542	179	277	367	206	523	533	718	69	294	315	315	361	381	427	528	1050	389	1443
ap	Query	95.2	57.8	53.0		٠		51.8			51.8				20.6	50.6	50.6	50.6	50.6	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4		48.8	48.8
	Score	79	48	44	44	43	43	43	43			43			42	42	42	42	42	41	41	41	41	41	41	41	41	41	40.5	
	Result No.	п	7	e	4	2	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

hypothetical prote	hyporhetical 14.6K hypothetical prote	hypothetical prote	WD-repeat family p	glyceraldehyde 3-p	hypothetical prote	nitrogenase (EC 1.	cytochrome-c oxida	cytochrome-c oxida	conserved hypothet	hypothetical prote	neurotoxin B-IV -	neurotoxin B-II -	cytochrome-c oxida	hypothetical prote
D86133	355573 T46295	T44896	D75470	H82245	G75423	B23874	C58888	S41837	T02857	C83339	NTHNB4	NTHNB2	S25424	G83348
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113	201	250	298	333	335	513	513	514	2241	5627	55	55	. 102	107
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8 4	48.2	48	48	48.2	48	48.2	48	48.2	48	48	47	47	47.0	47.0
0.4	4 4 0 4	40	40	40	40	40	40	40	40	40	39	39	39	39
30	37 32	33	34	35	36	37	38	36	40	41	42	43	44	45

# ALIGNMENTS

RESULT ò q

hypothetical protein Rv3905c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-du1-1998 #sequence\_revision 17-Ju1-1998 #text\_change 22-Oct-1999
C;Accession: B706c0
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon C;Connor, R.; Davies, R.; Pertwell, T.; Gentles, S.; Hanlin, N.; Holroyd, Raidnafream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-103 <COL> A;Residues: 1-103 <COL> A;Cross-references: GB:Z94121; GB:AL123456; NID:g3261736; PIDN:CAB08096.1; PID:e31227 A;Experimental source: strain H37Rv C;Genetics:

Matches

QΩ

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melanocyte-specific protein 1 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999
C; Accession: JG6113
R; Shioda, T:; Fenner, M.H.; Isselbacher, K.J.
Proc. Natl. Acad. Sci. U.S.A. 93, 12299-12303, 1996
A; Title: msgl, a novel melanocyte-specific gene, encodes a nuclear protein and is ass A; Reference number: JG6113; MUID:97057236
A; Accession: JG6113
A; Molecule type: mRNA
A; Residues: 1-203 <SHI>A; Residues: 1-203 <SHI>A; Cross-references: GB:U65091; NID:91854000; PIDN:AAC53048.1; PID:91854001
C; Comment: This protein is a nuclear protein whose expression is confined to pigmente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable ABC-type transport protein ycbE - Escherichia coli
C:Species: Escherichia coli
C:Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Feb-2001
C;Accession: D6483
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE000195; GB:U00096; NID:q1787156; PIDN:AAC74019.1; PID:q17871
                                                                                            Cispecies: Streptomyces coelicolor
Cispecies: Streptomyces coelicolor
Cispecies: Streptomyces coelicolor
Cispecies: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
Cispecession: T10919
A:Parkhill, J.: Barrell, B.G.: Rajandream, M.A.
Submitted to the EMBL Data Library, August 1998
A:Reference number: 217215
A:Accession: T10919
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-124 cPAR>
A:Cross-references: EMBL:AL031231; NID:e1315070; PID:e1315080
C:Genetics: 1-124 cPAR>
A:Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Mesidues: 1-255 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 203;
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16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 2;
Pred. No. 9.8;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 2
Pred. No. 16;
2; Mismatches
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70.0%;
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 LNSQYQGAAATAAA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LQGQWRGAAGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LQGQWRGAAG 12
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52 IQGGWQGAAG 61
                                                                             3C3.10 protein
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                                                                                                                                                                                                                                                                                                                                                                         C; Species: Mycobacterium tuberculosis

C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C; Accession: G70695

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Reference number: A70500; MUID:98295987

A; Accession: G70695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-666 <COL>
A;Residues: 1-666 <COL>
A;Cross-references: GB:Z80343; GB:AL123456; NID:g3261648; PIDN:CAB02458.1; PID:g1552862 A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable chromosome associated protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Dates 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Jun-2000
C;Accession: T35661
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, December 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molccule type: DDA
A;Residues; 1-1186 <AUC>
A;Residues: 1-1186 <AUC>
A;Cross-references: EMBL:AL034447; PIDN:CAA22420.1; GSPDB:GN00070; SCOEDB:SC7A1.21
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                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Rv37.79 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: Rv3779
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv3779
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0
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                                                                             Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 666;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Pred. No. 60;
0; Mismatches
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C;Superfamily: chromosome segregation protein SMC1
                                                                          DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB;
Pred. No. 34;
1; Mismatches
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                                                                                                                          Mismatches
                                                                          Score 48;
Pred. No.
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71.4%;
                                                                          57.8%;
57.1%;
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76.9%;
                                                                                                                            8; Conservative
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                                                                                                                                                                                                       | : | ||||:|:|
40 GQMLGGWRGASGSA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : [ | [ | [ | [ | ] | ] | ] | 231 EWRAAGAAGTAAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GSLOGOWRGAAGTA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: 221585
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Best Local Similarity
Matches 10; Conserv
                                                                       Query Match
Best Local Similarity
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Best Local Similarity
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A; Gene: Rv3905c
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δλ ΩD Matches

718

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δ

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Probable fadE8 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Daccession: A70826
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Parkhill, T.; Gentles, S.; Hanlin, N.; Holroyd, Rajandream, M.A.; Royers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70808; MulD:9829987
                                                                                                                                                                                                                                                                                                                                       R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se R; Kawarabayasi, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. S, S5-76, 1998
A; Title: Complete sequence and gene organization of the genome of a hyper-thermophili A; Reference number: A71000; MUID:98344137
A; Accession: H71135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29946.1; PID:g3257263
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa C;Genetics:
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A;Wolecule type: DNA
                                                                                                                                                                                       H71135
probable adenylosuccinate lyase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Date: H71135
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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34;
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0; Mismatches
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2; Mismatches
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64.3%;
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C;Superfamily: fumarate hydratase
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64.3%;
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Best Local Similarity 64.3
Matches 9; Conservative
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184 LVGKMRGAVGTAAS 197
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Best Local Similarity
'-hac 9; Conserve
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A;Molecule type: DNA
A;Residues: 1-255 <STO>
A;Cross-references: GB:AE005174; NID:g12514108; PIDN:AAG55418.1; GSPDB:GN00145; UWGP:Z1Z
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
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K.; Apodaca,
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A;Experimental source: strain K-12, substrain MG1655 C;Genetics:
C;Genetics:
A;Gene: yobE
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop; transport protein
F;27-209/Domain: ATP-binding cassette homology <ABC>
F;44-51/Region: nucleotide-binding motif A (P-loop)
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submitted to the EMBL Data Library, July 1999
A; Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
A; Reference number: A75001
A; Accession: C75033
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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Pred. No. 20;
1; Mismatches 4; Indels
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Pred. No. 34;
2; Mismatches
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Pred. No. 20;
1; Mismatches
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64.3%;
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C;Superfamily: fumarate hydratase
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Best Local Similarity 64.3
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Best Local Similarity 64.3
Matches 9; Conservative
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105 LKGQWRDAARRALA 118
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Best Local Similarity
Matches 9; Conserv
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-361, KEDK', 366 <RE2>
A;Cross-references: GB:D28491; NID:9808858; PIDN:BAA05852.1; PID:9808859
C;Genetics:
A;Gene: omlA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5, 2001, 11:48:35
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Best Local Similarity 55.0°
Matches 11; Conservative
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A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-506 <TAN>
                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                SLOGOWRGAAGTAA 15
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Best Local Similarity
Matches 6; Conserv
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Job time: 374 sec
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              C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
A;Accession: A88217
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold SprinNature 402, 769-777, 1999
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C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 17-Nov-2000
C;Accession: 139649; 139518; 552740
R;Bunka, S.; Christensen, C.; Potter, A.A.; Willson, P.J.; Gerlach, G.F.
Infect. Immun. 63, 2797-2800, 1995
A;Title: Cloning and characterization of a protective outer membrane lipoprotein of Acti
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A; Residues: 1-367 <RES>
A; Cross-references: EMBL: 248920; NID: 9757528; PIDN: CAA88756.1; PID: 9757529
R; Ito, H.; Uchida, I:; Sexizaki, T.; Ooishi, E.; Kawai, T.; Okabe, T.; Taneno, A.; Terak
Microb. Pathog. 18, 29-36, 1995
A; Title: Molecular cloning of an Actinobacillus pleuropneumoniae outer membrane lipoprot
A; Reference number: 139518; MUID: 95302932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the Protein Sequence Database, April 1998
A.Reference number: 213359
A.Reference number: 214441
                                                                                                A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488
A;Accession: A85217
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A;Cross-references: GB:NC_001268; NID:g7268715; PIDN:CAB78922.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4919200
A;Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T18B16.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C;Accession: T04441
R;Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Bancroft, I.
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A; Residues: 1-277 < CBEV>
A; Residues: 1-277 < CBEV>
A; Cross-references: EMBL:AL021687
A; Experimental source: cultivar Columbia; BAC clone T18B16
C; Genetics:
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A;Accession: 139649
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred No. 30;
0; Atsmatches
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Pred. No.
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A; Note: T18B16.170
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62.5%;
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Best Local Similarity 62.5
Matches 10; Conservative
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C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000 C;Accession: A40679 R;Tanimura, A.; Teshima, H.; Fujisawa, J.; Yoshida, M. Virol. 67, 5375-5382, 1993 A;Title: A new regulatory element that augments the Tax-dependent enhancer of human T A;Reference number: A40679; MUID:93353614
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                                                                                                                                                                                                                                                                                                     transcription enhancer regulatory element TRE-2S, splice form 1 - human T-ca
N.Alternate names: transcription holding protein 1 (THP-1)
C.Species: human T-cell lymphotropic virus type 1, HTLV-1
C.Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:D14827; NID:g439899; PIDN:BAA03568.1; PID:g488506
A;Experimental source: HUT102 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:136287, NCBIP:136288)
C;Superfamily: g1; transforming protein
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DB 2;
39;
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55.0%; Pred. No. 54;
ive 0; Mismatches
                                                      Mismatches
Score 42;
Pred. No.
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50.6%;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 5, 2001, 11:51:44; Search time 41.8 Seconds (Without alignments) 13.112 Million cell updates/sec Run on:

US-09-462-480-10 83 1 GSLQGQWRGAAGTAAA 16 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 segs, 34255486 residues Searched: 93435

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

· SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		P33682 streptomyce	_						Q9y8t5 aeropyrum p	_	-			P01526 cerebratulu	P01525 cerebratulu	P24984 coturnix co				archaec		Q33820 asterina pe	escheri	ednine	equine	eduine	ednj	anw snw	027600 methanobact	Q59579 methanobact	074031 methanobact	P52946 mus musculu	16	Q28479 macaca fasc
SUMMARIES		GUN1_STRHA	MSG1_MOUSE		PUR8_PYRAB	PUR8_PYRHO	SPD1_NEPCL	FMT_ECOLI	TRB1_AERPE	YJIW_ECOLI	COX1_ORNAN	NIFK_BRASP	COX1_HALGR	NXB2_CERLA	NXB4_CERLA	COX1_COTJA	YM19_MYCTU	FMT_HAEIN	NFIX_CHICK	PUR8_ARCFU	COX1_CHICK	COX1_ASTPE	MALT_ECOLI	VGLB_HSVEL	VGLB_HSVE1	VGLB_HSVEA	VGLB-HSVEB	GDF9_MOUSE	FWDC_METTH	FWDC_METIM	FWDC_METWO	IPF1_MOUSE	FMT_MYCTU	IDHB_MACFA
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IDHB_HUMAN BACE_HUMAN	BACE_MOUSE BACE_RAT	NIFK_BRAJA	ACEA_ARATH	SRC2_DROME	YA42_MYCPN	GELS_HORSE	Y355_HUMAN	PHR_THETH	NEF_HV2KR
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38 38	38 38	38	38	38	38	38	38	37.5	37
34 35	36 37	38	38	40	41	42	43	44	45

# ALIGNMENTS

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InterPro; IPR001617; -.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      STRAIN=K12;
PubMed=10506196;
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CBP/P300-INTERACTING TRANSACTIVATOR 1 (MELANOCYTE-SPECIFIC PROTEIN 1).
                                                                                                                                                                                                                                                                                     MEDLINE-9707236; PubMed-8901575; Shioda T., Fenner M.H., Isselbacher K.J.; Shioda T., Fenner M.H., Isselbacher K.J.; Shioda T., Fenner M.H., Isselbacher K.J.; a novel melanocyte-specific gene, encodes a nuclear protein and is associated with pigmentation."; Proc. Natl. Acad. Sci. U.S.A. 93:12298-12303(1996).
-!- FUNCTION: NOT KNOWN, SEEMS TO BE ASSOCIATED WITH PIGMENTATION.
-!- SUBCELLULAR LOCATION: UNCLEAR.
-!- TISSUE SPECIFICITY: EXPRESSED ONLY IN MELANOCYTES AND TESTIS.
EXPRESSED AT HIGH LEVELS IN THE STRONGLY PIGMENTED MELANOMA CELLS BUT AT LOW LEVELS IN THE WEAKLY PICHARITY: BELONGS TO THE CITED FAMILY.
                                    Gaps
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                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1994 (Rel. 30, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-2000 (Rel. 40, Last annotation update)
PUTATIVE ALIPHATIC SULPONATES TRANSPORT ATP-BINDING PROTEIN SSUB.
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Escherichia.
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            Length 321;
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BE968A5182873003 CRC64;
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            Score 44; DB Dred. No. 8.1; O; Mismatches
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64.3%;
          53.0%;
72.7%;
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          Query Match 53.0
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                       203 AA;
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Best Local Similarity
Matches 9; Conserv
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P38053; P75850;
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P97769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van der Ploeg J.R., Iwanicka-Nowicka R., Bykowski T., Hryniewicz M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Escherichia coli ssuEADCB gene cluster is required for the utilization of sulfur from aliphatic sulfonates and is regulated by the transcriptional activator Cbl.";
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattiner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
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                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 274:29358-29365(1999).
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EMBL, D90732; BAA35688.1; --
EMBL, AJ237695; CAB40393.1; --
EMBL, M15273; --; NOT_ANNOTATED_CDS.
HSSP; P13569; INBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87163509; PubMed-3549459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000195; AAC74019.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 3:137-155(1996).
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InterPro; IPR001617; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.";
Gene 48:145-153(1986).
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SPD1_NEPCL
P19837;
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                              FUMARATE + AMP).
PATHWAY: EIGHT STEP IN DE NOVO PURINE BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE LYASE I FAMILY. ADENYLOSSUCINATE LYASE
SUBFAMILY.
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                             IMIDAZOLECARBOXAMIDE (ALSO CATALYZES: N6-(1,2-DICARBOXYETHYL)AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                 Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=29292;
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                                                                                                                                                                                                   01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
ADENYLOSUCCINATE LYASE (EC 4.3.2.2) (ADENYLOSUCCINASE) (ASL)
                                                                                Score 43; DB 1; Length 255; Pred. No. 9.3; 4; Indels
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                   ATP (POTENTIAL).

GALDA -> RGAGR (IN REF. 4).

EL -> DV (IN REF. 4).

EV -> RS (IN REF. 4).

6FA276AD6E7FACE1 CRC64;
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BASE (BY SIMILARITY).
; 82A3C0131455CDBD CRC64;
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Pred. No. 16;
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PS00211; ABC_TRANSPORTER; 1.
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                                                       27738 MW;
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                                                                                                   Conservative
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                                                                                                                                                                                    STANDARD;
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          ATP-binding; Transport;
NP_BIND 44 51
                                                                                                                                     105 LKGOWRDAARRALA 118
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184 LVGKMRGAVGTAAS 197
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165
233
237
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Best Local Similarity
'-has 9; Conserve
                                                                       Query Match
Best Local Similarity
Lang 9; Conserve
                                                                                                                    LOGOWRGAAGTAAA
                                                      255 AA;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          PURB OR PAB0829
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Q9UZ99;
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ID PUR8_PYRHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA RES. 5:55-76(1998).
-!- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-4-(N-SUCCINO-CARBOXAMIDE)
-!- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-4-(N-SUCCINO-CARBOXAMIDE)
-5-AMINOIMIDAZOLE = FUNARATE + 5'-PHOSPHORIBOSYL-5-AMINO-4-
IMIDAZOLECARBOXAMIDE (ALSO CATALYZES: N6-(1,2-DICARBOXYETHYL)AMP =
                                                                                                                                                                                                                                                                                                                                                                                                                Kawarabayaai Y., Kawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamanoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii 073.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: EIGHT STEP IN DE NOVO PURINE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE LYASE I FAMILY. ADENYLOSSUCINATE LYASE
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                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID-53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ADENYLOSUCCINATE LYASE (EC 4.3.2.2) (ADENYLOSUCCINASE) (ASL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.8%; Score 43; DB 1; Length 450; 64.3%; Pred. No. 16;
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BASE (BY SIMILARITY).
A700A652ADB822BC CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).
Nephila clavipes (Orb spider).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            747 AA.
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InterPro; IPR000362; -
InterPro; IPR003031; -.
Pfam; PR00145; PR00145; PRNYS; PR00145; PURARATELIN.
PRINTS; PR00149; FUMRATELINE.
PROSITE; PS00163; FUMARATE_LYASES; 1.
PUTING biosynthesis; Lyase.
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98344137; PubMed=9679194;
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184 LVGKMRGAVGTAAS 197
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                                                                                                                                                                                 Pyrococcus horikoshii.
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
15-JUL-1999 (Rel.
15-JUL-1999 (Rel.
30-MAY-2000 (Rel.
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MEDLINE-97042366; PubMed-8887566; Schmitt E., Blanquet S., Mechulam Y.; Schmitture of crystalline Escherichia coli methionyl-tRNA(f)Met formyltransferase: comparison with glycinamide ribonucleotide formyltransferase.";
                                     FMT_ECOLI
                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 653-747 FROM N.A.
MEDLINE-94165058; PubMed-8120021;
MEDLINE-94165058; PubMed-8120021;
MEDLINE-94165058; PubMed-8120021;
MEGHER R., Arcidiacono S.;
"Sequence conservation in the C-terminal region of spider silk proteins (Spidroin) from Nephila clavipes (Tetragnathidae) and Araneus bleentenarius (Araneidae).";
J. Biol. Chem. 269:6661-6663(1994).
-!- FUNCTION: THIS SPIDER MAJOR AMPULLATE SILK POSSESSES UNIQUE CHARACTERISTICS OF STREWGTH AND ELASTICITY. IT MAY CONSIST OF PSEUDOCRISTALINE REGIONS OF ANTIPARALLEL BETA-SHEET INTERSPERSED WITH ELASTIC AMORPHOUS SEGMENTS.
-!- SUBUNIT: MAJOR SUBUNIT, WITH SPIDROIN 2, OF THE DRAGLINE SILK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQIVGQSVYQAL -> ILVFLDVMSSFKLFSRLFLLLSRS
                                                                                                                                                                                                                                                                                                           X APPROXIMATE TANDEM REPEATS.
                         structure or a protein superfiber: spider dragline silk."; Proc. Natl. Acad. Sci. U.S.A. 87:7120-7124(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N REF. 1).
850E44B0D649E012 CRC64;
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Pred. No. 35;
0; Msmatches
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90384959; PubMed-2402494;
                                                                                                                                                                   SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60528 MW;
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62.5%;
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                  Xu M., Lewis R.V.; "Structure of a pr
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Best Local Simil
Matches 10; C
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FMT_ECOLI STANDARD; PRT; 314 AA. P23882; P77040; 01-NOV-1991 (Rel. 20, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9)
100 GGLGGQGAGAAAAA 115
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MEDLINE-02325012; Pubmed-1624424; MEDLINE-02325012; Payat G.; Gulllon J.-M., Mechulam Y., Schmitter J.-M., Blanquet S., Fayat G.; Discription of the gene for Met-tRNA(fMet) formyltransferase severely impairs growth of Escherichia coll."; J. Bacteriol. 174:4294-4301(1992). SEQUENCE FROM N.A.
STRAIN-KIZ. / MG1657.
STRAIN-KIZ. / MG167.
STRAIN-KIZ. / MG167.
SIRAIN-KIZ. / MG167.
SIRAIN-KIZ. / MG167.
SIRAIN-F-9742617.
SIRAIN-F-9742617.
SIRAIN-F-9742617.
SIRAIN-F-7.
SIRAIN-PRELIMINARY SEQUENCE OF 81-161 FROM N.A.
MEDLINE-84272255; PubMed=6379605;
Meek D.W., Hayward R.S.;
Mucleotide sequence of the rpoA-rplQ DNA of Escherichia coli: a second requlatory binding site for protein S47";
Nucleic Acids Res. 12:5813-5821(1984). Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia. Meinnel T., Guillon J.-M., Mechulam Y., Blanquet S.;
"The Escherichia coli fint gene, encoding methionyl-tRNA(fMet)
[formyltransferase, escapes metabolic control.";
J. Bacteriol. 175:993-1000(1993). Mazel D., Coic E., Blanchard S., Saurin W., Marliere P.; "A survey of polypeptide deformylase function throughout the eubacterial lineage."; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997). SEQUENCE FROM N.A., AND PARTIAL SEQUENCE X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). MEDLINE=97240812; PubMed=9086272; STRAIN-K12 / K37; MEDLINE-93163064; PubMed-8432722; Mol. Biol. 266:939-949(1997). SEQUENCE OF 160-314 FROM N.A. STRAIN-K12 / MG1655; SEQUENCE FROM N.A. STRAIN-K12 / K37; Escherichia coli. NCBI\_TaxID=562;

METHIONYL-TRNA(FMET). THE FORMYL GROUP APPEARS TO PLAY A DUAL ROLE IN THE INITIATOR IDENTITY OF N-FORMYLMETHIONYL-TRNA BY: (I) PROMOTING ITS RECOGNITION BY IF2 AND (II) IMPAIRING ITS BINDING TO EMBO J. 15:4749-4758(1996).
-!- FUNCTION: MODIFY THE FREE AMINO GROUP OF THE AMINOACYL MOIETY OF METHIONYL-TRNA(FMET). THE FORMYL GROUP APPEARS TO PLAY A DUAL ROI IN THE INITIATOR IDENTITY OF N-FORMYLMETHIONYL-TRNA BY: (1) EFTU-GTP

; 0

Gaps

; 0

Indels

..

.; 0

Conservative

Similarity

GSLQGQWRGAAGTAAA 16

CATALYTIC ACTIVITY: 10-FORMYLTETRAHYDROFOLATE + L-METHIONYL-TRNA + H(2)0 = TETRAHYDROFOLATE + N-FORMYLMETHIONYL-TRNA. SUBUNIT: MONOMER. +

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YJIW_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
           DOMAIN CARRIES THE TETRAHYDROFOLATE (THF)-BINDING SITE AND THE C-FERMINAL DOMAIN IS PRESUMBLY INVOLVED IN POSITIONING THE MET-TRNA SUBSTRATE FOR THE FORMYLATION REACTION.
SIMILARITY: BELONGS TO THE FMT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-!- FUNCTION: THE BETA SUBUNIT IS RESPONSIBLE FOR THE SYNTHESIS OF L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99310339; PubMed-10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K. II., Kubota K.,
Makamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                         Pfan, PF00551; formyl_transf; 1.
PROSITE; PS00373; GART; 1.
Transferase; Methyltransferase; Protein biosynthesis; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 314;
Pred. No. 23;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      TETRAHYDROFOLATE (THF).
83D8AE62B616A1C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            N-TERMINAL DOMAIN.
C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) TRYPTOPHAN SYNTHASE BETA CHAIN 1 (EC 4.2.1.20)
 DOMAIN: COMPOSED OF AN N-AND A C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                           EMBL; X63666; CAA45207.1; -.
EMBL; X00767; CAA25339.1; ALT_SEQ.
                                                                                                                                                                                                               EMBL; U18997; AAAS8085.1; --
EMBL; X10307; CAA71358.1; --
EMBL; AE000407; AAC76313.1; --
PIR; S23108; S23108
PDB; IFWT; 28-JAN-98
SWISS-2DPAGE; P23882; COLI
                                                                                                                                                                                                                                                                                           SCO2DBASE; F033.6; 6TH EDITION. ScoGene; EG11268; fmt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                   34037 MW;
                                                                                                                                                                                        EMBL; X00767; CAA25339.1; ALT
EMBL; X77091; CAA54368.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.4%;
ilarity 72.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                    interPro; IPR001555;
InterPro; IPR002376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 GSLLPRWRGAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                  314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GSLOGOWRGAA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRPB1 OR APE2548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                                          209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRB1_AERPE
Q9Y8T5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                  INIT_MET
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                                                                                          OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRB1_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
-!- CATALYTIC ACTIVITY: L-SERINE + 1-(INDOL-3-YL)GLYCEROL 3-PHOSPHATE = L-TRYPYOPHAN + GIYCERALDEHYDE 3-PHOSPHATE + H(2)O.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- PATHWAY: LAST (FIFWH) STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 14.6 KDA PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRU01920; -.
Promise Target Synthase BETA; 1.
PROSTE; PS00166; TRP_SYNTHASE_BETA; 1.
PROSTE; PS00166; TRP_SYNTHASE_BETA; 1.
Tryptophan biosynthesis; Pyridoxal phosphate; Lyase.
Tryptophan biosynthesis; Pyridoxal phosphate (BY SIMILARITY).
BINDING 107 DAR: 45992 MW; DC8E165B40B65750 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blattner F.R.;
Analysis of the Escherichia coli genome VI: DNA sequence of the "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 427; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-K12 / MG165;
MEDLINE-95334362; Pubmed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14576 MW; 3E53097CD17B0C62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 AA.
                                                                                                                                                                                  SIMILARITY). SIMILARITY: BELONGS TO THE TRPB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP000064; BAA81565.1; -. InterPro; IPR001926; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U14003; AAA97244.1; -. EMBL; AE000505; AAC77303.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EcoGene; EG12584; yjiW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 GOWGLAASTAAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GOWRGAAGTAAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein SEQUENCE 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
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Query Match
Best Local S
Matches 8
                                                                                                                                                                                                               RESULT 11
NIFK_BRASP
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                                                                                                                                          q
                                                                                                                                                                                                                                                                   NO WEN BY A COURT OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The mitochondrial genome of a monotreme -- the platypus (Ornithoriyyoukus anathinus).";

(Ornithoriyyoukus anathinus).";

J. Mol. 42:153-159(1996).

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYEGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 FERRICYTOCHROME C.
-!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
-!- INNER MEMBRANE. CONTAINS 12, EDTENTIAL TRANSMEMBRANE DOMAINS.
-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; 1.
Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Janke A., Gemmell N., Feldmaier-Fuchs G., von Haeseler A., Paabo S.;
DB 1; Length 132;
15;
                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRON (HEME A) (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HEME A3) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ON (HEME A) (PROBABLE).
BC8758C005810841 CRC64;
                                                                                                                                                                                                                                                                                                   01-NOY-1997 (Rel. 35, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
MTCO1 OR COI OR COXI.
Ornithorhynchus anatinus (Duckbill platypus).
Score 40; DB
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Respiratory chain; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Heart, and Liver; MEDLINE-97077300; PubMed-8919867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56742 MW;
48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X83427; CAA58457.1; -.
                                                 Conservative
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000883; -.
InterPro; IPR002428; -.
Pfam; PF00115; COX1; 1.
                                                                                         2 SLQGQWRGAAGTA 14
                                                                                                                                          60 TLKGOWLEAAGFA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290
291
376
378
513 AA;
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P98002;
                                                                                                                                                                                                                                                            COX1_ORNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
SEQUENCE
                                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
NCBL_TaxID=377;
                                          ö
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                                                                                                                                                                                                                                                  01-57N-1988 (Rel. 06, Created)
01-5AN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NITROGENASE MOLYBDENUM-IRON PROTEIN BETA CHAIN (EC 1.18.6.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000318; -.
InterPro; IPR000510; -.
InterPro; IPR000510; -.
InterPro; IPR00048; oxidored_nitro; 1.
PROSITE; PS00090; NITROGENASE_1_2; 1.
PROSITE; PS00699; NITROGENASE_1_1; 1.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1; Length 513;
Pred. No. 50;
1; Mismatches 5; Indels
        Length 513;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  741373586CDD8A36 CRC64;
        DB 1;
                                                                                                                                                                                                                    513 AA
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                 (NITROGENASE COMPONENT I) (DINITROGENASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514
    Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobium sp. (strain ANU 289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56538 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COX1_HALGR STANDARD; E
1D COX1_HALGR STANDARD; E
AC P38595;
DT 01-0CT-1994 (Rel. 30, Created)
48.2%;
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Best Local Similarity 57.1
Matches 8; Conservative
                                          Conservative
                                                                                                                                                                                                                    STANDARD;
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                                                                                                             21 LFGAWAGMAGTA 32
                                                                                3 LOGOWRGAAGTA 14
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              Similarity
8; Conserve
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                                                                                                                                                                                                                  NIFK_BRASP
P06122;
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Amino

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Blumenthal K.M., Kem W.R.; "Structure and action of heteronemertine polypeptide toxins. Primary structure and action of heteronemertine primary structure of Gerebratulus lacteus toxin B-IV."; J. Biol. Chem. 251:6025-6029(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Howell M.L., Blumenthal K.M.;
"Mutagenesis of Cerebratulus lacteus neurotoxin B-IV identifies NH2-
terminal sequences important for biological activity.";
J. Biol. Chem. 266:12884-12888(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND REVISIONS.

MEDLINE-81264350; PubMed-7263698;
Blumenthal R.M., Keim P.S., Heinrikson R.L., Kem W.R.;
Structure and action of heteronemertine polypeptide toxins. Amino acid sequence of Cerebratulus lacteus toxin B-II and revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR. MEDLINE-93076792; Pubmed=1332861; Hansen P.E., Kem W.R., Bieber A.L., Norton R.S.; "IH-NMR study of neurotoxin B-1V from the marine worm Cerebratulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa; Nemertea; Anopla; Heteronemertea; Cerebratulus
                                                                                       Eukaryota; Metazoa; Nemertea; Anopla; Heteronemertea; Cerebratulus.
                                                                                                                                                                                      Blumenthal K.M., Keim P.S., Heinrikson R.L., Kem W.R.;
"Structure and action of heteronemertine polypeptide toxins.
acid sequence of Cerebratulus lacteus toxin B-II and revised
structure of toxin B-IV.";
J. Biol. Chem. 256:9063-9067(1981).
--- SIMILARITY: TO NEUROTOXIN B-IV.
HSSP; P01525; IVIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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0918C1D1FB2PA904 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
    01, Last sequence update)
19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.5;
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1; Mismatches
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                                                                     WOTIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39;
Pred. No.
                                                                 (Milky ribbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structure of toxin B-IV.";
J. Biol. Chem. 256:9063-9067(1981)
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MEDLINE=91302300; PubMed=2071577;
                                                                                                                                                                     MEDLINE=81264350; PubMed=7263698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=77006160; PubMed=972152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6028 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 47.0
Best Local Similarity 53.8
Matches 7; Conservative
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                                                                   Cerebratulus lacteus
                                                                                                                                                                                                                                                                                                                                                            Toxin; Hydroxylation MOD_RES 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 QGQWRGAAGTAAA
    21-JUL-1986 (Rel. 01-AUG-1991 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6221;
                                             NEUROTOXIN B-II
                                                                                                        NCBI_TaxID=6221;
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P01525;
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                               Arnason U., Gullberg A., Johnsson E., Ledje C.;
Arnason U., Gullberg A., Johnsson E., Ledje C.;
"The nuclectide sequence of the mitochondial DNA molecule of the
grey seal, Halichoerus grypus, and a comparison with mitochondial
sequences of other true seals.";
J. Mol. Evol. 37:323-330(1993).
-! FUNCTION EVYOCHROWE COXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBGNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CATALYTIC SUBUNIT OF THE ENXYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BINETALLIC CENTER FORMED BY HEME AS
AND COPPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 FERRICYTOCHROME C.
PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN: MITOCHONDRIAL
INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; 1.
Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 514;
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COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME A3) (PROBABLE).
IRON (HEME A) (PROBABLE).
37. 2A40DS5A0140F233 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40;
Pred. No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-94141933; PubMed-8308902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
NXB2_CERLA STANDARD; F
AC PO1526;
DT 21-JUL-1986 (Rel. 01, Created)
                                                                                    Halichoerus grypus (Gray seal)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X72004; CAA50879.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000883; -. InterPro; IPR002428; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00115; COX1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LOGOWRGAAGTA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514 AA;
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les 8; Conser
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                                                                                                                                                                   NCBI_TaxID-9711;
                                                                                                        Mitochondrion
                                                               MTCO1 OR COI.
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SEQUENCE

**TETAL** (ETAL Query Match

Matches

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Gaps

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INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS. SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                           EMBL; U36794; AAA76729.1; -.
PIR; S25424, S25424.
HSP; P00396; 120C.
InterPro; IPR000883; -.
Pfam; PF00115; COX1; 1.
PROSITE; PS00077; COX1; DARTIAL.
Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
Respiratory chain; Inner membrane.
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                                                                                                                                                                                              EMBL; X57246; CAA40524.1; -.
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Best Local Similarity
Matches 7; Conserv
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Job time: 503 sec
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SEQUENCE
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Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

-- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-

3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE

CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CYTOCHROME C ARE TRANSFERED VIA THE COPPER A CENTER OF SUBUNIT 2

AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
                                                                                  MEDLINE-97324210; Pubmed-9180379;
Barnham K.J., Dyke T.R., Kem W.R., Norton R.S.;
Barnham K.J., Dyke T.R., Kem W.R., Norton R.S.;
Barnham K.J.
Structure of neurotoxin B-IV from the marine worn Cerebratulus
lacteus: a helical hairpin cross-linked by disulphide bonding.";
J. Mol. Biol. 268:886-902(1997).
-i- FUNCTION: ONLY ACTS ON SOME CRUSTACEAN. INCREASE THE EXCITABILITY
OF NERVES PROBABLY BY AFFECTING THE INACTIVATION OF THE VOLTAGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desjarding P., Morais R.;
"Nucleotide sequence and evolution of coding and noncoding regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 FERRICYTOCHROME C.
PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
1-COT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENTS).
lacteus. Solution properties, sequence-specific resonance assignments, secondary structure and global fold."; Eur. J. Biochem. 210:231-240(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                          BB76B72E48DB050D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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Coturnix coturnix japonica (Japanese quail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 9.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA
                                                                                                                                                                                                                                                                                                    HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39;
                                                                                                                                                                                                           GATED SODIUM CHANNEL.
SIMILARITY: TO NEUROTOXIN B-II.
A01788; NTHNB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                PDB; 1VIB; 15-MAY-97.
Toxin; Hydroxylation; 3D-structur
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MEDLINE-91178819; PubMed-1706782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a quail mitochondrial genome.";
J. Mol. Evol. 32:153-161(1991).
[2]
SEQUENCE OF 103-156 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            47.0%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                          6107 MW;
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Best Local Similarity 53.00
Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 QGQWRGAAGTAAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OGKWAGKRGKCAA 39
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P24984;
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DISULFID
DISULFID
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DISULFID
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                                                                                                                                                                                                                                               PIR;
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Gaps

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Score 39; DB 1; Length 156; Pred. No. 24;.

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IRON (HEME A) (PROBABLE).

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OM protein - protein search, using sw model

July . 5, 2001, 11:50:50; Search time 123.78 Seconds (without alignments) 17.102 Million cell updates/sec Run on:

US-09-462-480-10 83 1 GSLQGQWRGAAGTAAA 16 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

425026 segs, 132305027 residues Searched:

425026 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_16:\* Database :

sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_fungi:\*
sp\_human:\*
sp\_nammal:\*
sp\_mammal:\* sp\_unclassified:\*
sp\_vertebrate:\*
sp\_virus:\* sp\_organelle:\*
sp\_phage:\*
sp\_plant:\*
sp\_rodent:\*

Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Description	O69739 mycobacteri	005440 mycobacteri	086441 pseudomonas	Q9xsr3 canis famil	Q9ewv9 streptomyce	Q9fts8 oryza sativ	P72045 mycobacteri	Q9zbq2 streptomyce	086643 streptomyce	Q9z1s6 rattus norv	Q910q5 streptomyce	Q9x7h6 paracoccus	088676 mus musculu	O86368 mycobacteri	Q9m0l8 arabidopsis	049678 arabidopsis	Q44163 actinobacil	Q44164 actinobacil	Q9zap9 actinobacil
	1	ID	069739	005440	086441	Q9XSR3	Q9EWV9	Q9FTS8	P72045	Q9ZBQ2	086643	Q921S6	Q9L0Q5	9н2х60	088676	086368	O9MOL8	049678	044163	044164	Q9ZAP9
		DB	7	7	7	9	7	10	7	~	7	11	7	7	11	Ċ	10	10	~	~	~
		Match Length DB	100	103	128	592	291	485	999	1186	124	203	314	331	391	542	179	277	366	367	367
æ	Query	Match	95.2	57.8	9.95	26.6	54.2	53.0	53.0	53.0	51.8	51.8	51.8	51.8	51.8	51.8	50.6	50.6	20.6	20.6	50.6
	·	score	79	48	47	47	45	44	44	44	43	43	43	43	43	43	42	42	42	42	42
	Result	S	1	7	e	7	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19

Q9rihB actinobacil Q9rcg3 actinobacil Q95932 homo sapien Q911MO Oryza sativ	oryza nephila nephila oryza nacaca	Q9xej9 dendroblum Q42394 gallus gall O79121 diastylis r Q9xm88 eudorella p O9xm87 campylassis		
Q9RIH8 Q9RCG3 Q9S932 0 Q9LIW0	10 004400 5 046171 5 046172 10 Q9XIXS 6 Q9N0B6	10 Q9XEJ9 13 O42394 8 O79121 Q9XM88 8 O9XM8		2 Q913E5 10 Q9SNH4 8 Q990A0 5 Q60978 11 Q88881
				513 8 513 8 528 8 605 1
500.0 500.0 500.0		4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4	
4444	4 4 4 4 2 2 2 2 1	4 4 4 4 4 1 1 1 1 1 1	44444 11111	· <del>4 4 4 4 4</del>
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# ALIGNMENTS

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RESULT 005440

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Gaps
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Actinomycetales; Streptomycineae; Streptomyces.
OCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pichon B., Mercan D., Poulllon V., Christophe-Hobertus C.,
Christophe D.;
                             Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Length 592;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
[3]
                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ388555; CAB46854.1; -- HSSP; P09651; 1HA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5952B93616CBE4E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 63.5 KDA PROTEIN.
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Last sequence update)
Last annotation update)
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                             DB 2;
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                                                                             Mismatches
                          Score 47;
Pred. No. 5
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Pfam; PRO0076; rrm; 3.
PROSTTE; PS00030; RNP_1; UNKNOWN_2.
SMART; SM00360; RNP; 1.
HYPOCHACICAL POCTEIN.
SEQUENCE 592 AA; 63523 MW. 5957
                                                                                                                                                                                                                                                                                                               PRT;
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                          56.6%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.0
Matches 9; Conservative
                                                                             Conservative
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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379 GSIRGRGRGAAGSRA 393
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Seeger K.J., Harris D.;
                                                                                                                              5 GOWRGAAGTAA 15
                                                                                                                                                         11111 1 111
38 GQWRGLAQTAA 48
                                                Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                          Query Match
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MEDLINE-98295987; PubMed-9634230;
MEDLINE-98295987; PubMed-9634230;
MEDLINE-98295987; PubMed-9634230;
MEDLINE-98295987; PubMed-9634230;
MEDLINE-98295987; PubMed-9634230;
Gordon S.V., Eiglmeier K., Parkhill J., Garnier T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Deviln K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Seeger K., Skelton S., Squares S., Sqares T., Sulston J.E.,
Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Mature 393:537-544(198).
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                                                        Gaps
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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Pseudomonas.
95.2%; Score 79; DB 2; Length 100; 100.0%; Pred. No. 6.1e-05;
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                                                   0; Indels
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de Groot A., Gerritse G., Lazdunski A., Filloux A.;
de Groot A., Gerritse G., Lazdunski A., Filloux A.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; X81085; CAS56987.1; -.
SEGUENCE 128 AA; 14154 MW; A32A79E69EAB6F18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 AA; 10460 MW; 3994E272A7BDFF02 CRC64;
                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 10.5 KDA PROTEIN.
RV3905C OR MTCX15F10.06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                    103 AA.
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                                                   Mismatches
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Pred. No. 3
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                                                                                                                                                                                                                                                                                       PRT;
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     95.20,
100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                   Conservative
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                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                1 GSLOGOWRGAAGTAA 15
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40 GQMLGGWRGASGSA 53
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                                                                                                                              Best Local Similarity
Matches 15; Conserv
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SEQUENCE FROM N.A.
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Best Local Similarity
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Query Match
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086441

RESULT 086441

Matches

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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map it the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
Mol. Microbiol. 21:77-96(1996).
InterPro: IPR001066;
InterPro: IPR001068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1902;
Submitted (SEP-1996) to the EMBL/Genbank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
EMBL; 280343; CAB02458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                         071B932A1BDC9BB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculist; Rv3779; -.
Interpro; IPR001064; -.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
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Pred. No. 81;
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TRANSMEM 1 21 POTENTIAL.
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                         71794 MW;
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76.9%;
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Pfam; PF02483; SMC_C; 1.
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428
460
493
666 AA;
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Best Local Similarity
Matches 10; Conserv
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                                                       Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinsshi H., Hopwood D.A.;
"A set of ordered cosmids and agetailed genetic and physical map for the B Mb Streptomyces coelicolor [3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL: AL512667; CAC21623.1;
                                                                                                                                                                                                                                                                                                     Gaps
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Noryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0409B08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 10; Length 485;
Pred, No. 59;
                                                                                                                                                                                                                                                          Length 291;
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                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002860; BAB18282.1; -- SEQUENCE 485 Aa; 50477 MW; 091B5D3AF14DF5FA CRC64;
                                                                                                                                                                                                291 AA; 30545 MW; 7C98648485F87C6F CRC64;
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Murphy L., Harris D., Barrell B.G., Rajandream M.A.;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 71.8 KDA PROTEIN CY13D12.13.
RV3779 OR MTCY13D12.13.
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Last annotation update)
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                                                                                                                                                                                                                                                          Score 45; DB
Pred. No. 25;
1; Mismatches
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                            STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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53.3%;
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Best Local Similarity 66.7%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.0
Best Local Similarity 53.3
Matches 8; Conservative
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284 GGLRAEWRGRAMTTA 298
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216 GRWRGAGGDPAA 227
                                                                                                                                                                                                                                                                                                                                        5 GOWRGAAGTAAA 16
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P0409B08.8.
  SEQUENCE FROM N.A.
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                                                                                                                                                                               Ligase.
SEQUENCE
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).

EMBL; AL160331; CAB77330.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 314;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A. Plisov S.V., Lerman M., Perantoni A.O.; Plisov S.Y., Ivanov S.V., Lerman M., Perantoni A.O.; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF104399; AAC98389.1; -.
                                                                                                                                                                  3; Indels
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12).
GAP.
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Last annotation update)
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                                                                                                                              51.8%; Score 43; DB 11; 64.3%; Pred. No. 34;
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                                                                                                                                                                  2; Mismatches
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SCD8A.09.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                          Created)
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Pfam; PF000888; SpoU_methylase; 1.
Transferase; Methyltransferase.
SEQUENCE 314 AA; 32967 MW; 609
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MEDLINE=97000351; PubMed=8843436;
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01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                Best Local Similarity 64.3
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                      102 LNSQYQGAAATAAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GSLQGQWRGAAGTAA 15
                                                                                                                                                                                                    3 LOGOWRGAAGTAAA 16
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                Query Match
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Q9X7H6
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Q9L0Q5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
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                                                                             Length 1186;
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                                                                           Score 44; DB 2; Length 118
Pred. No. 1.4e+02;
); Mismatches 4; Indels
         PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
1186 AA; 128722 MW; CB11027815373E99 CRC64;
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Murphy L., Harris D.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEOUENCE 124 AA; 13867 MW; F5E17CF4C5949FFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL031231; CAA20259.1; -
                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 13.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                             53.0%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MELANOCYTE-SPECIFIC PROTEIN
                                                                           Query Match 53.0
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
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                                                                                                                                                                  1 GSLOGOWRGAAGTA 14
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Best Local Similarity
Matches 7; Conserv
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52 IQGGWQGAAG 61
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         PROSITE; 1
SEQUENCE
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RESULT 10

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SMART; SM00409; IG; 1.
SEQUENCE 391 Aa; 44451 MW; 8C9675020F02F632 CRC64;
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m
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ilarity 63.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J.;
Submitted (JUN-1998) to the
EMBL, ALO21943; CAA17469.1;
Tuberculist; Rv0672; --
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Best Local Similarity 64.5.

Query Match
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01-NOV-1998 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
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|3 GAVQGRWLGAA 23
                                                                                                                                                     1 GSLQGQWRGAA 11
                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                     086368
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                                                                                                                                                                                                                                                   RESULT 14
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                                                                                     "CAMP, a matrix metalloproteinase without a classic cysteine switch."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
Paracoccus denitrificans.
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                               SIMILARITY).

-!-SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!-SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!-SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!-SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.

EMBL: AJ012158; CAB41844.1; -.
R EMBL: AJ012158; CAB41844.1; -.
R HSSP: P1721; 1HG.
R HSSP: P1721; 1HG.
R InterPro: IPR000173; -.
R Ffam: PF00044; gpdh; INROWN_1.
R PROSITE; PS00071; GAPDH; UNKNOWN_1.
R Glycolysis; NAD; Oxidoreductase.
W Glycolysis; NAD; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.8%; Score 43; DB 2; Length 331;
61.5%; Pred. No. 56;
ative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                     PATHWAY: STEP IN THE SECOND PHASE OF GLYCOLYSIS SIMILARITY).
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Last annotation update)
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InterPro; IPR003599; -.
Pfam; PF00047; 1g; 1.
Pfam; PF00413; Peptidase_M10; 1.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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STRAIN-BALB/C; TISSUE-SPLEEN;
Pei D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF085742; AAC34886.1;
HSSP; P03956; 1CGL.
MEROPS; MIO.022; ...
MGD; MGI:1347361; Mmp23.
InterPro; IPRO00130; ...
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08,
16,
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01-NOV-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
CAMP METALLOPROTEINASE.
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54 SVFGPWRGQVGTA 66
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Best Local Similarity
8, Conserve
                                                       NCBI_TaxID=266;
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Cole S.T., Brosch K., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squres S., Squres R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Taylor K., Whitehead S., Barrell B.G.;
Top-liphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCBI_TaxID=1773;
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  Length 391;
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08, Last sequence update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MARR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 17.7 KDA PROTEIN.
AT4619200.
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Pred. No. 93;
ore 43; DB ] ed. No. 67; Mismatches
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  Score 43;
Pred. No.
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                                                                                       SEQUENCE FROM N.A.
Benes V., Rechmann S., Borkova D., Ansorge W., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Gudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                    Query Match 50.6%; Score 42; DB 10; Length 179; Best Local Similarity 62.5%; Pred. No. 43; Matches 10; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                      SEQUENCE FROM N.A.

EN Arabidopsis sequencing project
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL161550; CAB78922.1; ...
InterPro; IPR00216; ...
PRINTS; PR00239; RHODPSNTAIL.
Hypothetical protein.
SEQUENCE 179 AA; 17745 MW; IDAC3F3D3C1A604D CRC64;
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SEQUENCE FROM N.A.
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Search completed: July 5, 2001, 11:50:51 Job time: 474 sec

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                                                                                                                                                     July 5, 2001, 11:45:43; Search time 130.35 Seconds (without alignments) 7.441 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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78
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

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	Description	M. tuberculosis LH	M. tuberculosis LH	Mycobacterium tube	Mycobacterium tube	M. tuberculosis im	Mycobacterium tube	M. tuberculosis an	M. tuberculosis re	Mycobacterium tube	Mycobacterium tube	M. tuberculosis im
SUMMARIES	ID	AAY03709	AAY03706	AAW32454	AAW32386	AAW81707	AAW64340	AAY39137	AAY38994	AAW32444	AAW32376	AAW81747
	DB	20	20	18	18	19	19	20	20	18	18	19
•	Query Match Length DB	16	49	80	80	80	80	80	80	95	95	95
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis - useful in vaccines, for diagnosis, and for expression of heterologous proteins

WPI; 1999-132249/11.

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### ALIGNMENTS

ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; immune response. M. tuberculosis LHP polypeptide antigenic fragment. Rasmussen PB; Gicquel B, AAY03709 standard; Protein; 16 AA. 97US-0052631. 98WO-IB01091. Mycobacterium tuberculosis. (INSP ) INST PASTEUR. (STAT-) STATENS SERUM INST. (first entry) Andersen P, Berthet F, WO9904005-A1 16-JUL-1998; 16-JUL-1997; 28-JAN-1999. 07-JUN-1999 

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The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the W. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6; and (b) for diagnosing tuberculosis infection by catection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two provide a synergistic increase lampability to induce a protective immune response. Sequences AAY03706-713 tepresent antigenic fragments of the
                                                                                                                                 21; Page 65; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 AA;
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\overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} \overset{\times}{\times} 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 Length 16;
                       Indels
100.0%; Score 78; DB 20; 100.0%; Pred. No. 4.4e-07;
                      Mismatches
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                       Conservative
Query Match
Best Local Similarity
Matches 16; Conserv
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1 GDLKTQIDQVESTAGS 16

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AAY03706 RESULT

AAY03706 standard; Protein; 49 AA. 07-JUN-1999 (first entry) AAY03706;

ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; M. tuberculosis LHP polypeptide antigenic fragment.

immune response 

Mycobacterium tuberculosis

WO9904005-A1

28-JAN-1999

16-JUL-1998;

97US-0052631 16-JUL-1997;

98WO-IB01091

(STAT-) STATENS SERUM INST. (INSP ) INST PASTEUR

Gicquel B, Andersen P, Berthet F,

Rasmussen PB;

WPI; 1999-132249/11.

Mycobacterium for expression New nucleic acid containing regulator and LHP gene of tuberculosis - useful in vaccines, for diagnosis, and of heterologous proteins

Claim 21; Page 64; 88pp; English.

The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the

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be used as immunogens and vaccines, to protect against bacteria of the with the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, the and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune response. Sequences AAY03706-713 represent antigenic fragments of the
                                                     polypeptide can
recombinant expression of the protein. The recombinant be used as immunores and waring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide.
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49 AA; Sednence

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Gaps
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 Length 49;
                       Indels
Score 78; DB 20;
Pred. No. 1.5e-06;
Mismatches 0;
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 100.0%;
                       Conservative
                                             GDLKTQIDQVESTAGS 16
                                                         23 gdlktgidgvestags 38
Query Match
Best Local Similarity
Matches 16; Conserv
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RESULT

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AAW32454 standard; Protein; 80 AA. AAW32454

AAW32454;

(first entry) 09-JAN-1998 Mycobacterium tuberculosis antigen Tb38-1F3.

vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis Antigen; immunogen;

Mycobacterium tuberculosis.

WO9709428-A2

13-MAR-1997

30-AUG-1996; 12-JUL-1996;

96US-0680574. 95US-0523436. 95US-0533634. 01-SEP-1995; 22-SEP-1995; 

96US-0620874 96US-0659683 22-MAR-1996; 05-JUN-1996;

(CORI-) CORIXA CORP.

Skeiky YAW;

Reed SG,

Houghton R,

Д Д

Campos-neto A, Dillon D Twardzik DR, Vedvick TH;

WPI; 1997-192903/17. N-PSDB; AAT91526.

New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis

Example 3; Page 149; 168pp; English.

A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, PBS-8-1F3. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins blus ESAT-6, are useful in vaccines, preferably when formulated with a

Sequence

SSSS

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Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis; infection; diagnosis; antigen; Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to A, Dillon DC, Houghton R, Lodes MJ;
Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                M. tuberculosis immunogenic polypeptide Tb38-1F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 78; DB 19;
100.0%; Pred. No. 2.5e-06;
tive 0; Mismatches 0;
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96US-0730510.
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                                                                                                                      AAW81707 standard; Protein;
                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
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 GDLKTQIDQVESTAGS 16
                  3 gdlktgidqvestags 18
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N-PSDB; AAV64509.
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-IP3. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
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non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
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                                                                                                      Length 80;
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illarity 100.0%; Pred. No. 2.5e-06;
Conservative 0; Mismatches 0;
                                                                                                      100.0%; Score 78; DB 18; 100.0%; Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed
                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 163; 190pp; English.
                                                                                                                                                                                                                                                                                                   AAW32386 standard; Protein; 80 AA.
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95US-0532136.
96US-0620280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skin testing; M.tuberculosis
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Twardzik DR, Vedvick TH;
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                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                  Query Match
Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserva
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N-PSDB; AAT91460.
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22-SEP-1995
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AAW32386;

AAW32386 RESULT

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Gaps

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Sequence

Length 80; Indels

method

Houghton R;

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AAX19294 to AAX19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                        New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis recombinant antigen protein Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 78; DB 20;
100.0%; Pred. No. 2.5e-06;
ive 0; Mismatches 0;
                                                                                   Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Hendrickson RC, Hor
SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                  Example 3; Page 134-135; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY38994 standard; Protein; 80 AA.
             98US-0072967.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 gdlktgidgvestags 18
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Lodes MJ, Reed SG,
                                                         (CORI-) CORIXA CORP.
                                                                                                                               WPI; 1999-527409/44.
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N-PSDB; AAZ19098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       80 AA;
                                                                                                                                            N-PSDB; AAZ19310
             05-MAY-1998;
18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence
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                                                                                                                                                                                                                                                                                                                                                                        This polypeptide comprises Mycobacterium tuberculosis antigen Tb38-1F3. A DNA molecule (see AAV44400) coding for Tb38-1F3 was isolated from a M. tuberculosis strain H37Kv genomic library. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigent portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                                                                                                                                                                                                                      New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
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                                                                                                                                                                                                     DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 7%; DB 19; 100.0%; Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
            Mycobacterium tuberculosis strain H37Rv.
                                                                                                                                                                                                                                                                                                                                                Example 3; Page 146; 250pp; English
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                                                                                                 97WO-US18214
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96US-0729622.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 gdlktqidqvestags 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                     Dillon
                                                                                                                                                                                                      Campos-Neto A, Dillon
Reed SG, Skeiky YAW,
                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                             WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 AA;
                                                                                                                                                                                                                                                           N-PSDB; AAV44400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis
                                        WO9816645-A2.
                                                                                                  07-OCT-1997;
                                                                                                                             13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09942076-A2
                                                                     23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY39137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY39137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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Gaps

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Indels

Houghton R; t, Vedvick TS;

Length 80;

Gaps

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ö DB 18; 3e-06;

Mismatches

Score 78;

Length 95; Indels

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jen; immunogen; vaccine; tuberculosis; non specific adjuvant;
testing; M.tuberculosis.
  M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                      AAW32376 standard; Protein; 95 AA.
                                                                                  ;
0
                                                          100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               96US-0680573.
95US-0523435.
95US-0532136.
96US-0620280.
96US-0658800.
                                                                                                                                                                                                                                                                                                                                                                                          96WO-US14675
                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillon DC,
                                                         Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                        1 GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GDLKTQIDQVESTAGS 16
                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-192904/17.
N-PSDB; AAT91445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conserv
                          95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95
                                                                                                                                                                                                                                                                                                                                            409709429-A2
                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1995;
22-SEP-1995;
                                                                                                                                                                                                                                      13-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-1996;
05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campos-neto
                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1997
                                                                                                                                                                                                               AAW32376;
                          Sequence
                                                                                                                                                                                                                                                                                  Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                 skin
                                                                                                                                                                           AAW32376
   SXS
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                                                                                                                                                                                                  ó:
                                             invention describes novel recombinant antigens and their encoding
                                                       nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the Polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or andifications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins preferably when formulated with a non-specific adjuvant, to induce an immune response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis - are
tuberculosis, also
                                                                                                                                                                                                                                                                                                                                                                                                  Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW;
                                                                                                                                                                           Length 80;
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunogenic polypeptide(s) from Mycobacterium useful in vaccines for prevention or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed SG,
                                                                                                                                                                         DB 20;
2.5e-06;
hes 0;
                                                                                                                                                                       100.0%; Score 7%; DF
100.0%; Pred. No. 2.5
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 124; 168pp; English.
                      Example 3; Page 180; 323pp; English
                                                                                                                                                                                                                                                                                                       AAW32444 standard; Protein; 95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0680574.
95US-0523436.
95US-0533634.
96US-0620874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US14674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campos-neto A, Dillon DC,
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                       GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                             3 gdlktgidgvestags 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-192903/17.
                                                                                                                                                                                    1 Similarity
16; Conserv
                                                                                                                                        80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT91509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09709428-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                     09-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-1996;
05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-MAR-1997
                                                                                                                                                                       Ouery Match
Best Local S
Matches 16
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                              AAW32444;
                                                                                                                                                                                                                                                                                             AAW324
                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                        A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                New immunogenic polypeptide(s) from soluble M. tuberculosis antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78; DB 18; Length 95;
Pred. No. 3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                  useful for diagnosis of M. tuberculosis infection
Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
Houghton R,
                                                                                                                                                                                                                                                                                              Example 3; Page 136; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
ilarity 100.0%;
Conservative 0
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This is an antigenic portion of Mycobacterium tuberculosis antigen TD38-1. A DNA sequence (see AAV44384) coding for antigen TD38-1. A DNA sequence (see AAV44384) coding for antigen TD38-1 was isolated from a M. tuberculosis strain HJRV expression library using sera from patients having pulmonary or pleural tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AMA4291-M46479) comprising an antigenic portion of as soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, contibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                     New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculosis; antigen; fusion protein; Tb38-1; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                   DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                core 78; DB 19;
red. No. 3e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78;
Pred. No.
Mycobacterium tuberculosis strain H37Rv.
                                                                                                                                                                                                                                                                                                                               Example 3; Page 123; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY32097 standard; Protein; 95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
                                                                                   97WO-US18214.
                                                                                                               97US-0818111
                                                                                                                            96US-0729622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 gdlktgidgvestags 33
                                                                                                                                                                                  Dillon
                                                                                                                                                                                   Campos-Neto A, Dillon
Reed SG, Skeiky YAW,
                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                            WPI; 1998-251292/22.
N-PSDB; AAV44384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 AA;
                            WO9816645-A2
                                                                                   07-OCT-1997;
                                                                                                               13-MAR-1997;
                                                                                                                           11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9951748-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-1999;
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                                                       23-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY32097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY32097
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 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducting protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                 Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculosis; infection; diagnosis; antigen; Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3e-06;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen Tb38-1 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 78; DB 19;
100.0%; Pred. NO. 3e-06;
ive 0; Mismatches 0;
                                                                                                                                                                     M. tuberculosis immunogenic polypeptide Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3b; Page 117; 230pp; English
                                                                                   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW64321 standard; Peptide; 95 AA
                                                                                AAW81747 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                       97US-0818112.
96US-0730510.
                                                                                                                                                                                                                                                                                                                              97WO-US18293
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.

Best Local Similarity 100.

Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 gdlktgidgvestags 33
CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-261042/23.
N-PSDB; AAV64491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
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11-OCT-1996;
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                                                                                                                                                                                                                                                                                                                            07-OCT-1997;
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                                                                                                                                        27-JAN-1999
                                                                                                                                                                                                                                                                                                  23-APR-1998
                                                                                                              AAW81747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW64321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                       RESULT 11
                                                                    AAW81747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW64321
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Gaps

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AAX19249 to AAX19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in biological sample by detecting antibodies which bind with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                              100.0%; Score 78; DB 20; Length 95; 100.0%; Pred. No. 3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20; Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis recombinant antigen protein Tb38-1
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on DC, Hendrickson RC, Hc
Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 159; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY38981 standard; Protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0072596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US03265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             Lodes MJ, Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-527416/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                   Local Similarity
es 16; Conserv
                                                                                                                                                                                                                                          95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9942118-A2
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Matches
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                                                                                                                                                                  New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                         TD38-1. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens such as TD38-1, e.g. TDF-2 (see AAY32063) and a TDH9-TD38-1 fusion. The new fusion proteins are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                           This sequence represents the Mycobacterium tuberculosis antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 95;
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Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78;
Pred. No. 3
                                                                                             Campos-Neto A;
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                                                                                                                                                                                                                       Claim 1; Fig 4D; 83pp; English.
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980S-0056556
                    98US-0223040
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98US-0025197
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                                                                                           Skeiky YAW, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Conservative
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                                                       (CORI-) CORIXA CORP
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Best Local Similarity
Matches 16; Conserv
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 07-APR-1998;
                   30-DEC-1998;
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18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                               components
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Best Local Similarity 100.0%; Pred. No. 3e-06; Matches 16; Conservative 0; Mismatches 0; Indels qq οy

Search completed: July 5, 2001, 11:45:43 Job time: 272 sec

Appli Appl Appl Appl Appli Appli

Appli Appl

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APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAMADA, Akiko
APPLICANT: YAMADA, Akiko
APPLICANT: KTO. Seishi
APPLICANT: KTONDO, Kiyosi
TITLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
TITLE OF INVENTION: Synthesizing Enzymes and Process for Froduction of
TITLE OF INVENTION: Eiscosapentaenoic Acid
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                   Sequence 4, Al
Sequence 4, Al
Sequence 4, Al
Sequence 10, Al
Sequence 4, Al
Sequence 29, P
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Sequence (
Sequence (
                         Sequence
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CID: 20007-5109

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOSTWARE: Patentin Release #1.0, Version #1.30

SOSTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/375,709

FILING DATE: 20-7AN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,251

FILING DATE: 14-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 4-147945

FILING DATE: 15-MAY-1992

ATTORNEY AGENT INFORMATION:

NAME: WEGNER, HATOLD C.

REGISTRATION NUMBER: 55,258

REGISTRATION NUMBER: 55,258

REGISTRATION NUMBER: 53466/150/AAOK

TELECOMMUNICATION INDERER: 53.000
US-08-446-100-31
US-08-446-100-31
US-08-316-308A-4
US-08-822-324-4
US-07-977-434-4
US-08-458-819-4
US-09-105-697-10
PCT-US91-07035-4
US-08-336-3312-29
US-08-336-3312-29
US-08-822-324-6
US-08-804-227C-8
US-08-804-198-2
US-08-804-198-2
US-08-320-878-1
US-09-320-878-1
US-08-320-878-1
US-08-320-878-1
US-08-320-878-1
US-09-06-6046-6
US-08-975-762-50
US-08-975-762-50
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08375709
Patent No. 5683898
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2756 amino acids
    454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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    USA
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TELEFAX: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: /cgn2_6/ptcdata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/laa/PCTUS_COMB.pep:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-444-189-18
US-08-430-024-2
US-08-782-009-2
US-09-017-302-2
US-08-756-317-13
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US-08-646-715-9
US-09-33-409-4
US-08-726-525-2
US-08-726-036A-2
US-08-781-560-1
US-08-792-014-3
US-08-792-014-3
US-09-443-948-3
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US-08-446-100-27
US-08-446-100-28
US-08-446-100-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-242-932-2
US-08-714-481-2
PCT-US95-06111-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                       1 GDLKTQIDQVESTAGS 16
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                        Run on:
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GENERAL INFORMATION:

APPLICANT: Ratti, Giulio

APPLICANT: Ratti, Giulio

APPLICANT: Tecce, Mario F.

APPLICANT: Giuliani, Marzia M.

APPLICANT: Giuliani, Marzia M.

APPLICANT: Giuliani, Marzia M.

APPLICANT: Giuliani, Marzia M.

TITLE OF INVENTION: TRACHOMATIS SENCYTPE D, ITS GENES AND PROTEINS ENCODED BY TITLE OF INVENTION: TRACHOMATIS SENCYTPE D, ITS GENES AND PROTEINS ENCODED BY TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 301 N. Washington Street

CITY: Falls Church

STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                          TITLE OF INVENTION: Production of polyunsaturated fatty acids by expression TITLE OF INVENTION: of polyketide-like synthesis genes in plants FILE REFERENCE: CONE.131.0105
CURRENT APPLICATION NUMBER: US/09/090,793
CURRENT FILING DATE: 1,998-06-04
EARLIER APPLICATION NUMBER: 60/048,650
EARLIER FILING DATE: 1,997-06-04
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 7
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64;
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ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAPR:
APPLICATION NUMBER: US/08/969,644
FILING DATE: 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42;
Pred. No. 6
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FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/661,820 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/969,644
13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 18, Application US/08969644
; Patent No. 6096519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/467,152
                                                                      Sequence 7, Application US/09090793
Patent No. 6140486
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Shewanella putrefaciens US-09-090-793-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 GSVKSQIGHTKSTAGT 412
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Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                     GENERAL INFORMATION:
APPLICANT: Calgene, LLC
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-08-969-644-18
                                                 US-09-090-793-7
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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APPLICANT: YRZAMA, Kazunaga
APPLICANT: YRZAMA, Kazunaga
APPLICANT: KANDA, Akiko
APPLICANT: KAND, Seishi
APPLICANT: KONDO, Kiyosi
TITLE OF INVENTION: Gene Coding for Elcosapentaenoic Acid Synthesizing
TITLE OF INVENTION: Enzymes and Process for Production of Elscosapentaenoic
TITLE OF INVENTION: Acid
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                                                                        Gaps
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                         DB 1; Length 2756;
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                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/752,929
FILING DATE: 20-00v-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,709
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
APPLICATION NUMBER: US 4-147945
FILING DATE: 15-MAY-1993
APPLICATION NUMBER: ST 4-147945
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: ST 4-147945
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: ST 5-258
REGISTRATION: NUMBER: 25.258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 1;
Pred. No. 64;
4; Mismatches
                                                                    4; Mismatches
                                              64;
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3000 K Street, N.W., Suite 500
                       Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               RESULT 2
US-08-752-929-11
; Sequence 11, Application US/08752929
; Patent No. 579829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
                       53.8%;
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(202)672-5399
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Ouery Match
Best Local Similarity 50.0
داره 8; Conservative
                                                                                                                                          397 GSVKSQIGHTKSTAGT 412
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397 GSVKSQIGHTKSTAGT 412
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Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                1 GDLKTQIDQVESTAGS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-752-929-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley
STREET: 3000 K St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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20007-5109
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Gaps
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GENERAL INFORMATION:
APPLICANT: Faulmann, Ervin L
TITLE OF INVENTION: NOVEL GENE AND METHOD FOR PRODUCTION OF
TITLE OF INVENTION: AN 19A BINDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Saliwanchik & Saliwanchik
STRRET: 2421 NW. 41st Street
CITY: Gainesville
                                                                                                                                                             Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
SUGTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,024
FILING DATE: 27-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/677,209
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
24;
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                                                                                                                                                                Score 41; DB.4
Pred. No. 6.1;
3; Mismatches
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Pred. No.
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Patent No. 5644030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Saliwanchik, David R
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
50.0%;
                                                                                                                                                                52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 amino acids
                                                                                                                                                                Query Match 52.6
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                       160 GDLKTKVDVIGKVCG 174
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                                       ; MOLECULE TYPE: protein US-08-444-189-18
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                                                                                                                                                                                                                                                                        1 GDLKTQIDQVESTAG 15
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DLKTQIDQVESTAG 15
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Best Local Similarity
7; Conserve
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US-08-430-024-2
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                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-08-430-024-2
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STATE:
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TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM, RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGGUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
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                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 3
Pred. No. 6.1;
3; Mismatches
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REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION:
TELEPHONE: 703-241-1300
REFERENCE/DOCKET NUMBER: 1267-202P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/444,189
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US-08-444-189-18
Sequence 18, Application US/08444189
Fatent No. 6110705
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comanducci, Maurizio
Tecce, Mario F.
Giuliani, Marzia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                       JENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-969-644-18
                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.6%;
Best Local Similarity 46.7%;
Matches 7; Conservative
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                  TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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APPLICANT:
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Misky, Timothy A.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Improved Rhodospirillum Rubrum
TITLE OF INVENTION: Poly-B-Hydroxyalkonoate Synthase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,317
FILING DATE: 25-NOV-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 24;
3; Mismatches
                                                    APPLICATION NUMBER: 08/782,009
FILING DATE: 07-JAN-1997
APPLICATION NUMBER: 08/430,024
FILING DATE: 27-APR-1995
APPLICATION NUMBER: US 07/677,209
FILING DATE: 29-WAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: BL-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 904-375-8100
TELEFAX: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 60/007,693
FILIND DATE: 29-NOV-1995
ATTORENYAGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBI:008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08756317 Patent No. 5849894 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              TELEPAX: 904-372-30vv
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 50.0
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-017-302-2
                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DLKTQIDQVESTAG 15
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ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Houston STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-08-756-317-13
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| Patent No. 6075128
| GENERAL INFORMATION:
| APPLICART: Faulmann, Ervin L
| TITLE OF INVENTION: NOVEL GENE AND METHOD FOR PRODUCTION OF
| TITLE OF INVENTION: AN 19A BINDING PROTEIN
| TUMBER OF SEQUENCES: 2
| CORRESPONDENCE SILWANCHIK & Saliwanchik STREET: 2421 N W. 41st Street
| CITY: Galnesville | STATE: FL
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó:
                  TITLE OF INVENTION: NOVEL GENE AND METHOD FOR PRODUCTION OF TITLE OF INVENTION: AN 19A BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 396,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,009
FILING DATE: 07-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/430,024
FILING DATE: 27-APR-1995
APPLICATION NUMBER: US 07/677,209
FILING DATE: 27-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: BL-1
TELECOMMUNICATION:
NAME: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39;
Pred. No.
                                                                                                         ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street
CITY: Gainesville
                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Faulmann, Ervin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-782-009-2
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DLKTQIDQVESTAG 15
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84 DIKKAVEPVEKTAG 97
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                                                                                                                                                                                                USA
                                                                                                                                                                                                                    32606
                                                                                                                                                                         STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-017-302-2
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Gaps
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TITLE OF INVENTION: Cloning of No. 5766606-1gA FC Binding Forms of
TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
TUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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                                                                                                                                                        Score 39; DB 1; Length 984;
Pred. No. 68;
3; Mismatches 4; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-SEP-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
68;
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Pred. No. 68;
3; Mismatches
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FILING DATE: 16-MAY-1994
ATONREY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF142
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           US-08-714-481-2; Sequence 2, Application US/08714481; Patent No. 576606; GENERAL INFORMATION:
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                                                                                                                                                              50.0%;
50.0%;
                                     984 amino acids
                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                        |:| :: || |||
47 DIKKAVEPVEKTAG 60
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                                                                                                                                                                                                                                      2 DLKTQIDQVESTAG 15
                                                                                                                                             Query Match
Best Local Similarity
'-hag 7; Conservē
                                                    amino acid
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Best Local Similarity
Matches 7; Conserv
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PCT-US95-06111-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                         US-08-242-932-2
                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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Patent No. 559540
GENERAL INFORMATION:
TITLE OF INVENTION: Cloning of No. 5595740-IGA FC Binding Forms of
TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                      Parent No. 5240706

Papelicann: FAQLDS, DARYL

HYDITLE OF INVENTION: INTRANASSAL ADMINISTATION OF MYCOPLASMA
HYDITLE OF SEQUENCES: 22

CURRENT APPLICATION DATA:
PILLOATION DATA:
PILLIAG DATE: 07-APR-1989
                                                                                                                                             Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Saliwanchik & Saliwanchik
: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB
Pred. No. 38;
                                                                                                                                         Score 39;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUCHRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,932
FILING DATE: 16-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFRX: 904-375-800
                                                                                                                                           50.0%;
               LENGTH: 577 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                       521 GDIETWMGKAKETAGS 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.7.

"The Conservative 7; Conservative 7.
                                                                                                                                         Query Match 50.0
Best Local Similarity 43.8
Matches 7; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                   1 GDLKTQIDQVESTAGS 16
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555 ELKLKLDQIEAAAQS 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:1:
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                     ; TOPOLOGY:
US-08-756-317-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Ga
STATE: FI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                          RESULT 10
5240706-1
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APPLICANT: Wang, Edith
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSES: FLEHK, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                             ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: Son Francisco STATE: California COUNTRY: USA
COUNTRY: USA
ZIP: 94.11-4.187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/188,582 FILING DATE: 28-JAN-1994 CLASSIFICATION: 435
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OPERATIMG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Osman, Richard A
REGISTATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERA: (415) 398-3249
TELERA: (415) 398-3249
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1
Pred. No. 24;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 278 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 43.87
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 GDLKMEVDSDAAAVGS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tjian, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comai, Lucio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-188-582-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-646-715-9
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APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert 0.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Cloning of Non-1gA Fc Binding Forms of TITLE OF INVENTION: the Group B Streptococcal Beta Antigens NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                             186 Grinter Hall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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904-392-8929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%; Score 39; 50.0%; Pred. No.
                                                                                                                                                    Florida
                                                                                                                                                                                                                                               : Phone number: 904-392-892
: Fax number: 904-392-6600
: Telex number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,932
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
Sequence 2, Application PC/TUS9506111
                                                                                    Street address:
City: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-188-582-9; Sequence 9, Application US/08188582; Patent No. 5534410; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dynlact, Brian D.
                                                                                                                                                                                        Country: U:
Postal code/2ip:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                    State/Province:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 984 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein PCT-US95-06111-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DLKTQIDQVESTAG 15
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Best Local Similarity
Matches 7; Conserv
                                GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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APPLICANT:
APPLICANT:
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Gaps

Search completed: July 5, 2001, 11:47:00 Job time: 314 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 5, 2001, 11:48:34; Search time 79.63 Seconds (without alignments) 15.306 Million cell updates/sec Run on:

US-09-462-480-9 78 1 GDLKTQIDQVESTAGS 16 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 segs, 76174552 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

SUMMARIES	Description	hypothetical prote		probable	probable		dextranase (EC 3.2		hypothetical	hypothetical	histidine kir	hypothetical prote	chorismate s				hypo		hypothetical									signal recognition	acetohydroxyacid	
SOS	Ð.	H70802	F84669	T38023	E81965	H81020	JC4076	T30183	S01924	F3738	B71677	G72593	H8684	T1891	S44809	T11560	T1687	S53945	T34496	A60234	FCSOAG	T3135	S0347	C69295	A49067	T03556	59	T3477	T11997	
	DB	5	~	7	7	7	7	7	7	~	~	7	~	7	7	~	~	~	7	~	٦	7	~	7	~	7	~	~	7	
	Length	100	1163	630	1068	1082	822	2756	247	247	497	533	388	442				523	774	1134	1164	1390	129	128	278	334	414	550	585	
de	Query Match		59.0	S	55.1	55.1	53.8	53.8	52.6	52.6	52.6	52.6	51.3	51.3	51.3	51.3	51.3	20.0	50.0	50.0	50.0	50.0		48.7			48.7		48.7	
	Score	78	46	43.5	43	43	42	42	41	41	41	41	40	40	40	40	40	39	39	39	39	3	38.5	38	38	38	38	38	38	
	Result No.	-	7	m	4	Ŋ	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	

hypothetical prote probable polyketid 240k tequment prot	large tegument pro large tegument pro probable aspartate	hypothetical prote parathymosin - rat zinc-binding prote	DNA-packaging prot probable host-nucl probable transcrip	transcription init probable glucan 1, hypothetical prote farnesyl-pyrophosp
S64439 D70887 WZBEZ4	T44178 C72547	T25296 B31512 S20422	JVBPFL E81897 T03990	E84243 T42370 T32232 A34441
777	000	000	400	2224
816 1733 2077	2077 2077 312	365 102 106	132 172 298	328 332 343 352
~~~	7.7.	L 4 4	4 4 4	4444
4 4 4 8 8 8	4 4 8 8 4 8	48	47	47.4 47.4 47.4 4.74
3 3 3 3 3 3 3 3 3	38 38 37.5	37.5 37 37	37 37 37	37 37 37 37
30 31 32	334 354 35	36 37 38	39 40 41	4 4 4 4 2 6 4 6

## ALIGNMENTS

RESULT 1 H70802 H70802 C:Species: Mycobacterium tuberculosis (strain H37RV) C:Species: Mycobacterium tuberculosis C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C:Accession: H70802 R:Cole, S:T: Brosch, R:Parkhill, J:, Garnier, T:; Churcher, C:; Harris, D:; Gordon Connor, R:; Davies, R:; Devlin, K:; Feltwell, T:; Gentles, S:; Hamlin, N:; Holroyd,	Nature 393, 537-544, 1998 A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Aitle: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987 A; Accession: H70802	A;Status: preliminary; nucleic acid sequence not snown; translation not snown A;Wolecule type: DNA A;Residues: 1-100 <col/> A;Cross-references: GB:AL022120; GB:AL123456; NID:93261558; PIDN:CAA17966.1; PID:9296 A;Experimental source: strain H37Rv C:Genetics: Ax3874
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Gaps ö Length 100; Query Match 100.0%; Score 78; DB 2; I Best Local Similarity 100.0%; Pred. No. 2.5e-06; Matches 16; Conservative 0; Mismatches 0;

g δλ

probable chromosome associated protein [imported] - Arabidopsis thaliana cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Daccession: F84669
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: R84669
A;Accession: F84669

A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-1163 <STO>
A; Cross-references: GB: AE002093; NID: 96598752; PIDN: AAD26882.2; GSPDB: GN00139
C, Genetics:

A; Gene: At2g27170 A; Map position: 2

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Serotype-1-specific antigen, probable NMB1969 (imported) - Neisseria meningitidis (st C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Janwar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: H81020
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58
A;Accession: H81020
A;Status: preliminary
A;Molacule type: DNA
A;Residues: 1-1082 < TETP>
A;Cross-references: GB:AR002545; GB:AR002098; NID:g7227229; PIDN:AAF42298.1; PID:g722
A;Experimental Source: serogroup B, strain MC58
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GENTRADASE (EC 3.2.1.11) precursor - Streptococcus salivarius

GENTRADASE (EC 3.2.1.11) precursor - Streptococcus salivarius

GENTRADASE (STREPTOCOCCUS SALIVARIUS

C.DATE: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 15-Oct-1999

C.ACCESSION: JC4076

R.Ohnishi, Y.; Kubo, S.; Ono, Y.; Nozaki, M.; Gonda, Y.; Okano, H.; Matsuya, T.; Mats

Gene 156, 93-96, 1995

A.Fitler: Cloning and sequencing of the gene coding for dextranase from Streptococcus

A.Fitler: JC4076

A.Reference number: JC4076

A.Recession: JC4076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-822 <OHN>
A;Cross-references: DDBJ:D29644; NID:9961504; PIDN:BAA06127.1; PID:d1006681; PID:9961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: M-33
A, Note: The authors' translation from residues 2303 to 2401 differs considerably from
C; Comment: This enzyme hydrolyzes the 1,6-alpha-glucosidic linkages of glucan d re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 5 - Shewanella sp. C;Species: Shewanella sp. C;Species: Shewanella sp. C;Species: Shewanella sp. C;Date: 0.2-Sep-2000 #sequence_revision 0.2-Sep-2000 #sequence_revision 0.2-Sep-2000 #sequence_revision 0.2-Sep-2000 #sequence_revision 0.3-Yearession: T30183 . R;Takeyama, H.; Takeda, D.; Yazawa, K.; Yamada, A.; Matsunaga, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-38/Domain: signal sequence #status predicted <SIG>F;39-822/Product: dextranase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ed. No. 38;
Mismatches
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Pred. No. 42;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43;
Pred. No.
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56.2%;
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ilarity 53.3%;
Conservative
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| 668 GGLLASLDSVEKTAGS 683
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334 GDLKARIDMVRNKTG 348
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: NMB1969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable outer membrane peptidase (EC 3.4.21.-) NMA0478 [imported] - Neisseria meningitid C; Species: Neisseria meningitidis C; Species: OS-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C; Accession: EB1965 F; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holroyd, S.; Jagels K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Astrile: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491. A; Reference number: A01775; MUID:20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1068 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83773.1; PID:g737922
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-630 A/Residues: 1-630 A/Residues: 1-630 Coss-references: EMBL:298598; PIDN:CAB11234.1; GSPDB:GN00066; SPDB:SPAC1B3.05
A; Experimental source: strain 972h-; cosmid c1B3
C; Genetics:
A; Gene: SPDB:SPAC1B3.05
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0
                                                                                                                                                                                                                                                                                                                                                                            probable transcription regulator - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C;Accession: T38023
E;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                             Length 1163;
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                                                                          DB 2;
13;
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A; Accession: T38023
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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                                                                             Score 46; DB 2
Pred. No. 13;
4; Mismatches
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Pred. No.
C; Superfamily: hypothetical protein YJL074c
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C,Genetics:
A;Gene: NMA0478
C;Keywords: hydrolase; serine proteinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDLKTQIKKLQRLRDQIKTWASS 57
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                                                                             59.0%;
61.5%;
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56.2%;
                                                    Query Match
Best Local Similarity 61.5.
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    1 GDLKTQIDQVEST 13

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Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
Matches 9; Conserv
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A; Introns: 75/3
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Gaps

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Indels

Length 247;

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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339
A;Accession: G72593
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A;Experimental source: strain K1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histidine kinase sensor protein (barA) RP229 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-NOV-1998 #sequence_revision 21-NOV-1998 #text_change 03-NOV-2000
C;Accession: B71677
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AJ235271; GB:AJ235269; NID:q3868717; PIDN:CAA14692.1; PID:q386
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C.Accession: G72593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 2;
Pred. No. 35;
4; Mismatches
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66.7%; Pred. No. 38;
iive 2; Mismatches
                                                                                                                                                                                                 Score 41; DB 2
Pred. No. 16;
3; Mismatches
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                                                                                                                                                                                             52.6%;
                                                                                                                                                                                                 Query Match 52.6
Best Local Similarity 46.7
Matches 7; Conservative
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      A; Residues: 1-247 <COM>
A; Cross references: GB:J03321
C; Genetics:
A; Genome: plasmid
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254 NLKAQIEKVEKTSSS 268
                                                                                                                                                                                                                                                                                                                                                                                     160 GDLKTKVDVIGKVCG 174
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388 DLNTRLDQVAST 399
                                                                                                                                                                                                                                                                                                                         1 GDLKTQIDQVESTAG
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-497 <AND>
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A; Molecule type: DNA
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A;Gene: barA; RP229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 6 - Chlamydia trachomatis plasmids
Nylternate names: hypothetical protein P-10
C;Species: Chlamydia trachomatis
08-0ct-1999
C;Accession: S01924; S00794
R;Comanducci, M.; Ricci, S.; Ratti, G.
MOI. Microbiol. 2, 531-538, 1988
A;Title: The structure of a plasmid of Chlamydia trachomatis believed to be required for A;Reference number: S01920; MUID:89013895
A;Reference number: S01920; MUID:89013895
A;Ross-references: EMBL:X07547; NID:940730; PIDN:CAA30426.1; PID:9581014
A;Residues: 1-247 <COM>A;COM>A;COM>A;COM>A;CoM>A;Residues: 1-24 <COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;CoM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A;COM>A
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C;Species: Chlamydia trachomatis
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Feb-1994
C;Accession: F37386
R;Comanducci, M.; Ricci, S.; Cevenini, R.; Ratti, G.
R;Comanducci, M.; Ricci, S.; Cevenini, R.; Ratti, G.
A;Smille: Diversity of the Chlamydia trachomatis common plasmid in biovars with different A;Reference number: A37386; MUID:90301796
A;Status: preliminary
A;Molecule type: DNA
Microbiology 143, 2725-2731, 1997
Affilte: Expression of the elcosapentaenoic acid synthesis gene cluster from Shewanella A; Reference number: 220764; MUID:97419510
A; Accession: T30183
A; Status: preliminary; translated from GB/EWBL/DDBJ
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A; Residues: 1-2756 <TAK>
A; Cross-references: EMBL:U73935; NID:g2529413; PID:g2529418; PIDN:AAB81123.1
A; Experimental source: strain SCRC-2738
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 2; Length 275
Pred. No. 1.6e+02;
4; Mismatches 4; Indels
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Pred No. 16;
3; Ansmatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Experimental source: plasmid pLGV440 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                          53.8%; 50.0%;
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46.7%;
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A; Residues: 175-247 <HAT>
A; Cross-references: EMBL:X06707
                                                                                                                                                                                                                                                                                                                         397 GSVKSQIGHTKSTAGT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GDLKTQIDQVESTAGS 16
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Best Local Similarity
Matches 7; Conserv
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A;Start codon: GTG
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Gaps

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Indels

Length 497;

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Gaps

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Length 533; Indels

Gaps

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Length 447; Indels

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DB 47;

Score 40; DB 2 Pred. No. 47; 5; Mismatches

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polyprotein - simian immunodeficiency virus SIVsm (strain E543) (fragment C;Species: simian immunodeficiency virus SIVsm (strain E543) (fragment C;Species: simian immunodeficiency virus SIVsm A;Variety: strain E543 (spacesion: E543 (spacesion: E543 (spacesion: T1156 (spacesion: T11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1019 <HIR>
A;Cross-references: EMBL:U72748; NID:g1695908; PIDN:AAC56559.1; PID:g1695910
C;Genetics:
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 - AMIP-
A;Cross-references: EMBL:L23648; NID:g388585; PIDN:AAA28028.1; PID:g388588
C;Genetics: A;Introns: 17/3; 53/1; 114/2; 375/1
C;Superfamily: phage T4 DNA polymerase accessory protein 44
C;Superfamily: phage T4 DNA polymerase accessory protein 44
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C;Superfamily: pol polyprotein
C;Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                               51.3%;
ilarity 50.0%;
Conservative
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Best Local Similarity
Matches 8; Conserv
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Job time: 374 sec
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                                                                        chorismate synthase (EC 4.6.1.4) [imported] - Lactococcus lactis subsp. lactis (strain I C; Species: Lactococcus Lactis subsp. lactis
C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C; Accession: H86843
R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrligenome Res. in press, 2001
A; Reference number: A86625
A; Accession: H86843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-442 < WIL:
A;Residues: 1-442 < WIL:
A;Cross-references: EMBL:Z81461; PIDN:CAB03839.1; GSPDB:GN00019; CESP:C04F12.10
A;Experimental source: clone C04F12
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                                                                                                                                                                                                                                                                                                                                                                                                            A Status: preliminary
A Molecule types: DNA
A:Molecule types: DNA
A:Residues: 1-388 (STO>
A:Cross.references: GB:AbE005176; NID:912724773; PIDN:AAK05850.1; GSPDB:GN00146
A) Experimental source: strain IL1403
C) Genetics:
A;Gene: aroC
C; Superfamily: chorismate synthase
C; Keywords: phosphorus-oxygen lyase
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18917
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C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decession: S44809
C;Accession: S44809
R;Antonacci-Fulton, L.
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A; Description: Sequence of the C. elegans cosmid F44B9.
A; Reference number: $44807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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Pred. No. 46;
5; Mismatches
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submitted to the EMBL Data Library, November 1996
A;Reference number: Z19044
A;Accession: T18917
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red. No. 40;
Mismatches
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Pred. No.
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A;Map position: 1
A;Introns: 30/2; 77/3; 318/1; 340/3
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ilarity 53.3%;
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47 GRMKIESDQVEITSG 61
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208 GDLKTKIEQLAAS 220
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Best Local Similarity
Matches 8; Conserv
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Gaps

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Q54443 streptococc
059979 streptococc
P1056 chlamydia t
P34429 caenorhabdi
P12502 simian immu
Q15040 saccharomyc
Q49539 mycoplasma
P50176 r poly-beta
Q14149 homo sapien
P2755 streptococc
Q27272 drosophila
050562 rhodobacter
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Q14696 P49842 P21745 P21745
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93435 seqs, 34255486 residues
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PHBC_RHIME
Y136_HUMAN
BAG_STRAG
T2D7_DROME
SAHH_RHOSH
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VPF1_LAMBD
FPPS_YEAST
YD36_AQUAE
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GP6D_CHLTR
AC11_CAEEL
POL_SIVSP
POL_SIVSP
YMR9_YEAST
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TEGU_HSV6G
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CHSB_PETHY
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Y081_HUMAN
G11_HUMAN
EA30_VICFA
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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78
1 GDLKTQIDQVESTAGS 16
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Maximum DB seq length: 2000000000
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EA92_VICFA	SVF3_VICFA	G3P_CHLTR	VE05_VARV	CICP_BOVIN	C140_MYCTU	NG79_SCHPO	YHDT_BACSU	FLAB_HELPJ	FLAB_HELPY	EST1_HUMAN
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268	268	334	341	437	438	438	461	513	513	267
46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2
36	36	36	36	36	36	36	36	36	36	36
34	35	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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                                                                                                                                                                                                                                      STRAIN=L1/440/LN; PLASMID=PLGV440;
MEDLINE=88233998; PubMed=2236808;
Hatt.C., Ward M.E., Clarke I.N.;
"Analysis of the entire nuclectide sequence of the cryptic plasmid of
Chlamydia trachomatis serovar L1. Evidence for involvement in DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-SERCOTYPE B; PLASMID-PCTT1;
MEDLINE-88177106; PubMed-3444859;
SIIPTARASh K.S., Macavoy B.S.;
"Characterization and sequence of a plasmid from the trachoma biovar of Chlamydia trachomatis.";
Plasmid 18:205-214(1987).
-i- MISCELLANEOUS: PGP6-D IS REQUIRED FOR GROWTH WITHIN MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                    Comanducci M., Ricci S., Cevenini R., Ratti G.;
bibversity of the Chlamydia trachomatis common plasmid in biovars
with different pathogenicity.";
Plasmid 23:149-154(1990)
                                                                                                                   STRAIN=L2/434/BU; PLASMID=PLGV440;
MEDLINE=89013895; PubMed=2845228;
Comanducci M., Ricci S., Ratti G.;
The structure of a plasmid of Chlamydia trachomatis believed to required for growth within mammalian cells.";
Mol. Microbiol. 2:531-538(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF PLASMID PLGV440.
                                           Plasmid pLGV440, Plasmid pCHL1, and Plasmid pCTT1.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
01-OCT-2000 (Rel. 40, Last annotation update) VIRULENCE PLASMID PROTEIN PGP6-D (PROTEIN P-10).
                                                                                                                                                                                                                                                                                                                                                          SEĞUENCE FROM N.A.
STRAIN-GG/86 / SEROTYPE D; PLASMID-PCHL1;
MEDLINE-90301796; Pubmed-2194229;
                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 16:4053-4067(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X07547; CAA30426.1; -.
EMBL; X06707; CAA29897.1; -.
EMBL; J03321; AAA91574.1; -.
EMBL; M19487; AAB02591.1; -.
PTR; S01924; S01924.
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47
186
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205
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28307 N
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                                Chlamydia trachomatis.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 AA;
                                                                                                     SEQUENCE FROM N.A.
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1183
1194
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                                                                         NCBI_TaxID=813;
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             CYTOPLASMIC (POTENTIAL).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohnishi Y., Kubo S., Ono Y., Nozaki M., Gonda Y., Okano H., Matsuya T., Matsushiro A., Morita T.;
"Cloning and sequencing of the gene coding for dextranase from Streptococcus salivarius.";
Gene 156:93-96(1995).
-! CARALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,6-ALPHA-D-GLUCOSIDIC LINKAGES IN DEXTRAN.
-! SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
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                                                                                                      DB 1; Length 850;
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                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DEXTRANASE PRECURSOR (EC 3.2.1.11) (ALPHA-1,6-GLUCAN-6-GLUCANOHYDROLASE).
                                                           D653CAA39C93D2AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEXTRANASE, 31857D38D3F2C761 CRC64;
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19;
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                                                                                                                                                                                                                                                                     822 AA.
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                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                      Score 46;
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Pred. No.
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                                                                                                                      Pred. No.
                                             PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=M-33;
MEDLINE=95255675; Pubmed=7737522;
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Hydrolase; Glycosidase; Signal.
                                                           MM;
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                                                                                                     59.0%;
53.3%;
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                                                                                                                                    Conservative
                                                                                                                                                                               Streptococcus salivarius.
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                                                           850 AA;
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                                                                                                                   Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
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059979;
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N -> D (IN PLASMIDS PCHL1 AND PCTT1).
CO -> R (IN PLASMIDS PCHL1 AND PCTT1).
LO -> CWIE (IN PLASMID PCTT1).
R -> T (IN PLASMID PCTT1).
S -> L (IN PLASMID PCTT1).
S -> I (IN PLASMID PCTT1).
H -> I (IN PLASMID PCTT1).
FIFAllF29037C221 CRC64;
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Pred. No. 7.6;
3; Mismatches
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                                                                                                                                                                         52.6%;
46.7%;
                                                                                                                                                                       Query Match 52.6
Best Local Similarity 46.7
Matches 7; Conservative
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AC11\_CAEEL P34429;

AC11\_CAEEL

RESULT

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F44B9.8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
                                                                                                                          01-OCT-1989 (Rel. 12, Last sequence update)
15-DEZ-1998 (Rel. 37, Last annotation update)
POL POL PROTEIN (CONTAINS: PROTESAE (RETROPEDSIN) (BC 3.4.23.16);
REVERSE TRANSCRIPTASE (BC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
                                                                                                                                                                                                                                                                               Simian immunodeficiency virus (F236/smH4 isolate) (sooty mangabey).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "An African primate lentivirus (SIVsm) closely related to HIV-2.";
Nature 339:389-392(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO KNOWN AS THE RETROPEPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; pF00078; rvt; 1.
PROSITE: PS00141; ASP_PROTEASE; 1.
PROSITE: PS50175; ASP_ROT_RETROV; 1.
AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
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52;
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89262053; PubMed-2786147;
Hirsch V.M., Olmstead R.A., Murphey-Corb M., Purcell R.H.,
Johnson P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 93 BY SIMILARITY.
1019 AA; 115465 MW; 8D3DE0B85FC92BIC CRC64;
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P19505, 088140,
P19505, 088140,
01-FB5-1991 (Rel. 17, Created)
01-FB2-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                           1019 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.3%; Score 40; DB 57.1%; Pred. No. 52; iive 2; Mismatches
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                                                                                        01-0CT-1989 (Rel. 12, Created)
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MEROPS; A02.002; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000477; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001584; -. InterPro; IPR001969; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00665; rve;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DETERMINED.
                           POL_SIVS4
P12502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
POL_SIVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                 SO THE TARKET AND DESCRIPTION OF THE TRANSPORT OF THE TRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ă
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensea agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
-i- FUNCTION: THE ELONGATION OF PRIMED DNA TEMPLATES BY DNA POLYMERASE DELTA AND EPSILON REQUIRES THE ACTION OF THE ACCESSORY PROTEINS PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) AND ACTIVATOR 1 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
MEDLINE-94150718; PubWed-7906398;
MEDLINE-94150718; PubWed-7906398;
Milson R., Alnacough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Button J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Lakitsen J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Sonnhammer E., Staden R.,
Sulston J., Thierry-Med J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HETEROPENTAMER OF SUBUNITS OF 140/145, 40, 38, 37, AND 36.5 KDA THAT FORMS A COMPLEX WITH PCNA IN THE PRESENCE OF ATP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA replication; ATP-binding; Nuclear protein.

ATP (POTENTIAL).

8255 MW; 8E5CE68DIAE131D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       '2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PUTATIVE ACTIVATOR 1 36 KDA SUBUNIT (REFLICATION FACTOR C 36 KDA SUBUNIT) (A1 36 KDA SUBUNIT) (RF-C 36 KDA SUBUNIT) (RF-C 36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
SIMILARITY: BELONGS TO THE ACTIVATOR 1 36 TO 40 KDA SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                          447 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 21;
5; Mismatches
                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L23648; AAA28028.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myorhetical protein; DNA NP RIND 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 GDMRTVINTLQSTAMS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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160 GDLKTKVDVIGKVCG 174
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wohldman P.;
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elegans

FAMILY

Query Match

RESULT

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NP\_BIND

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Gaps

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Indels

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                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
DNAK PROTEIN (HEAT SHOCK 70 KDA PROTEIN) (65 KDA PROTEIN) (P65).
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 59.3 KDA PROTEIN IN TAP42-CYK2 INTERGENIC REGION.
WMR029C OR YM9973.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=2099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COILED COIL (POTENTIAL).
3B2A3C95B2D575AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 39; DB 1;
53.3%; Pred. No. 37;
live 4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 249213; CAA89144.1; -. SGD; S0004631; YMR029C. Hypothetical protein; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN 26 76 CO
SEQUENCE 523. AA; 59301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U50209; AAB01921.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 DLKHQLNQIQSKAVS 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P04475; 1DKY.
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Q49539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=232;
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                                                                                                                                                                   MEDLINE-90272009; PubMed=1971917; Dewhurst S., Embretson J.E., Anderson D.C., Mullins J.I., Fultz P.N.; "Sequence analysis and acute pathogenicity of molecularly cloned
                                                             Simian immunodeficiency virus (PBj14/BCL-3 isolate) (sooty mangabey). Viruses; Retroid viruses; Retroid viruses; Retroid viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
POL POLYPROTEIN (CONTAINS: PROTEASE (RETROPEPSIN) (EC 3.4.23.16); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Res. Hum. Retroviruses 8:1179-1187(1992).
PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
                                                                                                                                                                                                                                                                                                                  MEDIJUE-92368737; PubMed-1503826; Dewhurst S., Embretson J.E., Fultz P.N., Mullins J.I.; Embretson J.E., Fultz P.N., Mullins J.I.; Molecular clones from a non-acutely pathogenic derivative of SIVSmmPBJ14: characterization and comparison to acutely pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DETERMINED.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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PROSITE; PS00141; ASP_PROT_RETROV; 1.
AIDS: Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1022; 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 96 BY SIMILARITY.
1022 AA; 115869 MW; 16DFBEA03F289D6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00552; integrase; 1.
Pfam; PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M31325; AAA47753.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L03298; AAA4777.1; -. HSSP; P04584; 1JLD.
HIV; M31325; POL$SMMPBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 57.1.
8; Conservative
                                                                                                                                                                                                                                                         Nature 345:636-640(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001037; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001584; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001995; -.
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Pfam; PF00077; rvp; 1
Pfam; PF00078; rvt; 1
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                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=11738;
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                                                                                                                                                                                                                                       SIVSMM-PB;14
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Q05040;
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Best Local Similarity
Matches 6; Conserv
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CONFLICT
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHEC_RHIME STANDARD; PRT; 611 AA.
P50176; 08731;
01-07-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-) (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE)
HYDROXYBUTYRADE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE)
(POLYHYDROXYALKANOATE) POLYMERASE).
                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Willis L.B., Walker G.C., "The phbC (poly-beta-hydroxybutyrate synthase) gene of Rhizobium (Sinorhizobium) meliloti and characterization of phbC mutants."; Can. J. Microbiol. 44:554-564(1998).
                                                                                                                                                                                                                                                                                                                                                                                                          Tombolini R., Povolo S., Buson A., Squartini A., Nuti M.P.;
*Poly-beta-hydroxybutyrate (PHB) biosynthetic genes in Rhizobium
                                                                                                                                                                                                                                                                                                                   Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                      Length 600
                                                                                                            Indels
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                                                      1F928F72EABBDB6B CRC64;
                                                                                     Score 39; DB 1;
Pred. No. 43;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MONOMER (PROBABLE),
SUBCELLULAR LOCATION: CYTOPLASMIC,
     PROSITE: PS00297; HSP70_1; 1.
PROSITE: PS00329; HSP70_2; 1.
PROSITE: PS01036; HSP70_2; 1.
Chaperone: ATP-binding; Heat shock.
SPONENCE 600 AA; 65575 MW; 1F92
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96036213; PubMed-7582015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98405222; PubMed-9734305;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiology 141:2553-2559(1995)
                                                                                   50.0%;
PRINTS; PR00301; HEATSHOCK70
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 35-611 FROM N.A.
                                                                                               Local Similarity 46.7 nes 7; Conservative
                                                                                                                                                    555 ELKLKLDQIEAAAQS 569
                                                                                                                              2 DLKTQIDQVESTAGS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N., "Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced analysis of cDNA clones from human cell line KG-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 611;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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ABE8A9B17F87D7A9
                                                                                                                                                                          PHB biosynthesis; Transferase; Acyltransferase
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-NOV-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PROTEIN KIAA0136 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                  REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Pred. No.
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Pred. No.
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EMBL; AP000692; BAA89432.1; JOINED.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE=96127530; PubMed=8590280;
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                                         EMBL; AF031938; AAC61899.1; -. InterPro; IPR000073; -. Pfam; PF00561; abhydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
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U17227; AAA90984.1;
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T; Conserve
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477
481
611 AA;
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950 AA;
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                                                                                                                                                                                                                                                                                                                                 STRAIN=LA239;
MEDILINE-913121121; PubMed-1857207;
MEDILINE-9131212121 PubMed-1857207;
Jerlstroem P.G. Chhatwal G.S., Timmis K.N.;
"The IgA-binding beta antigen of the c protein complex of Group B streptococci: sequence determination of its gene and detection of two binding regions.";
Mol. Microbiol. 5:843-849(1991).
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                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bateman A., Eddy S.R., Chothia C., Members of the immunoglobulin superfamily in bacteria.";
Protein Sci. 5:1939-1942(1996).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
-!- SIMILARITY: CONTAINS I IMMUNOGLOBULIN-LIKE DOMAIN.
-!- SIMILARITY: TO OTHER STREPPOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1164;
89;
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MEMBRANE ANCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE DOMAIN.
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                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGA-BINDING (POTENTIAL). IGA-BINDING (POTENTIAL).
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Parm, Pr00746; Gram, Pos_anchor; 1.
PROSITE: PS00143; GRAM_POS_ANCHORING; 1.
Cell wall; Transmembrane; Receptor; Repeat; Signal;
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50.0%; Pred. No. 89;
iive 3; Mismatches
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864 ELKTEVEQLKST 875
 DLKTQIDQVEST 13
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P27951;
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TRANSMEM
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Gaps

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4; Indels

Conservative

Best Local Similarity Matches 7; Conserv

2 DLKTQIDQVESTAG 15

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Amenicate P.G., Scherer S.E., Li P.M., Evans C.A., Gocayne J.D.,
Amenicated P.G., Scherer S.E., Li P.M., Bookins R.A., Galle R.F.,
Banantides P.G., Scherer S.E., Li P.M., Bookins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Pandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Pandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Baxter E.G., Helt G., Change M., Miklos G.L.G.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Baxuendale J., Baytarktaroglu L., Beasley E.M.,
RA Ballew R.M., Baxuendale J., Baytarktaroglu L., Beasley E.M.,
RA Burkle K.G., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burkle K.G., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burkle K.G., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burkle K.G., Bouch L.E., Downes M., Dugan-Rocha S., Plottov S.,
RA Burkle K.G., Evangelista C.C., Ferraz C., Ferraz C., Ferrac S., Fleischman W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plasser K.,
RA Dodson K., Cong E., Garrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Jalail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kecthum K.A.,
Jalail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kalup D., Lai Z.,
Las Nochrosh M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Mount S.M., Melson K.A., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Nelson K.A., Wanskern D.R., Parle W.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Zhan M., Zhang G., Zhao Q., Zhan B.,
Zheng X.H., Zhong W., Zhong W., Zhan S., Zhan X., Zhan X.
                                                                                                              T2D7_DROME STANDARD; PRT; 278 AA.

Q27272; Q9VX16;

Q1.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
01.OCT-2000 (Rel. 40, Last annotation update)
01.OCT-2000 (Rel. 40, Last annotation update)
01.OCT-2000 (Rel. 40, Last sequence update)
(TARISCRIPTION INTITATION FACTOR TFIID 42 KDA SUBUNIT (TAFII-42)
(TAFII40) (P42) (ENHANCER OF YELLOW I PROTEIN).
E(Y)1 OR TAF40 OR CG6474.
Drosophila melanogaster (Fruit fly).
E(Y)1 OR TAF40 OR CG6474.
Drosophila melanogaster (Fruit fly).
E(Y)2 CS CG6474.
Drosophila melanogaster (Fruit fly).
E(Y)1 OR TAF40 OR CG6474.
Drosophila melanogaster (Fruit fly).
E(Y)1 OR TAF40 OR CG6474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodrich J.A., Hoey T., Thut C.J., Admon A., Tjian R.; "Drosophila TAFII40 interacts with both a VP16 activation domain and the basal transcription factor TFIIB."; Cell 75:519-530(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-94150630; PubMed=7545910;
KOKUDO T., Gong D.W., Wootton J.C., Horikoshi M., Roeder R.G.,
Nakatani Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of Drosophila TFIID subunits."; Nature 367:484-487(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=OREGON-R;
MEDLINE=94037099; PubMed=8221891;
84 DIKKAVEPVEKTAG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                             YG3A_YEAST
P53278;
                                                                                                                                                                  NP_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                    RESULT 14
YG3A_YEAST
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TEGU_HSV6G
                                                                                                                                                                                                                                              Matches
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                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-97354111; Pubmed-9210332;
Mizoguchi H., Masuda T., Nishimura K., Shimada H., Ohta H., Shioi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                              (TFIID) COMPLEX THAT ARE ESSENTIAL FOR MEDIATING REGULATION OF RNA POLYMERASE TRANSCRIPTION (BY SIMILARITY).
SUBUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A NUMBER OF TBP-ASSOCIATED FACTORS (TAFS).
SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE TAF2G FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   that controls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence and transcriptional analysis of the flanking region of the gene (spb) for the trans-acting factor that control. light-mediated expression of the puf operon in Rhodobacter
                                   -1- FUNCTION: TAFS ARE COMPONENTS OF THE TRANSCRIPTION FACTOR IID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S-ADENOSYL-L-HOMOCYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- COFACTOR: NAD (BY SIMILARITY).
-1- PATHWAY: ACTIVATED METHYL CYCLE.
-1- SIMILARITY: BELONGS TO THE ADENOSYLHOMOCYSTEINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 1; Length 278;
Pred. No. 28;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Cell Physiol. 38:558-567(1997).
-1- CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)0
ADENOSINE + L-HOMOCYSTEINE.
                                                                                                                                                                                                                                                                                                                                                                        POLY-GLU (ACIDIC).
0EA442C80467001F CRC64;
             Drosophila melanogaster.";
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster. Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 463 AA.
                                                                                                                                                                                                                                                                                          TRANSFAC; T02125; -. FlyBase; FBgn0000617; e(y)1. Transcription regulation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                               POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                         274 E
29314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%;
                                                                                                                                                                                                                                           EMBL; U06458; AAC47347.1; -.
                                                                                                                                                                                                                                                                   EMBL; AE003506; AAF48767.1;
HSSP; P30129; 4DPV.
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 43...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 GDLKMEVDSDAAAVGS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROLASE) (ADOHCYASE).
                                                                                                                                                                                                                                                        EMBL; L29540; AAA28488.
                                                                                                                                                                                                                                                                                                                                                                                    278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodobacter.
NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                               202
250
250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rakamiya K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAHH_RHOSH
050562;
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on Instee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla E., Nawrocki A., del Bino S., Goffeau A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 92.7 KDA PROTEIN IN ASNZ-PHB1 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                             Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 816;
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                                                                                                                                                                                                                                                                                                                  NAD (POTENTIAL).
ACE8EB9D0D0CCBBA CRC64;
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D482327C9274C026 CRC64;
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89;
                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                        DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.7%; Score 38; 50.0%; Pred. No.
                                                                                                                                                                                                                                                                                      Hydrolase; NAD; One-carbon metabolism.
NP_BIND 247 278 NAD (POTE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER
                                                                                                                                                                                                               Pfam; PF00670; AdoHcyase; 1.
PROSITE; PS00738; ADOHCYASE_1; 1.
PROSITE; PS00739; ADOHCYASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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                                                                                                                                                                                                                                                                                                                                        50617 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z72915; CAA97143.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               48.7%;
40.0%;
                                                                                                                                                                    EMBL; U76671; AAB88245.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 NIKDQVDMIEMPSGS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0003362; YGR130C.
                                                                                                                                                                                             InterPro; IPR000043; -.
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460 DLQNQIDEIENS 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
DOMAIN 164 18
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                                                                                                                                                                                                                                                                                                                                           463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  816 AA;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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PRT; 2077 AA.

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 2077;
Pred. No. 2.5e+02;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S57540; AAB19786.1; -.
PIR; H40511; WZBEZ4.
SEQUENCE 2077 AA; 239909 MW; 28E297FDC2FAD2AE CRC64;
                                                                                        Human herpesvirus (type 6 / strain GS) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=10369;
                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.78;
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                LARGE TEGUMENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conservat
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5, 2001, 11:51:44 Search completed: July Job time: 503 sec

|:||:||::||:: 1084 DVKTEIDQMQKS 1095

2 DLKTQIDQVEST 13

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 5, 2001, 11:50:49; Search time 123.78 Seconds

Title: US-09-462-480-9

Perfect score: 78
Sequence: 1 GDLKTQIDQVESTAGS 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_bunda:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mncal:\*
7: sp\_mnc:\*
8: sp\_organelle:\*
9: sp\_phage:\*
10: sp\_phage:\*
11: sp\_rodent:\*
11: sp\_vertebrate:\*
14: sp\_virus:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_16:\*'

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SHIMMARTES

					SUMMAKES	
		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	Ω	Description
-	78	100.0	100	7	069739	069739 mycobacteri
7	46	59.0	1163	10	Q9SHT1	Q9sht1 arabidopsis
m	44	56.4	2954	14	096898	Q96898 hepatitis q
4	43.5	55.8	630	m	013870	013870 schizosacch
ഗ	43	55.1	1068	~	86MC6Q	Q9jw98 neisseria m
9	43	55.1	1082	~	Q9JXM7	Q9jxm7 neisseria m
7	43	55.1	1084	~	Q9JPL3	Q9jpl3 neisseria m
80	42	53.8	9	11	Q9EPM6	Q9epm6 mus musculu
6	42	53.8	2756	7	.033904	033904 shewanella
10	41	52.6	497	7	Q9ZDU5	Q9zdu5 rickettsia
11	41	52.6	533	٦	Q9YCP2	Q9ycp2 aeropyrum p
12	41	52.6	675	S	Q9VYB1	Q9vyb1 drosophila
13	41	52.6	779	S	Ø9W0U8	Q9w0u8 drosophila
14	41	52.6	1616	Ŋ	05x80	Q9vsj0 drosophila
15	40	51.3	271	7	032408	032408 rhodospiril
16	40	51.3	280	S	Ø9VL68	Q9v168 drosophila
17	40	51.3	442	Ŋ	Q9XVE5	Q9xve5 caenorhabdi
18	40	51.3	533	6	080226	O80226 bacteriopha
19	40	51.3	1019	14	P89154	P89154 chimpanzee

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Simons J.N., Desai S.M., Schultz D.E., Lemon S.M., Mushahwar I.K.;
"Translation initiation in GB viruses A and C: evidence for internal
ribosome entry and implications for genome organization.";
J. Virol. 70:6126-6135(1996).
-!- SIMILARITY: TO HEPATITIS C VIRUS RNA DEPENDENT RNA POLYMERASE.
BEMBL; U22303; ARS55983.1;
-- RSSP; P27958; 1HEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMO0487; DEXDC; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
SEQUENCE 2954 AA; 318835 MW; 4A0C35FCZED283B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002166; ...
InterPro; IPR002518; ...
InterPro; IPR002518; ...
Pfam; PF00098; HCV_RdRP; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS3a; 1.
Pfam; PF01506; HCV_NS2; 1.
Pfam; PF01538; HCV_NS2; 1.
PROS_TTE; PF00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                        Proc. Natl. Acad. Sci. U.S.A. 92:3401-3405(1995).
                                                               SEQUENCE FROM N.A.
MEDLINE=96323131; PubMed=8709237;
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50.0%;
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InterPro; IPR000745; -.
InterPro; IPR001410; -.
InterPro; IPR001490; -.
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630 AA;
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Best Local Similarity
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Best Local Similarity
Matches 11; Conserv
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KA MEDLINE-2008487; Pubmed-10617192;

KA MEDLINE-2008487; Pubmed-10617192;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Rujil C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Ruell C.R., Kerchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayama L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T. H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Adams M.D., Carrera A.J., Creasy T. H., Goodman H.M., Somerville C.R.,

Ralzberg S.L., Fraser C.M., Venter J.C.;

R. Sequence and analysis of chromosome II of Arabidopsis thaliana.";

R. Mature 402.761.768(1999).

R. InterPro; IPR003405; -.

R. InterPro; IPR03405; -.

R. Pfam; PF02483; SMC_C; I.
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MEDLINE-95241511; Pubmed-7724574;
Simons J.N., Pallot-Matias T.J., Leary T.P., Dawson G.J., Desai S.M.,
Schlauder G.G., Muerhoff A.S., Erker J.C., Buijk S.L., Chalmers M.L.,
van Sant.C.L., Mushahwar I.K.;
"Identification of two flavivirus-like genomes in the GB hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicates; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis GB virus A.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
NCBL_TaxID=39112;
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26;
  Length 100;
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A; 134366 MW; 775AD20AEA526B40 CRC64;
                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
100.0%; Score 78; DB 2; I 100.0%; Pred. No. 6.9e-06;
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Pred. No. 26;
4; Mismatches
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61.5%;
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Matches 8; Conservative
                                           Conservative
                                                                                   1 GDLKTQIDQVESTAGS 16
                                                                                                            23 GDLKTQIDQVESTAGS 38
                                                                                                                                                                                                                                         PRELIMINARY;
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710 GDIRTRIDQVRSS 722
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Matches 16; Conserv
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  Query Match
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 Length 2954;
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Score 44; DB 14; Length 29
Pred. No. 1.5e+02;
3; Mismatches 5; Indels
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Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR C1B3.05.
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llarity 47.8%; Pred. No. 36;
Conservative 3; Mismatches
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POLY-ALA.
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385 PG
627 PG
71715 MW;
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Complete genome sequence of Neisseria meningitidis serogroup B strain
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Turner D., Wooldridge K.G., Ala'Aldeen D.A.A.;
Turner D., Wooldridge K.G., Ala'Aldeen D.A.A.;
Tufentification and characterisation of an autotransporter serine protease in Neisseria meningitidis.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ277537; CAB89119.1;
InterPro; IPR000209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                               ore 43; DB 2; Length 1082; ed. No. 78; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1084;
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                                                                                                                                 Interpro; IPR000209; -.
Pfam: PF00082; Peptidase_S8; 2.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00138; SUBTILASE_SER; UNKNOWN.1.
SEQUENCE 1082 AA; 113614 MW; 377E9C7177FAF056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33BC30E9543D0AC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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ULWAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
FTVE-FINGER CONTAINING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 2;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1084 AA.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00082; Peptidase_S8; 2. PRINTS; PR00723; SUBTILISIN.
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                                                                                                                                                                                                                                                                                                                                  55.1%;
56.2%;
                                                                            EMBL; AE002545; AAF42298.1;
TIGR; NMB1969; -.
                                                    Science 287:1809-1815(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      668 GGLLASLDSVEKTAGS 683
                                                                                                                                                                                                                                                                                                                                  Query Match 55.1
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis
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Matches 9; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09EPM6;
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Q9EPM6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
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MEDLINE-20175755; Pubmed=10710307;
Tettelin H., Saunders N.J., Heldelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani W., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;

STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;

STRAIN-2022556 PubMed-10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamiin N., Holroyd (Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D8213CEAB86206A1 CRC64;
                                                                                                                                                                                                                                       09JW96,
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE OUTER MEMBRANE PEPTIDASE (EC 3.4.21.).
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Last annotation update)
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                                                                                                                                                                                                                      PRT; 1068 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEROTYPE-1-SPECIFIC ANTIGEN, PUTATIVE NMB1969.
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01-OCT-2000 (TrEMBLrel. 15, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1068 AA; 111854 MW;
                                                          35 GDLKTQIKKLQRLRDQIKTWASS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00082; Peptidase_S8; 2. PRINTS; PR00723; SUBTILISIN.
                          1 GDLKTQI-----DQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 404:502-506(2000).
EMBL; AL162753; CAB83773.1; -.
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56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=65699;
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
Cranarchaeon, Aeropyrum pernix KI.";
EMBL, APO00061; BAA802051; -.
                                                                                                                                                                                          Nature 396:133-140(1998).
-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE KINASES.
                                                        STRAIN-MADRID E;
MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aeropyrum pernix.
Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                         Interpro; IPR000410; -...
Interpro; IPR00354; -...
Pfam; PF00512; signal; 1...
PRINTS; PR00344; BCTRLSENSOR.
SMRTY; SM00387; HATPASS—C; 1...
Kinase; Phosphorylation; Sensory transduction; Transferase.
SEQUENCE 497 AA; 56908 WW; 781C9147531F388D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 533;
Pred. No. 80;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 56.5 KDA PROTEIN APE1216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00194; TROPOMYOSIN.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.6%; Score 41; DB
53.3%; Pred. No. 74;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K1;
MEDLINE-99310339; PubMed-10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEOUENCE 533 AA; 56481 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.6%;
66.7%;
                                                                                                                                                                                                                                                        EMBL; AJ235271; CAA14692.1;
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 NLKAQIEKVEKTSSS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000533; -. InterPro; IPR001865; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLKTQIDQVEST 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=56636;
    NCBI_TaxID=782;
                                                                                                                                                                                mitochondria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aeropyrum.
                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APE1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9YCP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9YCP2
    OX
RRN
RRT
RRT
RRT
RRT
DR
DR
DR
DR
DR
SO
SO
SO
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                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takeyama H., Takeda D., Yazawa K., Yamada A., Matsunaga T.; "Expression of the eicosapentaenoic acid synthesis gene cluster from Shewanella sp. in a transgenic marine cyanobacterium, Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
      Cormont M., Mari M., Galliche A., Le Marchand-Brustel Y.;
"Rablp4, a new FYVE-finger containing protein, is a Rab4 effector-involved in the fusion between Rab4 and Rab5 positive endosomes.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ50024, CAC17732.1;
NON_TER
                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shewanella sp. SCRC-2738.
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                              DB 11; Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2756;
                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Phosphopantetheine.
SEQUENCE 2756 AA; 292671 MW; 910FF442DB5F7759 CRC64;
                                                                                                                                   600 AA; 69054 MW; A2580582CC1249B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 292.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 2;
Pred. No. 3.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 2756 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 AA
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Last annota
HISTIDINE KINASE SENSOR PROTEIN (BARA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=SCRC-2738;
MEDLINE=97419510; PubMed=9274025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001227; - Pfam; PF00109; ketoacyl-synt; 1. Pfam; PF00550; pp-binding; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00698; Acyl_transf; 1.
PROSITE; PS50075; ACP_DOMAIN; 6.
                                                                                                                                                                                            53.8%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp.";
Microbiology 143:0-0(0).
EMBL; U73935; AAB81123:1; -.
InterPro; IPR000255; -.
InterPro; IPR000794; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 GSVKSQIGHTKSTAGT 412
                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.8
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GDLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
TISSUE=SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                             215 GDLQTKIDGLEKT 227
                                                                                                                                                                                                                                                                         1 GDLKTQIDQVEST 13
                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=53560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shewanella.
                                                                                                                   NON_TER
SEQUENCE
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Gaps

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Q9zbus ID Q9zbus **092DU5** 

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RESULT 033904

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Q9VYB1 Q9VYB1;

RESULT 12 O9VYB1

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RR STAIN-BERKELEY;
RAMIN-BERKELEY;
RAMIN-BERKELEY;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams H.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galla R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S.C., Champe M., Heafiffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.W., Bause D.A., Berman B.P., Banadari D., Bolshakov S.,
RA George R.Y., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.E., Butler H., Cadieu E., Center A., Chadra I.,
RA Graylos B., Delcher A., Dong Z., Mays A.D., Dow I., Dletz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J. Evorgelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J. Evorgelista C.C., Ferraz C., Ferriera S., Fleischmann M.,
RA Goog F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mosherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murphy D., Shu R.,
Rhaizzolo, M., Pittuman G.S., Pan S., Pollard J., Wan R.,
Rhaizzolo, M., Pittuman S.S., Pan S., Pollard J., Wan R.,
Rhaizzolo, M., Pittuman S.S., Pan S., Pollard J., Wan R.,
Rhaizzolo, M., Pittuman S., Supeler E., Scheller F., Shen H.,
Rhaizzolo, M., Pittuman S., Stapler E., Scheller F., Shen H.,
Rhaizzolo, M., Pittuman S., Stapler E., Scheller F., Shen H.,
Rhaizzolo, S., Stapler E., Staple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhu X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DICE 28 :2185 :2195 (2004)
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHARI, SHUUSEN, SHOUTHELICAL PROTEIN.
Alternative splicing; Hypothetical protein.
VARSPELC 1 211 MISSING (IN SHORT ISOFORM).
SERNIFRICE 779 AA: 84174 MW; 68B883F198CA45F6 CRC64;
                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0035101; p130CAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003467; AAF47336.1; -. HSSP; P29354; 1GRI.
                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003467; AAF47335.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - ALTERNATIVE PRODUCTS:
                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR001452;
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                                                                                                                                                                                                                                       P130CAS OR CG1212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
                                                                                                                                                                                                      P130CAS PROTEIN
                                                                                        09W0U7
                                                            Q9W0U8
   RESULT
                                 800M60
                                                                                        RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Amanatides P.G., Scherer S.E., I.I P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Batton G.G., Worthan J.R., Vandell M.D., Zhang O., Chen L.X.,
RA Batlaw R.W., Doyle C., Baxter E.G., Helt G., Nolson C.R., Mikhos G.L.G.,
RA Batlaw R.M., Basu A., Baxendale J., Baytaktarolu L., Beasley E.M.,
RA Besson K.Y. Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.D., Cavley S., Dallike C., Davenport L.B., Davies P.,
RA Burtis K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
RA Boson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,
Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,
RA Borlos B., Calcher A., Howland T.J., Wei M. -H., Ibeywan C.,
A Jalail M., Kalush F., Katpen G. H., Ke Z., Kannison J.A., Ketchum K.A.,
A Jalail M., Kalush F., Katpen G. H., Ke Z., Kannison J.A., Ketchum K.A.,
A Munch B.E., Kodira C.D., Kraft C., Kraft C., Morris J., Moshrefi A.,
R. Mamel B.E., Kodira C.D., Kraft C., Kraft C., Morris J., Moshrefi A.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Bazzolo M., Pittmano G.S., Pan S., Pollard J., Wang X.,
Rhung B.E., Sodira K. Musskern D.R., Parly W., Respenden J.,
Rhung S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Rhang Z.-Y., Wassarman D.A., Waltstoner R., Venter E., Wang K.,
Rhung Z.-Y., Santh T.,
Rhyer S., Shenliston M., Strong R., Walsenber B.,
Rhyers R., Tector C., Turner R., Venter E., Wang G., Zhon G., Zhon G., Shence S., Shence S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Epiydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C63451BF921E99E7 CRC64;
                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                  675 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0030500; CG9938.
SEQUENCE 675 AA; 77888 MW;
                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE003493; AAF48292.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 287:2185-2195(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1|||||: |:|:
309 GDLKTKLQQLEN 320
388 DLNTRLDQVAST 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GDLKTQIDQVES 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           CG9938 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY
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Search completed: July 5, 2001, 11:50:50 Job time: 473 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAINTH-BERKELEY;

RATAN-BERKELEY;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Holt R.A., Pabharer M., Henderson S.N.,

RA Burdon R.C., Rogers Y.-H.C., Blazes R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazes R.G., Relt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Rolsmicch C. R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Rolsmicch C. R., Miklos G.L.G.,

RA Berkova D., Botcham M.R., Bouck J., Borkstein P., Botchier P.,

RA Borkova D., Botcham M.R., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Gebroon R., Doup L.E., Downes M., Dugan Rocha S., Pleischman W.,

RA Botchin D., Houston K.A., Howland T.J., Wei M.-H., Ibegarer K.,

Alothin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,

RA Hartis N.L., Harvey D., Hamman T.J., Hernandez J.R., Houck J.,

RA Hartis N.L., Harvey D., Hamman T.J., Hernandez J.R., Houck J.,

Alothin M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,

Lasko P., Lei Y., Lewitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,

Lasko P., Lei Y., Lewitsky A.A., Li J., Marny D.M., Nelson D.L.,

Relear M., Moy M., Murphy E., Murphy L., Muzny D.M., Nelson D.R.,

Relear K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Rabics R., Jeckler C., Sten-Kiames I., Simpson M., Strong R., Shith T.,

Raber B.C., Siden-Kiamos I., Simpson M., Strong R., Weller E., Spradling A.C., Stabeler E., Spradling A.C., Stabeler E., Spradling A.C., Stabeler E., Spradling S.M., Woolage T., Worley R., Worley R.,
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBL_TaxID-7227;
                                                                            Gaps
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TISSUE-EMBRYO, AND IMAGINAL DISKS;

Clark K.E., vesenka G.D., Robertson J.P., Natzle J.E.,

"Itssue specific regulation of the ecdysone-inducible gene IMP-El.";

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

-: SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS A
                                                                         ö
                 Length 779;
Score 41; DB 5; Leuy...
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                O9VSJO, O9VSI9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ECDYSONE INDUCIBLE GENE E1.
IMPEI OR CG7116 OR CG13668.
                                                                                                                                                                                                                                                                                                                           PRT; 1616 AA.
              52.6%;
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        Query Match
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                              594 DLKTQFDTVIRTAES 608
                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                           2 DLKTQIDQVESTAGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LDLRA) DOMAIN.
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Q9VSJ0
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Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Phaeospirillum.
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                                                                                                                                                                                                                                                                                                                    D -> E (IN AAF50429).
K -> E (IN AAF50429).
G -> A (IN AAF50429).
S -> P (IN AAF50429).
EELHIP -> VECHIA (IN AAF50429).
WW: 83822D1A8E48D5FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .51.3%; Score 40; DB 2; Length 271; 72.7%; Pred. No. 57; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Nagashima K.V., Matsuura K., Shimada K.;
Nagashima K.V., Matsuura K., Shimada K.;
Photosyu. Res. 50:61-70(1996).
EMBL; D50654; BAA22794.1; -.
NON_TER 1 1
SEQUENCE 271 AA; 29711 MW; D483D34750FB2DF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         032408;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
BACTERIOCHLOROPHYLL BIOSYNTHETIC ENZYME (FRAGMENT).
                                                                                                                 Interpro; IPR002172; ...
Interpro; IPR003015; ...
Pfam; PR0057; ILL_recept_a; 4.
PRINTS; PR00261; LDLRECEPTOR.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01086; EGF_2; UNKNOWN_1.
PROSITE; PS010039; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE; PS010039; LDLRA_1; 2.
PROSITE; PS01009; LDLRA_1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 5; I
Pred. No. 2.6e+02;
5; Mismatches 1;
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1138 1138 S ->
1153 1158 EELHI
1616 AA; 176966 MW; E
EMBL, AE003555; AAF50429.1; AL
EMBL, AE0035555; AAF50430.1; AL
EMBL, AF217281; AAF27637.1; --
HSSP; P01130; 1AJJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
                                                          HSSP; P01130; 1AJJ.
FlyBase; FBgn0001253; ImpEl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.8°
"...a. 7; Conservative
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Matches 8; Conservative
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                                                                                                InterPro; IPR000561; -.
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890
1048
1138
1158
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| 651 DMESEIDQVEQSA 663
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188 LGTQLDQVEAT 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1083;
                                                                                                                                                                                                                                                                                                   Glycoprotein
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                        CONFLICT
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Thu Jul 5 13:59:14 2001

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OM protein - protein search, using sw model

Run on:

July 5, 2001, 11:45:43; Search time 130.35 Seconds (without alignments) 9.767 Million cell updates/sec

1 QEAGNFERISGDLKYTQIDQV 21 US-09-462-480-8 107 Perfect score: Sequence:

Scoring table:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** 

412676 segs, 60623988 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1981.DAT:\*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1982.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|   | Description              |   | M. tuberculosis LH | M. tuberculosis LH | Mycobacterium tube | Mycobacterium tube | M. tuberculosis im | Mycobacterlum tube | Mycobacterium tube | M. tuberculosis an | M. tuberculosis re | M. tuberculosis im | Mycobacterium tube |
|---|--------------------------|---|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|   |                          |   | AAY03708           | AAY03706           | AAW32444           | AAW32376           | AAW81747           | AAW64321           | AAY32097           | AAY39118           | AAY38981           | AAW81706           | AAWKA339           |
|   | EG                       | ; | 20                 | 20                 | 18                 | 18                 | 19                 | 19                 | 20                 | 20                 | 20                 | 19                 | 9                  |
|   | Query<br>Match Length DB |   | 70                 | 49                 | 95                 | 95                 | 95                 | 95                 | 95                 | 95                 | 95                 | 100                | 100                |
| - | Query                    |   | 83.6               | 83.6               | 83.6               | 83.6               | 83.6               | 83.6               | 83.6               | 83.6               | 83.6               | 83.6               | 83.6               |
|   | Score                    |   | 89.5               | 89.5               | 89.5               | 89.5               | 89.5               | 89.5               | 89.5               | 89.5               | 89.5               | 89.5               | 89.5               |
|   | Result<br>No.            |   | ٦                  | 7                  | 9                  | 4                  | 'n                 | 9                  | 7                  | 8                  | 6                  | 10                 | 11                 |

| M. tuberculosis an<br>M. tuberculosis re<br>M. tuberculosis LH<br>M tuberculosis Rv3<br>Mycobacterium tube<br>M. tuberculosis fu | y cobacterium a grobacterium t tuberculosis tuberculosis tuberculosis tuberculosis tuberculosis tuberculosis tuberculosis tuberculosis tuberculosis yoobacterium t | ulosi<br>ulosi<br>ulosi<br>ulosi<br>chai<br>chai                          | rabidopsi<br>rabidopsi<br>rabidopsi<br>rabidopsi<br>rabidopsi<br>rabidopsi<br>rabidopsi |
|----------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|
| AAY3913<br>AAY3899<br>AAY0370<br>AAB3521<br>AAB1984<br>AAW8174                                                                   | AAW3917<br>AAX3917<br>AAX3917<br>AAX3908<br>AAX3908<br>AAW3245<br>AAW3245                                                                                          | AAW8170<br>AAW8134<br>AAY3899<br>AAY3899<br>AAR9437<br>AAW3920<br>AAY0376 |                                                                                         |
|                                                                                                                                  | 8002 20<br>8002 20<br>8002 20<br>8002 20<br>28 119<br>80 20<br>80 20<br>80 20<br>80 10<br>80 10                                                                    |                                                                           |                                                                                         |
|                                                                                                                                  |                                                                                                                                                                    | 444446600                                                                 | 04444000<br>004444000<br>0000000000000000000                                            |
| 000000                                                                                                                           | 088888877744<br>00000000044477<br>1.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0                                                                                          | 4                                                                         | 44444444<br>666666770                                                                   |
| 12<br>13<br>14<br>15<br>17                                                                                                       | 7861222222222222222222222222222222222222                                                                                                                           | 9 3 3 3 3 3 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6                                 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                   |

## ALIGNMENTS

AAY03708 standard; Protein; 20 AA. AAY03708 RESULT

AAY03708;

(first entry) 07-JUN-1999

M. tuberculosis LHP polypeptide antigenic fragment.

ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; immune response. 

Mycobacterium tuberculosis.

WO9904005-A1.

28-JAN-1999

98WO-IB01091. 16-JUL-1998;

97US-0052631. 16-JUL-1997; (INSP ) INST PASTEUR. (STAT-) STATENS SERUM INST.

Rasmussen PB; Andersen P, Berthet F, Gicquel B,

WPI; 1999-132249/11.

New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis - useful in vaccines, for diagnosis, and for expression of heterologous proteins

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The present invention is directed to a polynucleotide carrying the regulatory expressions signals of the ESAT-6 protein as well as an open regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the M. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two provide a synergistic increase in ability to induce a protective immune process. Sequences AAV03706-713 represent antigenic fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid containing reguid for and LHP gene of Mycobacterium tuberculosis – useful in vaccines, for diagnosis, and for expression of heterologous proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. tuberculosis LHP polypeptide antigenic fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 89.5; DB 2
Pred. No. 5e-08;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersen P, Berthet F, Gicquel B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                 Claim 21; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; Page 64; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QEAGNFERISGDLKYTQIDQV 21
                                                                                                                                                                                                                                                                                                                                                                                                                    83.6%;
95.2%;
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(STAT-) STATENS SERUM INST
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                               20 AA;
                                                                                                                                                                                                                                                                                                                              polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response.
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recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the M. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein mycobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, the and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune response. Sequences AAY03706-713 represent antigenic fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, FDS3-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins ESAT-6, are useful in vaccines, preferably when formulated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW;
                                                                                                                                                                                                                                                      Length 49;
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                   Score 89.5; DB 20;
Pred. No. 1.3e-07;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis antigen Tb38-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAW32444 standard; Protein; 95
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                                                                                                                                                                                                                                                      83.6%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     skin testing; M.tuberculosis.
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95US-0523436.
95US-0533634.
96US-0620874.
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Twardzik DR, Vedvick TH;
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                                                                                                                                                                                                                                                                                                                                    1 QEAGNFERISGDLKYTQIDQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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N-PSDB; AAT91509.
                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                        49 AA;
                                                                                                                                                                            LHP polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-1995;
22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1996;
                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-1996
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Best Local S:
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW32444;
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                                                                                                                                                                                                                                                                                                                                                                Length 20;
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AAW32376

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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequencan be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                             Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculosis; infection; diagnosis; antigen; Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.6%; Score 89.5; DB 19;
95.2%; Pred. No. 2.7e-07;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis antigen Tb38-1 peptide
                                                                                                                                                                                                                              M. tuberculosis immunogenic polypeptide Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3b; Page 117; 230pp; English.
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                                                                                                                           95
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       21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                      27
                                                                                                                         AAW81747 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US18293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0818112.
96US-0730510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QEAGNFERISGDLKYTQIDQV
                       8 qeagnferisgdlk-tqidqv
                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QEAGNFERISGDLKYTQIDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis of tuberculosis.
                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-261042/23.
N-PSDB; AAV64491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                    WO9816646-A2
                                                                                                                                                                                              27-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1998
                                                                                                                                                             AAW81747;
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                                                                                                          AAW81747
                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic polypeptide can be used to diagnose antigen, Tb38-1. The immunogenic polypeptide can be used to diagnose antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW;
                                                                                                         95;
non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 95;
                                                                                                          Length
                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89.5; DB 18;
Pred. No. 2.7e-07;
0; M.smatches 0;
                                                                                                       Score 89.5; DB 18;
Pred. No. 2.7e-07;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 136; 190pp; English.
                                                                                                                                                                                                                                                                                              AAW32376 standard; Protein; 95 AA.
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                                                                                                                                                                            21
                                                                                                                                                                                            8 qeagnferisgdlk-tqidqv 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                          skin testing; M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9605-0680573.
9505-0523435.
9505-0532136.
9605-0620280.
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Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                       83.6%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US14675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campos-neto A, Dillon DC,
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                          1 QEAGNFERISGDLKYTQIDQV
                                                                                                                                                                                                                                                                                                                                                                   13-JAN-1998 (first entry)
                                                                                                                                         20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-192904/17.
N-PSDB; AAT91445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
                                                      95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-AUG-1996;
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05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-1997
                                                                                                                                                                                                                                                                                                                                  AAW32376;
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Gaps

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Length 95; Indels

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New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis
                                                                                                                                                                                                                This sequence represents the Mycobacterium tuberculosis antigen TD38-1. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens such as TD38-1, e.g. TDF-2 (see AAY32063) and a TB49-TD38-1 fusion. The new fusion proteins are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis; M. tuberculosis; antigen; immunimmunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. tuberculosis antigen Tb38-1 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                       83.6%; Score 89.5; DB 20;
95.2%; Pred. No. 2.7e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on DC, Hendrickson RC, Hor
Skeiky YAW, Twardzik DR,
                                                                                      Campos-Neto A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY39118 standard; Protein; 95 AA.
                                                                                                                                                                                        Claim 1; Fig 4D; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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             98US-0056556
98US-0223040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US03268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 qeagnferisgdlk-tqidqv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QEAGNFERISGDLKYTQIDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                      Skeiky YAW, Alderson
                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-527409/44.
                                                                                                                 WPI; 1999-601610/51
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                               95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9942076-A2.
               07-APR-1998;
30-DEC-1998;
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18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY39118;
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Matches
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ID AAY39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                         This is an antigenic portion of Mycobacterium tuberculosis antigen TD38-1. A DNA sequence (see AAV44384) coding for antigen TD38-1 was isolated from a M. tuberculosis strain H37Rv expression ID18-TSY. The invention relates to compositions and methods for diagnosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of as soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                    New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis; antigen; fusion protein; Tb38-1; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                   Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89.5; DB 19;
Pred. No. 2.7e-07;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis antigen Tb38-1.
             Mycobacterium tuberculosis strain H37Rv.
                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 123; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.6%;
95.2%;
                                                                                                97WO-US18214
                                                                                                                             97US-0818111
96US-0729622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                               WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 AA;
                                                                                                                                                                                                                                                         N-PSDB; AAV44384
                                        WO9816645-A2
                                                                                                  07-OCT-1997;
                                                                                                                             13-MAR-1997;
11-OCT-1996;
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                                                                       23-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Gaps

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95;

Length Indels

Example 3;

Sequence

Query Match

Matches

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Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis (MT) antigen which can be used in a methot for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunishing against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents an immunogenic portion of a soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to A, Dillon DC, Houghton R, Lodes MJ;
Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 89.5; DB 19;
Pred. No. 2.9e-07;
); Mismatches 0;
Score 89.5; DB 20;
Pred. No. 2.7e-07;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                           M. tuberculosis immunogenic polypeptide Tb38-IN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3B; Page 138-139; 230pp; English.
                                                                                                                                                                                   AAW81706
ID AAW81706 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 100 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.6%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0818112.
96US-0730510.
   83.6%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US18293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QEAGNFERISGDLKYTQIDQV
                                                                          1 QEAGNFERISGDLKYTQIDQV
                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                         (first entry)
 Query Match 83.6
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-261042/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9816646-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1997;
                                                                                                                                                                                                                                                                         27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1998
                                                                                                                                                                                                                                       AAW81706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                            δ
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                                The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                             95;
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                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                  Indels

    M. tuberculosis recombinant antigen protein Tb38-1.

                                                                                                                                                                                                                                                                                                         Score 89.5; DB 20;
Pred. No. 2.7e-07;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hendrickson RC, Ho
YAW, Twardzik DR,
Page 113; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY38981 standard; Protein; 95 AA
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                                                                                                                                                                                                                                                                                                           83.6%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto A, Dillon DC,
Lodes MJ, Reed SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US03265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 159; 323pp;
                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-527416/44
                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                        95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ19082
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05-NOV-1999

AAY38981;

AAY38981

05-MAY-1998; 18-FEB-1998;

17-FEB-1999; 26-AUG-1999

WO9942118-A2

vaccine;

method

ij

Indels

95

Sequence

Length 100;

13-MAR-1997; 11-OCT-1996;

SG.

07-OCT-1997;

23-APR-1998

WO9816645-A2

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The present invention describes polypeptides comprising an immunogenic are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis: Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AAX19494 to AAX19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89.5; DB 20; Length 100;
Pred. No. 2.9e-07;
0; Mismatches 0; Indels 1
                                                                                                                                                              Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on DC, Hendrickson RC, Houghton R;
Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. tuberculosis recombinant antigen protein Tb38-IN.
                                                                                                                                                              Dillon DC, Hendrickson RC, Ho
SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                        Example 3; Page 133-134; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY38993 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 qeagnferisgdlk-tqidqv 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.6%;
95.2%;
                    99WO-US03268
                                                          98US-0072967
98US-0025197
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98US-0024753
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Reed SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 83.6
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                   Reed SG,
                                                                                                                                                                                                                        WPI; 1999-527409/44.
                                                                                                                      (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 AA;
                                                                                                                                                            Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campos-Neto A,
                    17-FEB-1999;
                                                            05-MAY-1998;
                                                                               18-FEB-1998;
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                                                                                                                                                                                     Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises a partial sequence of Mycobacterium tuberculosis antigen Tb38-IN. It is encoded by genomic DNA isolated from a M. tuberculosis strain H37Rv genomic library using a probe derived from clone Tb38-1 (see AAV44384). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA. sequences encoding such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis antigen, as well as DNA sequences encoding such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 100;
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immunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                       infection; diagnosis; antigen; Tb37-FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis antigen Tb38-IN amino acid sequence.
                                                                                                                                                                                                                                                                                                                                         Dillon DC, Houghton R, Lodes MJ; YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89.5; DB 19;
Pred. No. 2.9e-07;
); Mismatches 0;
Mycobacterium tuberculosis antigen Tb38-IN
                                                                               tuberculosis strain H37Rv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 145; 250pp; English.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.6%;
95.2%;
                                                                                                                                                                                                                                       97US-0818111.
96US-0729622.
                                                                                                                                                                                                 97WO-US18214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 qeagnferisgdlk-tqidqv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.6
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                              Skeiky YAW,
                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 AA;
                                                                                                                                                                                                                                                                                                                                           Campos-Neto A,
                                                                               Mycobacterium
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Sequence

05-NOV-1999

AAY39136;

RESULT 12 AAY39136

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26-AUG-1999

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Gaps

1;

FX8X0000000X8

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100 AA;
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15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query ...
Best Local Simi.
                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001
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                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                              AAB35218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXX DEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the other immunogenic proteins of the bacteria of the interrulosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in
                                                                      This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                               83.6%; Score 89.5; DB 20; Length 100; 95.2%; Pred. No. 2.9e-07;
                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid containing regulator and LHP gene of tuberculosis - useful in vaccines, for diagnosis, and of heterologous proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rasmussen PB;
                                                                                                                                                                                                                                                                                                                      Mismatches
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                                 Example 3; Page 179; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY03705 standard; Protein; 100 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis LHP polypeptide.
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hes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andersen P,
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                                                                                                                                                                                                                          Sequence
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mycobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune response. The present sequence represents the LHP polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences for members of the esat-6 gene family from Mycobacterium tuberculosis. Thes proteins include Rv0287, Rv1036c, Rv1037c, Rv2346c, Rv2348c, Rv2553c, Rv25654c, Rv33020c, Rv344c, Rv3445c, Rv3890c, Rv3891c, Rv3904c and Rv3905c. These can be used to produce vaccines against, and in the diagnosis of, tuberculosis (TB) infection. The present sequence is one
                                                                                                                                                                                                                                                        Gaps
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Immunizing against and diagnosis of tuberculosis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculosis; TB; vaccine; esat-6 gene family; Rv0287; Rv1036c; Rv1037c; Rv2346c; Rv2348c; Rv2653c; Rv2654c; Rv3020c; Rv3444c; Rv3445c; Rv3890c; Rv3891c; Rv3904c; Rv3905c.
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95.2%; Pred. No. 2.9e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                   Score 89.5; DB 20;
Pred. No. 2.9e-07;
0; Mismatches 0;
                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M tuberculosis Rv3874 protein.
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95.2%;
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99US-0144011.
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Search completed: July 5, 2001, 11:45:43 Job time: 272 sec

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                                                                                                                                July 5, 2001, 11:46:59; Search time 61.79 Seconds (without alignments) 6.846 Million cell updates/sec
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Sequence 2
Sequence 2
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Patent No.
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/cgn2_6/ptodata/3/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-470-179-19
US-08-470-179-19
US-08-470-179-19
US-08-136-1-2
US-08-138-133-2
US-08-138-133-2
US-08-170-179-20
US-08-77-27-2
US-08-70-179-21
US-08-70-179-179-21
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US-09-059-849A-2
US-09-213-632-2
PCT-US95-12675-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                  1 QEAGNFERISGDLKYTQIDQV 21
                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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107
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| 38 35.5 1230 2 US-08-968-542C-35<br>38 35.5 1551 4 US-09-425-665-2<br>37 37 141 1 US-08-470-176-25 | 8 35.5 1551 4 | r 141 3 45 7 | 7 757 0.50 | 6 221 1 | 7 34.6 707 4 | 7 34.6 708 4 | 34.1 358 1 | 34.1 358 2 | 34.1 358 3 | 1 436 3 | 33.6 141 1 | 33.6 241 1 | 33.6 241 2 | 33,6 241 5 | 33.6 | 33.6 402 2 | 33.6 402 3 |  |
|----------------------------------------------------------------------------------------------------|---------------|--------------|------------|---------|--------------|--------------|------------|------------|------------|---------|------------|------------|------------|------------|------|------------|------------|--|
| ď                                                                                                  | 9             | 38           | 37         | 37      | 37           | 37           | 36.5       | 36.5       | . 36.5     | 36.5    | 36         | 36         | 36         | 36         | 36   | 36         | 36         |  |

### ALIGNMENTS

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Sequence 2, Application US/08317223
Patent No. 5585267
GENERAL INFORMATION:
APPLICANT: Jones, Jonathan C.R.
APPLICANT: Quaranta, Vito
APPLICANT: Tamura, Richard
TITLE OF INVENTION: CELLULAR ATTACHMENT TO TRANS-EPITHELIAL
TITLE OF INVENTION: APPLIANCES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,223
FILING DATE:
CLASSIFICATION NUMBER: US 08/042,727
FILING DATE:
CLASSIFICATION NUMBER: US 08/042,727
FILING DATE: O5-APR:1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/151,134
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,460
FILING DATE: 12-NOV-1993
ATTONEY/AGENT INFORMATION:
APPLICATION NUMBER: 29,655
REGISTRATION NUMBER: 29,655
RELECOMMULCATION INFORMATION:
TELECHONE: (619) 235-8550
TELEBRAX: (619) 235-8550
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRARACTERISTICS:
IFNORMATION FOR SEQ ID NO: 2:
FENGTH.
                                                                                                                                                                                                                                                             AUURESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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  US-08-317-223-2
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US-08-836-567-2

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APPLICANT: Craig Halberstadt
TITLE OF INVENTION: CELLULAR ATTACHMENT TO LAMININ 5-COATED
TITLE OF INVENTION: TRANS-EPITHELIAL APPLIANCES
AUDRER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELLULAR ATTACHMENT TO TRANS-EPITHELIAL APPLIANCES
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,849A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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55.0%; Pred. No. 3.4;
tive 4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFRENCE/DOCKET NUMBER: DESMOS.015A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-6176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                      Sequence 2, Application US/09059849A Patent No. 6034068 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-213-632-2
Sequence 2, Application US/09213632
Patent No. 6110/11
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jones, Jonathan C.R. APPLICANT: Quaranta, Vito APPLICANT: Tamura, Richard TITLE OF INVENTION: CELLULAR AT TITLE OF INVENTION: APPLIANCES
    17 KDAGNF-LINGDLTLNQINQ 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laminin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                             92660
                                                                                                                                                                                                                                                                                                                                                          S
                                                                                 RESULT 3
US-09-059-849A-2
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                  CITY: PSTATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Quaranta, Vito
APPLICANT: Unaranta, Marketta
TITLE OF INVENTION: Promotion of Epithelial Cell Adhesion
TITLE OF INVENTION: and Hemidesmosome Assembly by a Laminin-Like Molecule
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                          Gaps
                                                                                                                                                             Score 46.5; DB 1; Length 360; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46.5; DB 1; Length 360;
Pred. No. 3.4;
4; Mismatches 4; Indels
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,135
                                                                                                                                                                                    ed. No. 3.4;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESMOS.002CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/151,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08445135
Patent No. 5658789
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Israelsen, Ned A. REGISTRATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: DESTELECOMMUNICATION INFORMATION:
                                                                                                                                                             Ouery Match
Best Local Similarity 55.0%;
Matches 11; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.5%;
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                                                                                                                                                                                                                                                                                     17 KDAGNF-LINGDLTLNQINQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QEAGNFERISGDLKYTQIDQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                        internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                     ANTI-SENSE: NO
FRAGMENT TYPE: inter
IMMEDIATE SOURCE:
CLONE: laminin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
                                                                                                   US-08-317-223-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     US-08-445-135-3
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Cloning, Tissue Distribution, and Functional Analysis Of The Human Na+/H+ Exchanger Isoform, NHE3.
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Pred. No. 3.4;
4; Mismatches 4; Indels
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  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12675
                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,727
APPLICATION NUMBER: US 08/042,727
FILING DATE: 05-APR-1993
APPLICATION NUMBER: US 08/151,134
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/151,134
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: 1878-818-81, Ned A.
REFERENCE/DOCKET NUMBER: DESMOS.002CP1
TELEOPHONE: (619) 235-0176
TELEPHONE: (619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08677734A Patent No. 5871919 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Brant, Steven R. APPLICANT: Yun, Chris C.H. APPLICANT: Donowitz, Mark APPLICANT: Tse, Chung-Ming TITLE OF INVENTION: Cloning, TITLE OF INVENTION: Functiona TITLE OF INVENTION: NHE3. NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QEAGNFERISGDLKYTQIDQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 KDAGNF-LINGDLTLNQINQ 35
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IMMEDIATE SOURCE:
; CLONE: laminin A
PCT-US95-12675-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.0°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-677-734A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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GENERAL INFORMATION:
APPLICANT: DESMOS, IEC.
TITLE OF INVENTION: CELLULAR ATTACHMENT TO TRANS-EPITHELIAL
TITLE OF INVENTION: APPLIANCES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46.5; DB 4; Length 360;
Pred. No. 3.4;
4; Mismatches 4; Indels
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                    COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/151,134
FILING DATE: 12-NOV-1993
PRIOR APPLICATION NUMBER: US 08/152,460
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: DESMOS.002CP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (619) 235-0176
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 maino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/317,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 KDAGNF-LINGDLTLNQINQ 35
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Best Local Similarity 55.09
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
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IMMEDIATE SOURCE:
CLONE: laminin A
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                   92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
PCT-US95-12675-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-213-632-2
                                                                                                                                               COUNTRY:
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Sequence 18, Application US/08470179

Sequence 18, Application US/08470179

Patent No. 564594

GENERAL INFORMATION:

APPLICANT: Huang Ph.D. Wai Mun

TITLE OF INVENTION: Method and Compositions for

TITLE OF INVENTION: Identification of Species in a Sample

NUMBER OF SEQUENCES: 207

CORRESPONDENCES: 207

CORRESPONDENCE ADDRESS:

ADDRESSEE: Trask, Britt and Rossa

STRET: U. Box 2550

CITY: Salt Lake City

STATE: Utah

CONNTRY: USA
                                                                                                                                              38.3%; Score 41; DB 1; Length 141; 47.4%; Pred. No. 9.8; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.3%; Score 41; DB 1; Length 141; nilarity 47.4%; Pred. No. 9.8; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/470,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Svedgert Ph.D. Susan E.
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801-531-1922
TELEPHONE: 801-531-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Shigella dysenteriae US-08-470-179-18
                       ; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
US-08-470-179-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  4 GNFERISGD----LKYTQI 18
                                                                                                                                                                                                                                                          4 GNFERISGD----LKYTQI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                              Query Match
Best Local Similarity 47.4*
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
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  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                       US-08-470-179-18
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Patent No. 5645994
GENERAL INFORMATION:
APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Identification of Species in a Sample NUMBER OF SEQUENCES: 207
CORRESPONDE ADDRESS:
ADDRESSEE: Trask, Britt and Rossa STREET: P.O. Box 2550
CORTY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 2; Length B31;
Pred. No. 49;
5; Mismatches 3; Indels
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WIMBER: 05/08/677,734A
FILING DATE: 10-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,179
                                                                                                                                                                                                             05387.0043-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OGTWARE: PatentIn Polacing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sweigert Ph.D. Susan E.
REGISTRATION NUMBER: 36,289
REPERENCE/DOCKET NUMBER: 2601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801-531-1922
TELEFAX: 801-531-1928
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: FORDIS, Jean B.
REGISTRATION NUMBER: 32,984
REFRENCE/DOCKET NUMBER: 0538'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 801-531-9168
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SS: not relevant
not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 141 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 39.3
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 EEATNYEEISGGIEF 733
                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-677-734A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QEAGNFERISGDLKY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: Koblan, Kenneth S.
APPLICANT: Pompliano, David L.
TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
TITLE OF INVENTION: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE DAVID A. Muthard
ADDRESSE: David A. Muthard
STREET: P.O. BOX 2000, 126 E. Lincoln Avenue
CITY: Rahway :
STATE: New Jersey
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1;
Pred. No. 72;
4; Mismatches
                                                                                                                                                                                  PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/649,565
FILING DATE: 01-FEB-1991
APPLICATION NUMBER: U.S. 07/487,038
FILING DATE: 02-MAR-1990
ATTORNEY AGENT INFORMATION:
NAME: POLTEY, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 0627.2100004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 833-753
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AGG11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,304
   United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 18937
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-138-641-2; Sequence 2, Application US/08138641; Patent No. 5474921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 ODNGNLORLSGNATLTLI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QEAGNFERISGDLKYTQI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 828 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 44.4*
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-261-304-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                        FILING DATE:
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Patent No. 5708147
GENERAL INFORMATION:
APPLICANT: Cybulsky, Myron I.
APPLICANT: Collins, Tucker
TITLE OF INVENTION: Endothelial Adhesion Molecule Associated With
TITLE OF INVENTION: Atherosclerosis
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
             Sequence 19, Application US/08470179
Patent No. 5645994
GENERAL INFORMATION:
APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Method and Compositions for
TITLE OF INVENTION: Identification of Species in a Sample
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSE: Trask, Britt and Rossa
STRRET: P.O. Box 2550
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Avenue, N.W. STREET: Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.3%; Score 41;
47.4%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Salmonella typhimurium US-08-470-179-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     District of Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 GNFGSIDGDSAAAMRYTEI 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.4'
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                             Utah
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                                                                                                                                                                                                     CITY: Sal
STATE: Ut
COUNTRY:
US-08-470-179-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-261-304-2
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Gaps

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TELEPHONE: 801-532-1922
TELEFAX: 801-531-9168
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GNFERISGD----LKYTQI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||| : || ::||:|
69 GNFGSVDGDSAAAMRYTEI 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.4
Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal
                                                                                                                                                                                                                                                                         ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: PI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
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                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-367-227-2
                                                                                                                                                                                                                                          STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GIBBS, JACKSON B.
APPLICANT: KOBLAN, KENNETH S.
APPLICANT: MACLEOD, ANGUS M.
APPLICANT: MACLEOD, ANGUS M.
TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC TITLE OF INVENTION: PHOSPHOLIPASE C
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADAPESS:
ADDRESSEE: DAVID A. MUTHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1290;
                                                                                                                                                                                  Length 1290;
                                                                                                                                                                Score 41; DB 1; Length 123.
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 129
Pred. No. 1.2e+02;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: DAVID A. MUTHARD
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
TARHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MOTHARD, DAVID A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18936
TELECOMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAS: (908) 594-3903
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08138133
Patent No. 5519163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.3%;
INFORMATION FOR SEQ ID NO: 2:
                 SEQUENCE CHARACTERISTICS:
LENGTH: 1290 amino acids
                                                                                                                                                                                Ouery Match 38.3%;
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1290 amino acids
                                                                                                                                                                                                                                                                               :||: |||: | | :
200 DFEQRSGDITYGQFAQL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||: |||: | |:
200 DFEQRSGDITYGQFAQL 216
                                                                                                                                                                                                                                                          5 NFERISGDLKYTQIDQV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 NFERISGDLKYTQIDQV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.3
Best Local Similarity 47.1
Matches 8; Conservative
                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-138-641-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-138-133-2
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                               LENGTH:
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Sequence 20, Application US/08470179
GENERAL INFORMATION: Add Mun
APPLICANT: Hung Ph.D. Wal Mun
TITLE OF INVENTION: Method and Compositions for TITLE OF INVENTION: Method and Compositions for TITLE OF INVENTION: Method and Compositions for Comparison of SEQUENCES: 2071 [Cartification of Species in a Sample Compassion of Security ```

us-09-462-480-8.rai

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Length 140;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                           36.4%; Score 39; DB 1;
illarity 36.8%; Pred. No. 21;
Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: July 5, 2001, 11:46:59 Job time: 313 sec
                                                                                                                                                                                                     FRAGMENT TYPE: internal ORIGINAL SOURCE:
CREANISM: Pseudomonas aeruginosa US-08-470-179-21
                                                                                                                                                                                                                                                                                                                                                                                                                 4 GNFERISGD----LKYTQI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| : || ::||::
68 GNFGSVDGDNAAAMRYTEV 86
                                                            LENGTH: '140 amino acids TYPE: amino acid
                                                                                                                      TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
TELEFAX: 801-531-9168 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                      8
                                                                                                  STRANDEDNESS:
TOPOLOGY: no
                                                                                                                                                                                      ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Method and Compositions for
TITLE OF INVENTION: Method and Compositions for
TITLE OF INVENTION: Identification of Species in a Sample
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask, Britt and Rossa
ADDRESSEE: Trask, Britt and Rossa
STRE: Utah
COUNTY: USA
ZIP: Utah
COUNTY: USA
ZIP: 04110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,227
FILING DATE: 17-JAN 1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FP PCT/FF94/00589
FILING ADPLICATION DATA:
APPLICATION NUMBER: FF 93/06003
FILING APPLICATION NUMBER: FF 93/06003
FILING APPLICATION NUMBER: 18 PAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 384-42-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
COFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.5; DE
Pred. No. 80;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Sweigert Ph.D, Susan E.
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801-532-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/08470179
Patent No. 5645994
GENERAL INFORMATION:
APPLICANT: Huang Ph.D, Wai Mun
                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.9%;
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GNF-ERISGDLKYTQIDQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 540 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-367-227-2
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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OM protein - protein search, using sw model

July 5, 2001, 11:48:32; Search time 79.63 Seconds (without alignments) 20.089 Million cell updates/sec Run on:

US-09-462-480-8 107 1 QEAGNFERISGDLKYTQIDQV 21 Title: Perfect score: Sequence:

Scoring table:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Ouery Match	Length	DB	ID	Description
:	89.5	83.6	100	10	H70802	hypothetical prote
		47	296	(	T27375	
	46.5	4	3712	~	S18253	
	46	4	297	7	F69595	multidruq resistan
	46	4	547	~	S44841	K06H7.1 protein -
	44	4	411	7	A86741	phosphopentomutase
	43	40	317	7	F85650	hypothetical prote
	43	40	643	7	G72320	penicillin-binding
	43	40	606	7	C84965	oxoglutarate dehyd
	43	40	948	7	JC2190	preprotein translo
	43	40	1023	7	LEECA	4
	43	4	1279	7	A47363	(1)
	43	40.2	1287	7	146032	nuclear DNA helica
	42.5	39.7	314	7	JC1276	dihydroorotate oxi
	•	39.7	1014	Н	S75023	sensory transducti
	42	39.3	462	7	S55114	hypothetical prote
	42	39.3	480	7	G75313	molybdate metaboli
	42	39.3	540	7	T51390	TCP-1 chaperonin-1
	42	39.3	702	7	A69140	ATP-dependent heli
	42	39.3	831	7	B40204	Na+/H+-exchanging
	42	39.3	859	7	T26134	hypothetical prote
	42	σ	1616	~	T47801	hypothetical prote
	41.5	œ	307	7	S47244	C-raf protein - ze
	41.5	38.8	1439	7	T02087	qaq/pol polyprotei
	41	38.3	95	7	S54254	DNA topoisomerase
	41	38.3	189	~	A38577	lumazine protein L
	41	38.3	192	7	A64098	molybdopterin-quan
	41	38.3	305	~	C83967	aspartate carbamoy
	41	38.3	341	~	T26552	hypothetical prote

inulin fructotrans	replicative DNA he	conserved hypothet	DNA topolsomerase	DNA gyrase, subuni	DNA topoisomerase	hypothetical prote	1-phosphatidylinos	probable membrane	hypothetical prote	hypothetical prote	DNA topoisomerase				_
JC4318	G72217	D72356	ITECAP	D85862	S47332	T21403	A31317	S60932	A96719	B86677	S49447	G75351	T22886	E83386	T49938
7	~	~	-	7	~	7	7	7	7	7	7	7	~	7	~
393	451	463	875	875	878	1217	1290	1511	1028	93	95	125	148	213	213
38.3	38.3	38.3.	38.3	38.3	38.3	38.3	38.3	38.3	37.9	37.4	37.4	37.4	37.4	37.4	37.4
41	41	41	41	41	41	4.1	41	41	40.5	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1	
H70802	
hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV)	
C;Species: Mycobacterium tuberculosis	
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000	0
C; Accession: H70802	
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon	D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,	.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	, s.
Nature 393, 537-544, 1998	
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno	mplete geno
A; Reference number: A70500; MUID:98295987	
A; Accession: H70802	
A; Status: preliminary; nucleic acid sequence not shown; translation not shown	Own
A; Molecule type: DNA	
A; Residues: 1-100 <col/>	
A; Cross-references: GB: AL022120; GB: AL123456; NID: 93261558; PIDN: CAA17966.1; PID: 9296	1; PID:9296
A; Experimental source: strain H37Rv	
C; Genetics:	
A;Gene: Rv3874	
Query Match 83.6%; Score 89.5; DB 2; Length 100;	
Pred. No. 1.6e-07;	
Matches 20; Conservative 0; Mismatches 0; Indels 1; Gaps	
OV 1 OPAGNERETSCOLKVHOTDOV 21	

ò g

7

RESULT

Pypothetical protein Y75B12B.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999 C;Accession: T27375 S;White, S. Submitted to the EMBL Data Library, October 1998 A;Reference number: 220360 A;Accession: T27375 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Accession: T27375 A;Status: preliminary; canslated from GB/EMBL/DDBJ

A; Residues: 1-296 <WIL> A; Cross-references: EMBL:AL032663; PIDN:CAA21764.1; GSPDB:GN00023; CESP:Y75B12B.1 A; Experimental source: clone Y75B12B

C; Genetics:

A;Gene: CESP: V75B12B.1 A;Map position: 5 A;Introns: 99/3; 173/2; 199/3; 248/3

```
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C; Accession: F69595
R; Kunst, F; Ogasawara, N; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Ccaldwell, B.; Capuano, V.; Carter, N.M.; Ai; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Pabret, C.; Perrari, Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galisch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevilc, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, A.; Tanaka, T.; Terpstra, P.; Tosato, V.; Othiya A; Authors: P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tosato, V.; Voshida A; Authors: P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tosato, V.; Yata, K.; Yoshida A; Authors: P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Janane, M.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Yoshida A; Authors: Preliminary, Nucleic acid sequence of the Gram-positive bacterium Bacillus subtill A; Reference number: And Sequence of the Gram-positive bacterium Bacillus subtill A; Reference preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 25/3; 36/3; 80/3; 149/3; 186/2; 229/3; 311/3
C;Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase hom
C;Keywords: ATP: serine/threonine-specific protein kinase
F;265-518/Domain: protein kinase homology xKIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Lactococcus lactis subsp. lactis (strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:299116; GB:AL009126; NID:g2634723; PIDN:CAB14331.1; PIN
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W06H7.1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: S44841
R;Favello, A.D.
S;Acvello, A.D.
S;Acvello, A.D.
S;Acvello, C the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid K06H7.
A;Reference number: S44620
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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-547 <FAV>
A;Cross-references: EMBL:L15314; NID:9289690; PIDN:AAA28084.1; PID:9289691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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Pred. No. 15;
4; Mismatches
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EQGSIDRFTGELSYVQASRI 258
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50.0%;
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Best Local Similarity 50.00,
Acconservative
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170 NVEKVTGDLKCTNYDR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 35.0
Matches 7; Conservative
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A:Residues: 1-547 <FAV>
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F;3049-3223/Domain: repeat G3 <RG3>
F;3079-3223/Domain: laminin G repeat homology <LG3>
F;3079-3200/Domain: repeat G4 <RG4>
F;3324-3528/Domain: repeat G5 <RG5>
F;3529-3712/Domain: repeat G5 <RG5>
F;3529-3712/Domain: repeat G5 <RG5>
F;1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3
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A; Moseduces: 1-3712 cKDS.
A; Residuces: 1-3712 cKDS.
A; Residuces: 1-3712 cKDS.
A; Cross-references: GB: M96388; NID:g157799; PIDN: AAA28662.1; PID:g157800
B; Garrison, K.; MacKrell, A.J.; Fessler, J.H.
B; Garrison, K.; MacKrell, A.J.; Fessler, J.H.
A; Btol. Chem. 266, 22899-22904, 1991
A; Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct A; Reference number: S18253; MUID:92078147
                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila none: 1999
Richard S28399; S18253
Richard S28399; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A;Title: Laminin A chain: expression during Drosophila development and genomic sequence. A;Reference number: $28399; MUID: 93049203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: FlyBase:FBgn0002526
Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h. Seywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular 273-330/Domain: laminin-type EGF-like homology (LEG)
333-400/Domain: laminin-type EGF-like homology (LEG)>
5313-400/Domain: laminin-type EGF-like homology (LEG1)>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
                                                                                                               Gaps
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                                         Length 296;
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n: laminin-type EGF-like homology cLE2>
n: laminin-type EGF-like homology cLE3>
n: laminin-type EGF-like homology cLE4>
n: laminin-type EGF-like homology cLE4>
n: laminin-type EGF-like homology cLE6>
n: laminin-type EGF-like homology cLE6>
n: laminin-type EGF-like homology cLE6>
n: JII, heptad repeats cDOM2>
n: G cDOM3>
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Pred. No. 1.1e+02;
4; Mismatches 4;
                                             DB 2;
                                                                                                           Mismatches
                                             Score 51;
Pred. No.
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                                         47.7%;
50.0%;
                                                                                                                                                                                                                1 QEAGNFERISGDLKYTQI 18
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                                                                                                           Conservative
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A; Residues: 1762-3712 <GAR>
                                                                         Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 11; Conserv
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                                                Query Match
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C;Species: Buchnera sp. C. Carlotte of Species: Buchnera sp. C;Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: C84965  
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H. Nature 407, 81-86, 2000  
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUID:20445173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL:X74592; NID:9505309; PIDN:CAA52669.1; PID:9505310 C; Comment: This protein participates in protein translocation across both the cytopla C; Comment: The "nucleotide-binding motif B" and "DEAD motif" features as annotated ar is adjacent to the identified motif and a third conserved motif is approximatly 120-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding C;Reywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Keywords: ATP: homodimer; membrane-associated complex; P-loop; protein transport F:106-113/Region: nucleotide-binding motif A (P-loop) #status atypical F:209-214/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Synechococcus sp.
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 17-Nov-2000
C;Accession: JC2190
E;Nakai, M.; Nohara, T.; Sugita, D.; Endo, T.
Blochem. Biophys. Res. Commun. 200, 844-851, 1994
A;Title: Identification and characterization of the sec-A protein homologue in the A;Reference number: JC2190; MUID:94235036
A;Accession: JC2190; MUID:94235036
                                                                                                                                                                                                                                                                                                                                                                                                                          oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) el component [imported]
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Pred, No. 84;
3; Mismatches
                                                                                                                                                      DB
57;
                                                                                                                                                                                                  7; Mismatches
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A; Experimental source: strain MSB8
C;Genetics:
C;Gene: TMO886
C;Superfamily: penicillin-binding protein 1B
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Pred. No.
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Best Local Similarity
7; Conserve
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270 FQKISGDVKY 279
                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-909 <STO>
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A; Status: preliminary
A; Molecule type: DNA
A; Medecule type: DNA
A; Residues: 1 -643 < ARN>
A; Cross-references: GB: AE001754; GB: AE000512; NID: g4981417; PIDN: AAD35967.1; PID: g498143
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A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: 21551
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                     R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Genome Res. in press, 2001
As Title: The complete genome sequence of the lactic acid bacterium.
A;Reference number: A86625
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A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-411 <STO>
A; Cross-references: GB: AE005176; NID: g12723864; PIDN: AAKO5027.1; GSPDB: GN00146
A; Experimental source: strain IL1403
C; Genetics:
C; Genetics:
C; Superfemily: phosphopentomutase
C; Keywords: intramolecular transferase; isomerase
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C; Date: 16 Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C; Accession: F85650
R; Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-317 <STC>
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C;Species: Escherichia coli
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A;Title: Evidence for lateral gene transfer between Archaea and
A;Reference number: A72200; MUID:99287316
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 411;
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Pred. No. 23;
0; Mismatches
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Pred, No. 25;
3; Mismatches
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64.38;
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9; Conserv
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Best Local (
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nuclear DNA helicase II - bovine
C;Species: Bos primigentius taurus (cattle)
C;Species: Bos primigentius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 02-Feb-2001
C;Accession: 146032; S49822
R;Zhang, S.; Maacke, H.; Grosse, F.
J. Biol. Chem. 270, 16422-16427, 1958
A;Fitle: Molecular cloning of the gene encoding nuclear DNA helicase II. A bovine hom A;Reference number: 146032; MUID:95332357
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Residues: 1-314 <ALE>
A;LES-ALES-ACIDE: DNIB: 228216; NID: 9486386; PIDN: CAA82061.1; PID: 9486387; GSPDB: GNO
A;Cross-references: EMBL: 228216; NID: 9486386; PIDN: CAA82061.1; PID: 9486387; GSPDB: GNO
A;Experimental source: strain $288C
B;Tzermia, M.; Horaitis, O.; Alexandraki, D.
Yeast 10, 663-679, 1994
A;Note: this sequence follows the published nucleotide sequence and translation and C;Keywords: ATP; nucleotide binding; nucleus; P-loop F;H1-418/Region: nucleotide-binding motif A (P-loop) F;510-512/Region: nucleotide-binding motif B F;511-514/Region: DEXH motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1287 <2HA>
A;Cross-references: EMBL:X82829; NID:9577738; PIDN:CAA58036.1; PID:9577739
C;Genetics:
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A:Accession: JC1276
                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.2e+02;
3; Mismatches 2;
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Pred. No. 1.3e+02;
3; Mismatches 2;
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C;Keywords: ATP: nucleotide binding; P-loop
F;408-415/Pegion: nucleotide-binding motif A
F;504-509/Region: nucleotide-binding motif E
F;508-511/Region: DEXH motif
                                                                                                                                                                                                        40.2%;
58.3%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Matches 7; Conservative
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192 EKIQGEYKYTQV 203
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189 EKIQGEYKYTQV 200
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Gene 118, 149-150, 1992
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A; Residues: 1-314 <ROY>
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C; Superfamily: hemolysin A; hemolysin—A homology
C; Keywords: calcium binding; cytolysis exotoxin; hemolysis; lipoprotein; tandem repeat;
F; 246-791/Domain: hemolysin A homology </rr>
F; 246-791/Acmain: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIVF]-X)
F; 553,689/Binding site: palmitate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Molecule type: DNA
A.Residues: 1-1033 <- FELD
A.Cross-references: GB:M10133; GB:M12863; NID:g146377; PIDN:AAA23975.1; PID:g146379
A.Cross-references: GB:M10133; GB:M12863; NID:g146377; PIDN:AAA23975.1; PID:g146379
A.Experimental source: strain J96, O4 serotype
R:Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C.
Science 266, 1992-1996, 1994
A.Fitle: Fatty acylation of two internal lysine residues required for the toxic action A.Reference number: A5387; MUID:95099325
A.Contents: annotation; lysine palmitoylation
A.Note: lysine modification is performed by the hlyC gene product
B.Haertlein, M.; Schiessl, S.; Wagner, W.; Rdest, U.; Kreft, J.; Goebel, W.
J. Cell Biol. 22, 87-97, 1983
A.FILLE: Transport of hemolysin by Escherichia coli.
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C;Species: Homo sapiens (man)
C;Aatce,OB MAY-1995 #sequence_revision 12-May-1995 #text_change 02-Feb-2001
C;Aatcession: A47363
R;Lee, C.G.; Hurwitz, J.
D Biol. Chem. 268, 16822-16830, 1993
A;Title: Human RNA halicase A is homologous to the maleless protein of Drosophila. A;Reference number: A47363; MUID:93346440
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                                                                                                                                                                                                                                                                                         hemolysin A - Escherichia coli
C;Species: Escherichia coli
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 18-Jun-1999
C;Accession: A24433; I41280
R;Felmlee, T.; Pellett, S.; Welch, R.A.
J. Bacteriol. 163, 94-105, 1985
A;Fitle: Nucleotide sequence of an Escherichia coli chromosomal hemolysin.
A;Reference number: A24433; MUID:85234404.
                                 Gaps
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1,'T',3,'V',5,'T',7-44 <RES>
A:Cross references: GB:M29173; NID:g146337; PIDN:AAA23957.1; PID:g146338
C;Genetics:
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Pred. No. 97;
4; Mismatches
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1279 <LEE>
A; Cross-references: GB:L13848
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A; Accession: 141280
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Best Local Similarity
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Residues: 1-1014 (KRN-A)
A;Residues: 1-1014 (KRN-A)
A;Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17885.1; PID:g165296
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: sensory transduction histidine kinase; response regulator homology
A;Title: The complete sequencing of a 24.6 kb seqment of yeast chromosome XI identified e dehydratases, membrane transporters, hydantoinases and the phospholipase A(2)-activatian: A;Reference number: S44319; MUID:95028164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Genes. SGD:URA1; MIPS:YKL216w
A.Genes. SGD:URA1; WIPS:YKL216w
A.Map position: 11L
C.Superfamily: dihydroorotate oxidase
C.Superfamily: dihydroorotate oxidase
C.Keywords: flavoprotein; FMN; oxidoreductase; pyrimidine nucleotide biosynthesis
                                                                                                                                                                      A; Accession: 544322
A; Status: translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
C; Molecule 
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Pred. No. 1.2e+02;
7; Mismatches 3; Indels 1;
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F; 20-131/Domain: sensor histidine Kinase homology <SRKH>
F; 293-542/Domain: sensor histidine Kinase homology <SRKH>
F; 742-854/Domain: response regulator homology <SRKH2>
F; 786/Binding site: phosphate (Asp) (covalent) #status predicted
F; 790/Binding site: phosphate (Asp) (covalent) #status predicted
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Pred. No. 30;
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Best Local Similarity 50.0%;
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Best Local Similarity 42.1%;
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997 AASYERVQGELK-TMLDRL 1014

3 AGNFERISGDLKYTQIDQV 21

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 5, 2001, 11:51:42; Search time 41.8 Seconds (without alignments) 17.210 Million cell updates/sec

US-09-462-480-8 107 Perfect score:

1 QEAGNFERISGDLKYTQIDQV 21 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosem parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% . Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	drosophi]	P390/4 bacillus su p34500 caenorhabdi				P09983 escherichia	homo	QZ8141 bos taurus O70133 mus musculu	2 sacc	Q04235 saccharomyc	~	048400 bacteriopha			P25082 photobacter			_	m			P75049 mycoplasma			P35401 dictyosteli	Q10432 schizosacch		P14829 klebsiella	P26221 thermomonos	0	P08715 escherichia
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# ALIGNMENTS

LETHOUGHT TO WEDIATE THE ATTACHMENT, WIGNATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

-!- FUNCTION: DIVERSE FUNCTIONS DURING MORPHOGENESIS IN DROSOPHILA.

COMPLETE LOSS-OF-FUNCTION MUTATIONS LEAD TO LATE EMBRYONIC
LETHALITY: CERRAIN PARTIAL LOSS-OF-FUNCTION MUTATIONS GIVE RAISE
TO ESCAPER ADULTS, WHICH HAVE ROUGH EYES ASSOCIATED WITH CHANGES
IN CELL FATE AND PATTERN, MISSHAPPEN LEGS AND DEFECTS IN WING
STRUCTURE.

-!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLIFEPTIDE GLAINS (ALPHA, BETA, GAMAA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

-!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
MENBRARMS (MADOR COMPONENT).

-!- TISSUE SPECIFICITY: NEWLY FOUND MESODERM AND LATER PROMINENTLY
EXPRESSED IN HEMOCYTES, WHICH ALSO SYNTHESIZE COLLAGEN IV. 8888888888888888888888

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LAMININ G-LIKE REPEATS (DOMAIN G)
               LAMININ G-LIKE 1.

LAMININ G-LIKE 2.

LAMININ G-LIKE 3.

POLY-THR.

LAMININ G-LIKE 4.

LAMININ G-LIKE 4.

LAMININ G-LIKE 4.

LAMININ G-LIKE 4.

LAMININ G-LIKE 5.

COLLED COLL (POTENTIAL).

COLLED COLL (POTENTIAL).

COLLED COLL (POTENTIAL).

COLLED COLL (POTENTIAL).

EXILLARITY.

BY SIMILARITY.

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                                                          DOMAIN
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                                                                                                                                                                                                                                    DEVELOPMENT AT 10-12 HOURS.

DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT DOMAIN: THE ALPHA-HELICAL DOMAINS I OF FORM A COILED COIL STRUCTURE.

WITH OTHER LAMININ CHAINS 10 FORM A COILED COIL STRUCTURE.

SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAINS (DOMAIN VI).

SIMILARITY: CONTAINS 1.5 LAMININ BGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV (DOMAIN IV' IS NOT SIMILARITY: CONTAINS 5 LAMININ GLANIN DOMAIN IV (DOMAIN IV' IS NOT SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         III B).

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 13.

LAMININ EGF-LIKE 14.

LAMININ EGF-LIKE 14.

LAMININ EGF-LIKE 15.

LAMININ EGF-LIKE 16.

LAMININ EGF-LIKE 16.

LAMININ EGF-LIKE 16.

LAMININ EGF-LIKE 17.

LAMININ EGF-LIKE 17.

LAMININ EGF-LIKE 19.

LAMININ EGF-LIKE 20.

LAMININ EGF-LIKE 21.

LAMININ EGF-LIKE 21.

LAMININ EGF-LIKE 22.

DOMAIN II AND I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAMININ ALPHA CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
10.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
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LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 9.
LAMININ EGF-LIKE 9.
LAMININ EGF-LIKE 10.
DOMAIN IV'.
1. S. LAMININ EGF-LIKE 11.
THE 11.
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Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mormbep; K06H7.1; CE00252.
InterPro; IPR000719; -.
InterPro; IPR002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkinase; 1
PROSITE; PS00107; PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 NFERISGDLKYTQIDQ 20
                   Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
273
296
390
547 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEOB LACLC
                                                                                                                                                                                                                                                     elegans."
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SEQUENCE
                                                                             SEQUENCE
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BINDING
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DEOB_LACLC
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                                ä
                                                                                                                                                                                                                                                                                                                                                                                      Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,
Sato T., Takeuchi M.,
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO B.COLI YEGS AND TO SYNECHOCYSTIS PCC 6803 SLL0036.
                               Gaps
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-168 / MARBUIG;
MARBLINE-95050642; PubMed-7961792;
Ahmed M., Borsch C.M., Taylor S.S., Vazquez-Laslop N., Neyfakh A.A.;
"A protein that activates expression of a multidrug efflux
transporter upon binding the transporter substrates.";
J. Biol. Chem. 269:28506-28513(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PUTATIVE SERINE/THREONINE-PROTEIN KINASE K06H7.1 IN CHROMOSOME III
                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
        Length 3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.0%; Score 46; DB 1; Length 297; 35.0%; Pred. No. 2.1; tive 6; Mismatches 7; Indels
                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2EB5B9DC35F90CDD CRC64;
                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group;
         DB 1;
                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BMRU PROTEIN.
                                                                                                                                   297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 AA.
                               Mismatches
                    32;
       Score 46.5;
Pred. No. 32
                                                                                                                                                                                                                                 Bacillus/Staphylococcus group; Bacillus.
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                                                                  2366 KDAGNF-LINGDLTLNQINQ 2384
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SEQUENCE 297 AA; 32461 MW;
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       43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L25604; AAB81538.1; -.
                                                      1 QEAGNFERISGDLKYTQIDQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D84432; BAA12602.1; -. EMBL; Z99116; CAB14331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EAGNFERISGDLKYTQIDQV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 43.0
Best Local Similarity 35.0
Matches 7; Conservative
                  Local Similarity 55.0 nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SubtiList; BG10302; bmrU.
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001206;
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168 / JH642;
                                                                                                                                                                                                                 Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
YMX1_CAEEL
ID YMX1_CAEEL
AC P34509;
                                                                                                                                  BMRU_BACSU
P39074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interPro;
         Query Match
                                                                                                            RESULT 2
BMRU_BACSU
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                                Matches
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                                                                                                                                                                                                                                Wilson R., Ainscough R., Adderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Adderson K., Copser J., Coulson A.,
Craxton M., Dear S., Durbin R., Favello A., Fraser A.,
Tolanton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latrella P., Lightning J., Lloyd C., Morthnore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Smith M., Sonnhammer B., Staden R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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15-UUL-1998 (Rel. 36, Created)
15-UL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOPENTOMUTASE (EC 5.4.2.7) (PHOSPHODEOXYRIBOMUTASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
W; OCD28C2FEAC63101 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00108; PROTEIN_KINASE_ST; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
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                                                                                                                                                                             STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
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Gaps

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                                                                                                                                                                          EMBL; AP001118; BAB13011.1; -.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate.
SEQUENCE 909 AA; 105806 MW; AE739F8ÇD9F9CF8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                                                                                                                       1; Length 909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 948 AA
                                                                                                                                                                                                                                                                                   40.2%; Score 43; DB 70.0%; Pred. No. 25; Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SECA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREPROTEIN TRANSLOCASE SECA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01043; SecA_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107257 MW;
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                       948 AA;
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Q55357;
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SEQUENCE
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SEQUENCE FROM N.A.

SEQUENCE TO 1998;

MEDLINE-20445173; bubMed-10993077;

MEDLINE-20445173; bubMed-10993077;

MEDLINE-20445173; bubMed-10993077;

The medical symbiont of aphids

The medical symbionidary

The medical symbionid
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                 Duwat P., Cochu A., Ehrlich S.D., Gruss A.;
"Characterization of Lactococcus lactis UV-sensitive mutants obtained by ISSI transposition.",
J. Bacteriol. 179:4473-4479(1997).
-!- CATALYTIC ACTIVITY: D-RIBOSE 1-PHOSPHATE = D-RIBOSE 5-PHOSPHATE.
-!- CATALYTIC ACTIVITY: 2-DEOXY-D-RIBOSE 1-PHOSPHATE = 2-DEOXY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Bacteria, Firmicutes, Bacillus/Clostridium group, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2) (ALPHA-SUCA OR BU302.
                                                                                                                                                                                                                                                                                                     -i- PATHAY: NUCLEOTIDE AND DEOXYRIBONUCLEOTIDE CATABOLISM.
-i- SIMILARITY: BELONGS TO THE PHOSPHOPENTOMUTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 1; Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 AA; 45818 MW; C6EDD47C563322B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBL_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    909 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                               MEDLINE=97369814; PubMed=9226255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002599; -. Pfam; PF01676; Metalloenzyme; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U80410; AAC45496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.18;
64.38;
                                                                                                                                                                                                                                                                                   D-RIBOSE 5-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1111111 | 1 | 1 | 232 | 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EAGNFERISGDLKY 15
                                                                                      SEQUENCE FROM N.A.
                                           NCBL_TaxID=1359;
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P57388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                         in the cyanobacterium synchrococus PCC7942.*;
Biochem. Biophys. Res. Commun. 200:844-851(1994).
-! FUNCTION: INVOLVED IN PROTEIN EXPORT. LIKELY PARTICIPATES IN
PROTEIN TRANSLOCATION ACROSS BUT THE CYTOPLASMIC AND THYLAKOID
MEMBRANES IN CYANOBACTERIAL CELLS.
-! SUBUNIT: HOMODIMER. PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION
APPARATUS WHICH COMPRISE SECA, SECB, SECE, SECF, SECG
AND SECY (BY SIMILARITY).
-! SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
MEDLINE-94235036; Pubmed-8179618;
Nakai M., Nohara T., Sogita D., Endo T.;
"Identification and characterization of the sec-A protein homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01312; SECA; 1.
Protein transport; ATP-binding; Membrane; Translocation; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.2%; Score 43; DB 1; Length 948; 64.3%; Pred. No. 26; 1ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-9720962; PubMed-9111062; Zhang S., Grosse F.; Human nuclear DNA helicase II (RNA helicase A)."; "Domain structure of human nuclear DNA helicase II (RNA helicase A)."; J. Biol. Chem. 272:11487-11494(1997).
-I- FUNCTION: UNWINDS DOUBLE-STRANDED DNA AND RNA IN A 3' TO 5' DIRECTION. GENERATES MULTIPLE SECONDARY STRUCTURES THAT INFLUENCE RNA-BINDING PROTEINS. MAY PLAY A ROLE IN X-LINKED GENE EXPRESSION.
-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE. DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 2 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDX9_HUMAN STANDARD; PRT; 1270 AA.
008211; Q99556;
01-FEB-1995 (Rel. 31, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-007-2000 (Rel. 40, Last annotation update)
ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II)
(DEAD-BOX PROTEIN 9)
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MEDILINE=93346440; PubMed=8344961;
Lee C.-G., Hurwitz J.;
"Human RNA helicase A is homologous to the maleless protein of
                                                                                                                                                                                                                                                                                                                                                                                                Length 1023;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                       PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
A -> T (IN STRIN 2001).
W; 196D5C0A9A28B54D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 268:16822-16830(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L13848; AAB48855.1; -. EMBL; Y10658; CAA71668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              40.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                 109867
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563
689
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1023 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDX9 OR NDH2
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelabs-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Felmlee T., Pellett S., Welch R.A.; "Nucleotide sequence of an Escherichia coli chromosomal hemolysin."; J. Bacteriol. 163:94-105(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicaud J.-M., Mackman N., Gray L., Holland I.B.;
"Characterisation of HlyC and mechanism of activation and secretion of haemolygin from E. col1 2001.";
FEBS Lett. 187:339-344(1985).
-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INVOLVED IN PORE FORMATION BY THE CYTOTOXIN. PTM: PALMITOYLATED BY HLYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY BY STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE OF
                                                                                                                                                                                                                                                                                                   Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfan; PF00353; hemolysincabind; 2.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
16 X REPEATS, GLY-RICH.
                                                                                                                                                                              01-WAR-1989 (Rel. 10, Created)
01-WAR-1989 (Rel. 10, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ransmembrane; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: SECRETED. DOMAIN: THE GLY-RICH REGION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-85258115; PubMed-3894051;
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=J96 / SEROTYPE 04;
MEDLINE=85234404; PubMed=3891743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M10133; AAA23975.1; -. EMBL; X02768; CAA26546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-44 FROM N.A.
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A24433; LEECA.
InterPro; IPR001343; -.
                       ||: ||| ||||:
847 RIAYDLKEAQIDQI 860
                                                                                                                                                                                                                                               HEMOLYSIN, CHROMOSOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326
410
869
728
737
  RISGDLKYTQIDQV 21
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URINARY TRACT
                                                                                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MODIFIED.
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                                                                                                                                            HLY1_ECOLI
P09983;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kisielow P., Miazek A.;
Submitted (MRR-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: UNWINDS DOUBLE-STRANDED DNA AND RNA IN A 3' TO 5'
DIRECTION. GENERATES MULTIPLE SECONDARY STRUCTURES THAT INFLUENCE
RNA-BINDING PROFESINS. MAY PLAY A ROLE IN X-LINKED GENE EXPRESSION.
-!- SUBCELLULAR LOCATION: NOLLEAR.
-!- SUBLIBLARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE. DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY: SIMILARITY: CONTAINS 2 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAINS.
               SIMILARITY: CONTAINS 2 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAINS
                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
DEIH BOX.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee C.-G., Eki T., Okumura K., da Costa Soares V., Hurwitz J.; "Molecular analysis of the cDNA and genomic DNA encoding mouse RNA helicase A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDX9_MOUSE STANDARD; PRT; 1380 AA.

O70133; O35931; O54703;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II)
(DEAD-BOX PROTEIN 9) (MHEL-5).
                                                                                                                                                                                                                                                PROSITE; PS00699; DEMLATP_HELICASE; 1.
PROSITE; PS50137; DS_RBD; 2.
Helicase; RNA-binding; DNA-binding; Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                            40.2%; Score 43; DB 1; Length 1287; 58.3%; Pred. No. 37; 2; Indels 1:ve 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                    ARG/GLY/TYR-RICH.
W; DC908095AB683ED4 CRC64;
                                                                                                                                                                                                                                                                                                              DRBM 1.
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                                                                                                                                                                                         InterPro; IPR001650; -.
InterPro; IPR002464; -.
Pfam; PF00035; dSrm; 2.
Pfam; PF00271; helicase_C; 1.
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                                                                                                                                                              EMBL; X82829; CAA58036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    141943
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592
1287
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249
415
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189 EKIQGEYKYTQV 200
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408 41
508 51
583 55
1167 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ERISGDLKYTQI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
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SEQUENCE
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NP_BIND
SITE
                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDX9_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 270:16422-16427(1995).
- FUNCTION: UNMINDS DOUBLE-STRANDED DNA AND RNA IN A 3' TO 5'
DIRECTION. GENERATES MULTIPLE SECONDARY STRUCTURES THAT INFLUENCE
RNA-BINDING PROTEINS. MAY LAX A ROLE IN X-LINKED GENE EXPRESSION.
- SUBCELLUTAR LOCATION: UNCLEAR.
- SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE. DEAH
                                                                                                                                                                                                       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                               NSFRAGYG -> TPSGRIC (IN REF. 1).
FGQGRGGGGY -> LDIEEEVAAIKLGYVSSVCRQ (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang S., Maacke H., Grosse F.;
"Molecular cloning of the gene encoding nuclear DNA helicase II.
bovine homologue of human RNA helicase A and Drosophila Mle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OJ-NOV-1997 (Rel. 35, Last sequence update)
OJ-OGT-2000 (Rel. 40, Last annotation update)
ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II)
DDX9 OR NDH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                           Helicase; RNA-binding; DNA-binding; Repeat; Nuclear protein; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.2%; Score 43; DB 1; Length 1270; 58.3%; Pred. No. 36; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                        (IN REF. 1). -> SLKLW (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3DEBB9ED3D6C9B2D CRC64;
                                                                                                                                                                                                                                            t (IN REF. 1).
REF. 1).
                                                                                                                                                                                                                   ARG/GLY/SER/TYR-RICH.
S -> T (IN REF. 1).
TM -> HH (IN REF. 1).
PPH -> LHI (IN REF. 1).
N -> I (IN REF. 1).
S -> T (IN REF. 1).
                                                                                                                                                                        ATP (BY SIMILARITY).
DEIH BOX.
                                                                                                                                                                                                                                                                                                                                                                    I -> V (IN REF. I
R -> Q (IN REF. 1
K -> N (IN REF. 1
R -> E (IN REF. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1287 AA.
                                                                                                                                                                                                                                                                                                                          D -> S (IN R
L -> F (IN R
IIEVYG -> SI
          Interpro; IPR001159; -.
Interpro; IPR001569; -.
Interpro; IPR002464; --
Pfam; PF00271; dsrm; 2.
Pfam; PF00271; helicase___; 1.
PROSITE; PS06590; DEAM_ATP_HELICASE; 1.
PROSITE; PS50137; DS_RBD; 2.
                                                                                                                                                                                                                                                                                                              NI) V <- I
                                                                                                                                                DRBM 1.
DRBM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Thymus;
MEDLINE=95332357; PubMed=7608213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1270 AA; 140876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| |: ||||:
192 EKIQGEYKYTQV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ERISGDLKYTQI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
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CONFLICT
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NP_BIND
SITE
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Gaps

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Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
SEQUENCE
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YMA5_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MARY REPARENCE OF THE PROPERTY                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@labs.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

ARG/GLY/SER/TYR-RICH.

R -> A (IN AAC05301).

N -> M (IN REF. 2).

T -> I (IN REF. 2).

I -> V (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of the URA1 gene of Saccharomyces cerevisiae."; Gene 118:149-150(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ×
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1-DEC-1992 (Rel. 24, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tzermia M., Horaitis O., Alexandraki D.; Trhe complete sequencing of a 24.6 kb sequent of yeast chromosome identified the known loci URA1. SAC1 and TRP3, and revealed 6 new open reading frames including homologues to the threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                               Helicase; RNA-binding; DNA-binding; Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.2%; Score 43; DB 1; Length 1380;
58.3%; Pred. No. 40;
tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T -> I (IN REF. 2).
I -> V (IN REF. 2).
W; 0F23755C29ID2FE1 CRC64;
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DEAH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 AA.
                                                                                                                                                                                                                                                                           InterPro; IPR001650; -.
InterPro; IPR002464; -.
Pfam; PF00035; darm; -.
Pfam; PF00271; hellcase_C; 1.
PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
PROSITE; PS50137; DS_RBD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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STRAIN-ATCC 28383 / FL100;
MEDLINE-92380485; Pubmed-1511880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95028164; Pubmed-7941750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                        EMBL; 091922; AAC05725.1; -.
EMBL; AF023530; AAC05301.1; -
EMBL; 092080; AAB72087.1; -.
MGD; MGI10817; DAY9.
InterPro; IPR001159; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149582
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194 EKIQGEYKYTQV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ERISGDLKYTQI 18
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding
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P28272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHODEHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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SITE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
PYRD_YEAST
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                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Biolinformatics and the EMED cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    OROTATE + H(2)O(2).

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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO S.POMBE SPAC4G8.06C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 52.7 KDA PROTEIN IN PDR4-GLO1 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42.5; DB 1; Length 314;
Pred. No. 8.9;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrimidine biosynthesis; Oxidoreductase; Flavoprotein; FAD.
dehydratases, membrane transporters, hydantoinases and the phospholipase A2-activating protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAD (NAD PART) (POTENTIAL).
0F1FF9BDA7F8D68E CRC64;
                                                                                                                                                                          -!- PATHWAY: FOURTH STEP IN PYRIMIDINE BIOSYNTHESIS.
                                                                                                       1- CATALYTIC ACTIVITY: L-DIHYDROOROTATE + O(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00911; DHODEHASE_1; 1. PROSITE; PS00912; DHODEHASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 FERIEKELKDIMEAKGYTSIDQ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 FERISGDLK-----YTQIDQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 AA; 34801 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X59371, CAA42014.1; -. EMBL, X75951, CAA53557.1; -. EMBL, M83295, AAA34566.1; -. EMBL, Z28216; CAA82061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.7%;
Best Local Similarity 50.0%;
Matches 11; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z49810; CAA89947.1; -. SGD; S0004464; YML005W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001295; -.
Pfam; PF01180; DHOdehase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                         Keast 10:663-679(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
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PIR; S44322; S44322.
HSSP; P54321; 1DOR.
                                                                                                                                            !- COFACTOR: FAD.
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Query Match
Best Local Similarity
Matches 7; Conserv
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10685;
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SEQUENCE 77
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ID GP46_BPSP1
AC 048400;
                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
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TRANSMEM
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TRANSMEM
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                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
INTSUE SPECIFICITY: MOST ABUNDANT IN COLON AND SMALL INTESTINE,
FOLLOWED BY KIDNEY AND STORAGH.
PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALLIZATION AND DENOMINATION OF HYDROPHOBIC
DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
                                                                                                                                                                                                                                                                                                                                                                                                                 SLC9A3 OR NHE3.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related proteins.";
J. Biol. Chem. 267:9331-9339(1992).
-I- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INNARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orlowski J., Kandasamy R.A., Shull G.E.;
"Molecular cloning of putative members of the Na/H exchanger gene family. CDNA cloning, deduced amino acid sequence, and mRNA tissue expression of the rat Na/H exchanger NHE-1 and two structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein; Sodium transport; Transport; Symport; Multigene family; Phosphorylation.

CYTOPLASMIC (POTENTIAL).
                                                                                                        ;
                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
SODIUM/HYDROGEN EXCHANGER 3 (NA(+)/H(+) EXCHANGER 3) (NHE-3).
                                                            Length 462;
                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A (M1) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
B (M2) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
D (M4) (POTENTIAL).
52726 MW; C581EF189A7D733C CRC64;
                                                            1;
                                                      DB 7
                                                                                                                                                                                                                                                                                         831 AA
                                                                                                     Mismatches
                                                            Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney; MEDLINE-92250539; PubMed-1577762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00999; Na_H_exchanger; 1. PRINTS; PR01084; NAHEXCHNGR. PRINTS; PR01087; NAHEXCHNGR3.
                                                      39.3%;
milarity 57.1%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M85300; AAA41702.1; -.
PIR; B40204; B40204.
InterPro; IPR000676; -.
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                          2 EAGNFERISGDLKY 15
                                                                                                                                                                    IPR001118; -
  462 AA;
                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSDUCTION
SEQUENCE
                                                                                                                                                                                                                                                                                         NAH3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
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TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation—
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-I - SIMILARITY: SOME, TO PHAGE SPP1 HYPOTHETICAL 10.2 KDA PROTEIN IN GP2-GP6 INTERGENIC REGION (AC 038400).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae; SPO1-like Viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.3%; Score 42; DB 1; Length 831; 46.7%; Pred. No. 33; Live 5; Mismatches 3; Indels
                                                                CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
G (MSB) (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
H (MG) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
I (M7) (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
G (M8) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
K (M9) (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
L, HYDROPHOBIC.
EXTRACELLUTAR (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                       E (M5) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINKED (GLCNAC. . .) (P. 77A4BF10DFF99E3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     M (M10) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFA3E89975061FAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE GENE 46 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF031901; AAC29015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93105 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l protein.
77 AA; 8989 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|| |:| ||| :::
719 EEATNYEEISGGIEF 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QEAGNFERISGDLKY 15
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PROSITE;
PROSITE;
                                                                                                                                                                           SEQUENCE
                                                                                                                                              METAL
METAL
                                                                                                                   METAL
                                                                        CHAIN
                                                                                       METAL
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                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ARGINASE II PRECURSOR (EC 3.5.3.1) (NON-HEPATIC ARGINASE) (KIDNEY-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SV/EV;
MEDINE=98427201; PubMed=9745037;
MEDINE=98427201; PubMed=9745037;
SS11 O.U., Kepka-Lenhart D., Morris S.M. Jr., O'Brien W.E.;
"Structure of the murine arginase II gene.";
Mamm. Genome 9:822-824(1998).

-i- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF EXTRA-UREA CYCLE
ARGININE METABOLISM AND ALSO IN DOWN-REGULATION OF NITRIC OXIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- PATHWAY: FIRST STEP IN ARGININE DEGRADATION IN THE UREA CYCLE.: SUBMIT: HOWOTRIMER (BY SIMILARITY).
-i- SUBMELLUIAR LOCATION: MITOCHONDRIAL.
-i- SIMILARITY: BELONGS TO THE ARGINASE FAMILY.
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Soldrognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                             oxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHESIS (BY SIMILARITY).

CATALYTIC ACTIVITY: L-ARGININE + H(2)0 = L-ORNITHINE + UREA.

COFACTOR: MANGANESE.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN-(2751BL/61; TISSUE-Kidney;
MEDLINE-9903259; PubMed-9814991;
Morris S.M. Jr., Kepka-Lenhart D., Chen L.C.;
"Differential regulation of arginases and inducible nitric synthase in murine macrophage cells.";
Am. J. Physiol. 275:E740-E747(1998).
                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                   354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC78460.1; JOINED.
AAC78460.1; JOINED.
AAC78460.1; JOINED.
                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00147; ARGINASE_1; 1.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-C57BL/6; TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF032466; AAB86959.1; -. AF045965; AAC78460.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U90886; AAC22548.1; -.
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AAC78460.1;
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AF045964; AAC78460.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC78460.1;
               EAGNF----ERISGDLKY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00491; arginase; 1. PRINTS; PR00116; ARGINASE.
                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1330806; Arg2.
                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF045960;
EMBL; AF045961;
                                                                                                  ARG2_MOUSE
                                                                                                                                                                                                                                                                                                                      yer R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                        ARGINASE).
                                                                                                                008691;
                                                                     RESULT 15
ARG2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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Gaps
                                                                        ARGINASE II.
MANGANESE I (BY SIMILARITY).
MANGANESE I (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE I (BY SIMILARITY).
MANGANESE I (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
W; B372DF68A19473F2 CRC64;
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,
                                                                                                                                                                                                                                       DB 1; Length 354;
                                                                                                                                                                                                                                                                       Indels
                                            ransit peptide; Mitochondrion.
RANSIT 22 MITOCHONDRION (POTENTIAL).
                               Urea cycle; Arginine metabolism; Hydrolase; Manganese;
                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                       Score 41.5; DF
                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                     1 QEAGNFERIS------GDLKYTQIDQ 20
                                                                                                                                                                                                                                                                                                                                   REAGLLKRLSRLGCHLKDFGDLSFTNVPQ 78
                                                                                                                                                                                                                                                                                                                                                                                                Search completed: July 5, 2001, 11:51:43
Job time: 502 sec
ARGINASE_2; 1.
ARGINASE_3; 1.
                                                                                                                                                                                         38878 MW;
                                                                                                                                                                                                                                       38.8%;
34.5%;
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                    Query Match
Best Local Similarity
Thes 10; Conserve
                                                                            23
120
143
145
147
251
253
354 AA;
PS00148;
PS01053;
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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: July 5, 2001, 11:50:48; Search time 123.78 Seconds

(without alignments)
22.446 Million cell updates/sec

Title: US-09-462-480-8

Perfect score: 107
Sequence: 1 OEAGNFERISGDLKYTQIDQV 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

2	Description	O69739 mycobacteri	09xwb8 caenorhabdi	O9vrw0 drosophila	O9w766 ambystoma m	Q9reb6 enterobacte	Q98856 cynops pyrr	09f799 salmonella	09fa27 clostridium	Q9f9q7 clostridium		09wzy8 thermotoga	082969 bacillus sp	P73828 synechocyst		09srh5 arabidopsis	Q9w5u2 drosophila	Q9rs16 deinococcus	Q9m888 arabidopsis	091fr8 arabidonsis
	ID	069739	Q9XWB8	Q9VRW0	09W766	Q9REB6	098856	Q9F799	Q9FA27	Q9F9G7	Q9EYK0	Q9WZY8	082969	P73828	Q9VP53	Q9SRH5	Q9W5U2	Q9RSL6	Q9M888	Q9LFR8
	DB	2	Ŋ	S	13	7	13	7	7	7	N	7	7	7	ß	10	Ŋ	7	10	10
	Query Match Length DB	100	296	3712	108	653	619	464	610	610	306	643	248	1014	119	276	458	480	535	540
æ	Query Match	83.6	47.7	43.5	43.0	43.0	43.0	41.1	41.1	41.1	40.7	40.2	39.7	39.7	39.3	39.3	39.3	39.3	39.3	39.3
	Score	89.5	51	46.5	46	46	46	44	44	44	43.5	43	42.5	42.5	42	42	42	42	42	42
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O26412 methanobact O18167 caenorhabdi Q9mlz7 arabidopsis Q9deb2 seriola qui	<b>α</b> α ο α .	O9ez78 klebsiella O9ez77 klebsiella O9ez76 klebsiella O9ez75 klebsiella O9ez71 klebsiella	klebsiell klebsiell klebsiell klebsiell klebsiell	091bj8 shigella so 091bj7 shigella so 09rd43 streptomyce 068890 enterobacte 032394 klebsiella 052978 enterobacte 09r936 escherichia 09wdj3 bacteroides
026412 018167 0 09M127 3 09DEB2	3 Q90458 Q56014 Q28714 069153	096278 096277 096276 096275 096273	Q9E270 Q9EUD6 Q9ETC0 Q9EXI5 Q9LBJ9	091537 091037 098043 068890 05294 052978 098936
702 1 1071 5 1616 1 285 1	307 69 73 81 2	2 721 2 721 2 721 2 721 2 721	127 127 127 127 136 140	140 2 140 2 140 2 140 2 140 2 140 2 2 140 2 2 2 4 2 2 2 3 4 3 4 3 4 3 4 3 4 3 4 3
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20 21 23 23	24 25 27	28 30 32 32	33 35 37	8.66444444 8.0001161846

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PROSITE;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Parsons J., Percy C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudnin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LANA OR CG10236.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Mooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
MCHT maxTn=6330.
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0
Score 89.5; DB 2; Length 100;
Pred. No. 4.5e-07;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                    Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natúre 368:32-38(1994).
EMBL; ALO32663; CAA21764.1; -.
SEQUENCE 296 AA; 34018 MW; E39256933B926E91 CRC64;
                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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Last annotation update)
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                                                                                                                           296 AA.
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3; Mismatches
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                                                                                                                           PRT;
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STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
MEDLINE-94150718; PubMed=7906398;
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                                                        13 QEAGNFERISGDLK-TQIDQV 32
                                             1 QEAGNFERISGDLKYTQIDQV 21
 83.6%;
95.2%;
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 EETSQLQRVSGDSKYLQI 204
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                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                        Caenorhabditis elegans.
 Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                      01-NOV-1999 (TrEMB)
Y75B12B.1 PROTEIN.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                             X75B12B.1
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gocayne G.R.A., Lewiss S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Beson K.Y., Beach P.V., Barnan B.P., Bhandari D., Bolshakov S., Bortchan M.R., Bouther H., Cadieu E., Center P., Bottchan M.R., Butler H., Cadieu E., Center A., Chandra I., RA Burtis R.C., Busam D.A., Bullek C., Davenport L.B., Davies P.M., RA Burtis R.C., Busam D.A., Bullek C., Davenport L.B., Davies P.M., RA Burtis R.C., Daplike C., Gaptielian A.E., Downson M. Dietz S.M. Achtis M., Cawley S., Dahlke C., Perraz C., Ferraz C., Busam D.A., Burtis M., M., Gabser K., Goog F. Gorrell J.H., Gu Z., Galbart W.M., Glasser K., Goog F. Gorrell J.H., Gu Z., Galbart W.M., Glasser K., Authouston K.A., Harvey D., Hehman T.J., Herrandez J.R., Harvey D., Hehman T.J., Herrandez J.R., Hostin D., Houston K.A., Harvey D., Hehman T.J., Herrandez J.R., Hock D., Lai Z., Lasko P., Eal Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X., Lasko P., Eal Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X., Liang Y., Lin X., Martel B.W., McIntosh T.C., Mcrendon D., Moshrefi A., Mont K.A., Nison K., Nusskern D.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., Shifner K., Wassarman D.A., Welsenbach J., Mang Z.Y., Wassarman D.A., Welsenbach J., Wallenger E., Spradling R.W., Rubin G.W., Wallenger E., Wang G.Y., Wassarman D.A., Wellenger E., Stan G., Zhao Q., Zhao Q., Zhao Q., Zhao G., Z
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PS01186; EGF_2: 5.
PS01248; LAMININ_TYPE_EGF_19.
PS00294; PRENTATION: UNKNOWN_1.
PS00030; RNP_1: UNKNOWN_1.
PS00030; RNP_1: LUKNOWN_1.
PS00031; PSPASE_1_3: UNKNOWN_1.
domain; Glycoprotein; Laminin EGF_like domain; Repeat.
3712 AA; 411126 MW; 2B6260435E06B84A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.5%; Score 46.5; DB 5; 55.0%; Pred. No. 2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00011; EGFLAMININ.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00054; laminin_G; 5.
Pfam; PF00055; laminin_Nterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00052; laminin_B; 1.
Pfam; PF00053; laminin_EGF; 20.
Pfam; PF00054; laminin_G; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QEAGNFERISGDLKYTQIDQ 20
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HSSP; P02468; 1TLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000034; Interpro; IPR0000345; Interpro; IPR000504; Interpro; IPR000508; Interpro; IPR000508; Interpro; IPR001230; Interpro; IPR001886; Interpro; IPR001886; Interpro; IPR001896; Interpro; IPR001896; Interpro; IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.0
Matches 11; Conservative
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PRELIMINARY;
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InterPro; IPR000130; -.
TPR000562; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000585; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001818;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GELATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
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                                                         098856
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                                      098856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                         Yang E.V., Gardiner D.M., Carlson M.R.J., Nugas C.A., Bryant S.V., "Expression of matrix metalloproteinase genes during axolot1 limb regeneration.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFISO055; AAD40666.1;
HSSP; P03956; ICGL.
                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
MATRIX METALLOPROTEINASE MMP-9 (FRAGMENT).
MATRIX METALLOPROTEINASE MMP-9 (FRAGMENT).
Eukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Nunez B., Avila P., de la Cruz F.;

"Mobilization functions of ClopF13.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12105 MW; 373757F60B73303C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D69F5922FEE8A79F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 2
Pred. No. 44;
1; Mismatches
                                    108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00413; Peptidase_M10; 1.
PRINTS; PR00138; MATRIXIN.
SMART; SM00235; ZNMc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       653 AA; 72897 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
43.0%;
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, MOBB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DVGNFQTFDGDLKWDHND 20
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Best Local Similarity 75.0
Matches 9; Conservative
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000130; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacter cloacae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                       NCBI_TaxID=8296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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                                    09W766
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RESULT
Q9W766
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Q9REB6
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Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824(1996).
-!- FUNCTION: COULD PLAY A ROLE IN BONE OSTBOCLASTIC RESORPTION. MAX
BE INVOLVED IN TISSUE REMODELLING OF THE REGENEATING LIMB.
-!- CATALYTIC ACTIVITY: CLEAVAGE OF GELATIN TYPES I AND V AND COLLAGEN
                                                                                                                                                                                                                                                                                                                                              TISSUE-RECENERATING LIMB BLASTEMA;
MEDLINE-967570627; PubMed-9692902;
MADIZAKI K., UChiyama K., Imokawa Y., Yoshizato K.;
"Cloning and characterization of cDNAs for matrix metalloproteinases
                       01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
92 KDA TYPE IV COLLAGENASE PRECURSOR (EC 3.4.24.35) (92 KDA
GELATINASE) (MATRIX METALLOPROTEINASE-9) (MMP-9) (GELATINASE B).
Cynops pyrrhogaster (Japanese common newt).
Eukaryota: Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi;
Amphibia: Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00120; HX; 1.
Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular matrix; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEMOPEXIN-LIKE.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GICNAC. . .) (POTENTIAL).
W, 573CDDB9DBF85524 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 3 FIBROMECTIN TYPE II-LIKE DOMAINS.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MIOA (ZINC METALLOPROTESE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
EMBL; D82052; BAA11523.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
ACTIVATION PEPTIDE (BY SIM)
92 KDA TYPE IV COLLAGENASE.
AUTOINHIBITOR REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRONECTIN TYPE-II.
FIBRONECTIN TYPE-II.
FIBRONECTIN TYPE-II.
679 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00546; CYSTEINE_SWITCH; 1.
PROSITE; PS00023; FIBRONECTIN_2; 3.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00045; fn2; 3.
Pfam; PF00045; hemopexin; 4.
Pfam; PF000413; Peptidase_M10; 1.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR00138; MATRIXIN.
ProDom; PD000995; -; 3.
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                                                                                                                                                                                                                                                                  of regenerating newt limbs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75581
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679 AA;
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SEQUENCE
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Query Match

:1111 | 1111 560 REAGNVEHISGD 571 1 QEAGNFERISGD 12

à g

43.0%; Score 46; DB 13; Length 679;

2 EAGNFERISGDLKYTQID 19

ŏ g PRELIMINARY;

Q9F799; 09F799

RESULT Q9F799

Salmonella typhimurium

SEQUENCE FROM N.A.

Salmonella. NCBI\_TaxID=602;

Conservative

Best Local Similarity

Matches

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Waligora A.-J., Hennequin C., Mullany P., Collignon A., Bourlioux P., Karjalalnen T., Karjalalnen T., Karjalalanen T., Collignon A., Bourlioux P., Collignon, C. aracterization and expression of a gene encoding a surface protein of C. difficile with adhesive properties."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF194870; AAG28425.1; SEQUENCE 610 AA, 66765 MM; BADEFC23DIAA1140 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactobacillus paracasei.
Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                Clostridium difficile.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-VTT E93490;
Makayama J. Akkermans A.D.L., de Vos W.M.;
"Genomic survey of three component regulatory system putatively
"Genomic survey of three component regulatory system putatively
involved in quorum sensing.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF322594; AAG48147.1;
SEQUENCE 306 AA; 35484 MW; 1E123E79905BE756 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.1%; Score 44; DB 2; Length 610; ilarity 72.7%; Pred. No. 86; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Last annotation update)
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Last annotation update)
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                                                                                     610 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 AA
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44.0%; Pred. No. 47;
:ive 3; Mismatches
                                                                                                                       Created)
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                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 ERGINERFINELRYYFPKGTQFDQV 270
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                                                                                                          U1-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01 MAR-2001 (TrEMBLrel. 16, CWP.66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, PUTATIVE TRANSPOSASE PRCB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.0
Matches 11; Conservative
                                                                                     PRELIMINARY;
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128 NFERISGNSRY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 NFERISGNSRY 138
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 NCBI_TaxID=1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1597;
                                                                                                                                                                                                                                                                                                       STRAIN=C253;
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Q9WZY8;
                                                                                    09F9G7
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                                                  RESULT
Q9F9G7
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ID Q9
AC Q9
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                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Stevenson G., Lan R., Reeves P.R., ^{\circ} "The colanic acid gene cluster of salmonella enterica has a complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium difficile.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 610;
                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE UNDECAPRENTLEHOSPHATE GLUCOSEPHOSPHOTRANSFERASE.
               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF093106; AAG13990.1; -SEQUENCE 610 AA; 66323 MW; C4720E5E0AE28F7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 AA; 52548 MW; B36027A2231957DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2;
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2;
Pred. No. 86;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.1%; Scor.
47.4%; Pred. No. v.,
4; Mismatches
                                                                                                                                                                    464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           610 AA
                 Mismatches
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEMS Microbiol. Lett. 191:11-16(2000)
EMBL; AF285085; AAG24818.1; -.
Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20461159; PubMed-11004393;
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72.78;
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44.48;
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                                                                       104 DVGNFQTFDGDLKWDHND 121
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Conservative

Local Similarity

Matches

ò qq

Query Match

SEQUENCE

history.

PRELIMINARY;

Q9FA27 Q9FA27

RESULT **Q9FA27**  01-MAR-2001 ( 01-MAR-2001 ( 01-MAR-2001 (

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1;

Query Match
Best Local Similarity 72.7
Matches 8; Conservative

SEQUENCE FROM N.A. NCBI\_TaxID=1496;

5 NFERISGDLKY 15

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SEQUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfelifer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium "Sequence analysis of the Synechocystis sp. strain PCC6803, II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA RES. 3:109-136(1996).
-!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.7%; Score 42.5; DB 2; Length 1014; 42.1%; Pred. No. 2.7e+02; tive 7; Mismatches 3; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation; Sensory transduction; Transferase. 1014 AA; 111604 MW; 989CB8AACGFF8050 CRC64;
                                                                                                                                                                                             stis sp. (strain PCC 6803).
Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                       Last sequence update)
Last annotation update)
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     PRT; 1014 AA
                                                                                                                                        SENSORY TRANSDUCTION HISTIDINE KINASE
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997 AASYERVQGELK-TMLDRL 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00072; response_reg;
Pfam; PF00512; signal; 1.
Pfam; PF00989; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90910; BAA17885.1; -.
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     PRELIMINARY;
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                                                             (TrEMBLrel.
                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P06628; IFSP.
InterPro; IPR000014; -.
InterPro; IPR000410; -.
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                                                                                                                 (TrEMBLrel
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Best Local Similarity
The 8; Conserve
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                                                                                                                                                                                                                                                    NCBI_TaxID=1148;
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                                                                                                                                                                                                Synechocystis
                                                             01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KINASES
                                                                                                                                                                                                                             Bacteria;
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                                                                                                                                                                                                                                                                                                                             Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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"Alkalophilic Bacillus DNA fragment involving MBP, CGTase, CDase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.2%; Score 43; DB 2; Length 643; 37.5%; Pred. No. 1.38+02; Ative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan; PF00905; Transpeptidase; 1.
Pfam; PF00912; Transglycosyl; 1.
SEQUENCE 643 AA; 73672 MW; 152291C19EBB717F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 248 AA; 27286 MW; DB9322A115442722 CRC64;
Created)
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Last annotation update)
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1409;
                                                                                 PENICILLIN-BINDING PROTEIN, CLASS 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                       Bacteria; Thermotogales; Thermotoga.
NCBI_TaxID-2336;
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STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
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EMBL; AE001754; AAD35967.1; -.
TIGR; TM0886; -.
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142 EEASDFEKSRAGDIEFLLVDQ 162
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  (TrEMBLrel. 12, (TrEMBLrel. 12,
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                                                          (TrEMBLrel. 16,
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Matches 8; Conservative
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01-NOV-1998 (TremBirel. 042-5A ORFI (FRACMENT.
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Best Local Similarity
Local 6; Conserve
                                                                                                                                           Thermotoga maritima
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01-NOV-1999 (
01-NOV-1999 (
01-MAR-2001 (
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InterPro; IPR001925; -

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And Antil J.K., Agbayani A., An H.-J., Andrews-Prainkoch C., Beasley E.M., Ballew R.M. Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Beeson K.Y., Benos P.V., Brokstein P., Berotter P., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Dodson K., Doup L.E., Garg N.S., Gelbart W.M., Glasser K., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harriss M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J. M., Allash F., Karpen G.H., Ke Z., Kulp D., Harris M., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Degwam C., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Mattei B., McIntosh T.C., Morris J., Moshrefi A., Mortulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mulshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Parley J., Patleb J.M., Rabara C., Siden Krämos I., Simpson M., Stupski M., Shen H., Wang X., Rahazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Mang Z., Tay, Wassarman D.A., Weinsted B., Wang Z., Yao Q.A., Wallsham S.M., Woodage T., Worlex E., Wang A.H., Wang S., Yao Q.A., Wang Z.Y., Wassarman D.A., Weinsted G., Zhon W., Zhon X., Zhu N., Zhon S., Zhon X., Zhon W., Zhon X., Zhon Y., Zhon Y., Zhon Y., Zhon X., Zhon Y., Zhon X., Zhon Y., Zhon
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Baldwin D.,
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Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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LIN X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thallana chromosome III BAC T22N4 genomic sequence.";
Submitted (OCT-1999) to EMBL/GenBank/DDBJ databases.
EMBL; AC010676; AAR03498.1;
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Agbayani A., An H.-J., Andrews-Pfannkoch C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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FlyBase; FBqn0037069; CG7658.
InterPro; IPR000618; -
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SEQUENCE 119 AA; 12674 MW;
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Best Local Similarity
Matches 9; Conserv
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Q9SRH5;
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Gaps
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                                                                                                 39.3%; Score 42; DB 10; Length 276; 35.0%; Pred. No. 72; 6; Indels 1; Mismatches 6; Indels
                                                       276 AA; 29425 MW; 7F33F53E56E9765C CRC64;
            Pfam; PF01459; Euk_porin; 1.
PROSITE; PS00558; EUKARYOTIC_PORIN; 1.
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151 KSGNFTKINAGLSFTKEDLI 170
                                                                                                                                                              2 EAGNFERISGDLKYTQIDQV 21
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Best Local Similarity 35.0*
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                  4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                     Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                         412676 seqs, 60623988 residues
                    GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1: /SIDSP///
                                                                                                                                                                                                                                       US-09-462-480-7
                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                         OM protein
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M. tuberculosis an M. tuberculosis an M. tuberculosis im Mycobacterium tube M. tuberculosis Ev M. tuberculosis IF M. tuberculos

AAX32097
AAX3118
AAX8118
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AAX32063
AAX39176
AAX391

AAY39128 AAW32459 AAW31697 AAY39127 AAY03713 AAY097313 AAW19540 AAW94391

## ALIGNMENTS

AAY00152 AAW32458 AAW81696 AAY39126

S-region transfer

	RESULT	LT 1						
-	AAY0	AAY03707						
	61	AAY03707 sta	AAY03707 standard; Protein; 42 AA.	in; 42 AA.				
	×							
-	AC	AAY03707;						
	XX							
	DŢ	07-JUN-1999	(first entry)	Y)				
	×							
	DE	M. tuberculosis LHP	sis LHP poly	peptide antic	polypeptide antigenic fragment.			
+	×							
-	ΚM	ESAT-6 prote	in; antigeni	c protein; L	ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosi	ium t	uberc	ulosi
	ΚM	immunogen; vaccine;	accine; bact	eria; tubercu	bacteria; tuberculosis; regulatory; synergist	tory;	syne	ergist
	ΚW	immune response.						
-	XX							
-	SO	Mycobacteriu	Mycobacterium tuberculosis.	is.				
	XX							
0	PN	W09904005-A1						
	XX							
	PD	28-JAN-1999.						
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٠	PF	16-JUL-1998;	98WO-IB01091	091.				
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	PR	16-JUL-1997;	97US-0052631	631.				
	XX							
	ΡA	(INSP ) INST	INST PASTEUR.					
•	PA	(STAT-) STAT	STATENS SERUM IN	INST.				
_	XX							
	ΡΙ	Andersen P,	Berthet F,	Gicquel B,	Rasmussen PB;			
	 XX							
	DR	WPI; 1999-132249/11	2249/11.					
_	X							
	PŢ	New nucleic	acid contain	ing regulato	New nucleic acid containing regulator and LHP gene of		4ycob?	Mycobacter
	ΡŢ	tuberculosis	- useful in	vaccines, fo	tuberculosis - useful in vaccines, for diagnosis, and		or e	for expres:
_	ΡŢ	of heterolog	of heterologous proteins					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ü

DB

Length

Query Match

Score

Result No.

/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

220 220 220 220 220 220 220 220 220

is; tic;

New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis - useful in vaccines, for diagnosis, and for expression of heterologous proteins

Mycobacterium tube
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AAY03707 AAW32454 AAW32386 AAW81707 AAW64340 AAY39137

20 118 118 118 118 118

996.1 996.1 996.1 996.1 996.1 996.1 996.1

1198 1198 1198 1198 1198 1198

AAW32444 AAW32376 AAW81747 AAW64321

Description

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New
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                                      The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open regulatory expression signals of the ESAT-6 protein as well as an open cading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the M. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, or specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antiboddes. The regulatory region present in the polynucleotide may be used to express almost any heterologus protein in mycobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                          Sequences AAY03706-713 represent antigenic fragments of the
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                   Length 42;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reed SG,
                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                Score 198; DB 20;
Pred. No. 5.5e-20;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon DC, Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 149; 168pp; English.
              Claim 21; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW32454 standard; Protein; 80
                                                                                                                                                                                                                                                                                                                                                96.18;
97.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0680574.
95US-0523436.
95US-0533634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US14674.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0620874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-neto A, Dillon D
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-192903/17.
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                     42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT91526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9709428-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-1996
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW32454;
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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-IF3. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                Gaps
                        (or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ^{\rm sW} immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection
A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (of is variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1F3. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins ESAT-6, are useful in vaccines, preferably when formulated with a mon-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YAW;
                                                                                                                                                                                                                                             Length 80;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                   Houghton R, Reed SG,
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                                                                                                                                                                                                                                         Score 198; DB 18;
Pred. No. 1.2e-19;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis antigen Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 163; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW32386 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             skin testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0523435.
95US-0532136.
96US-0620280.
96US-0658800.
                                                                                                                                                                                                                                         Query Match 96.1%;
Best Local Similarity 97.6%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campos-neto A, Dillon DC,
Twardzik DR, Vedvick TH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0680573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-192904/17.
N-PSDB; AAT91460.
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                                                                                                                                                                                      80 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-1995,
22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-1996
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Sequence

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Matches

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39

AAW81707;

AAW81707

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This polypeptide comprises Mycobacterium tuberculosis antigen Tbi8-1F3. A DNA molecule (see AAV4440) coding for Tbi8-1F3 was isolated from a M. tuberculosis strain H37Rv genomic library. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                         Tuberculosis; infection; diagnosis; antigen; Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculosis antigen Tb38-1F3 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF 42
                                                                                                                                                                                                                                                                                                                                                                            DC, Houghton R, Lodes M.
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 96.1%; Score 198; DB 19; 1 Similarity 97.6%; Pred. No. 1.2e-19; 41; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis antigen Tb38-1F3
                                                                                                                                            Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 146; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY39137 standard; Protein; 80 AA.
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96US-0729622
                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                            Dillon
                                                                                                                                                                                                                                                                                                                                                                              o A, Dillon
Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-251292/22.
N-PSDB; AAV44400.
                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of tuberculosis
                                                                                                                                                                              WO9816645-A2.
                                                                                                                                                                                                                                                  07-0CT-1997;
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11-OCT-1996;
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                                     09-NOV-1998
                                                                                                                                                                                                                 23-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                Campos-Neto
                                                                                                                                                                                                                                                                                                                                                                                           Reed SG,
 AAW64340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY39137;
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                                                                                                                                                                                                                                                                                                                                                                                             Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;
vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
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                                                     80;
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                                                                                        1; Indels
                                                     Length
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                                                                                                                                            1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                   , DB 18;
1.2e-19;
                                                                                                                                                                                                                                                                                                                                                          M. tuberculosis immunogenic polypeptide Tb38-1F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 198; DB 19;
Pred. No. 1.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                        0; Mismatches
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                                                   Score 198;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW64340 standard; Protein; 80 AA.
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97.6%;
                                                 96.18;
97.68;
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96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                        41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-261042/23.
N-PSDB; AAV64509.
                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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80
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Gaps

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Sequence

Query Match

Matches

AAW64340 ID AAW6

RESULT

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Length 80; Indels M. tuberculosis

Vedvick TS:

Houghton R;

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This invention describes novel recombinant antigens and their encodin nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizating against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A new immunogenic polypeptide has been developed comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunogenic polypeptide(s) from Mycobacterium useful in vaccines for prevention or treatment of
                                                                                                                       New polypeptide comprising antigenic portions of
                o A, Dillon DC, Hendrickson RC, Hor
Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                             Score 198; DB 20;
Pred. No. 1.2e-19;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis antigen Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houghton R,
                                                                                                                                                     Example 3; Page 180; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 124; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW32444 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                                         96.1%;
illarity 97.6%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skin testing; M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0523436.
95US-0533634.
96US-0620874.
96US-0659683.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Twardzik DR, Vedvick TH;
                                                                   WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-192903/17
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 41; Conserv
                                                                                                                                                                                                                                                                                                                           80 AA;
                                                                                     N-PSDB; AAZ19098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT91509
                   Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campos-neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9709428-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1995
22-SEP-1995
                                     Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Si
Matches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW32444;
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW32444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes polypeptides comprising an immunogenic art of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. Bor natural killer cells and/or macrophages in tuberculosis-immune subjects. AAX19249 to AAX19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                         New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                       o A, Dillon DC, Hendrickson RC, Houghton R;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis recombinant antigen protein Tb38-1F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 198; DB 20;
Pred. No. 1.2e-19;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QEAANKOKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qeaankqkqeldeistnirqagvqysradeeqqqalssqmgf
                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 134-135; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY38994 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.1%;
97.6%;
                                                                                                   99WO-US03268
                                                                                                                                     98US-0072967
98US-0025197
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98US-0024753
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Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                         WPI; 1999-527409/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 AA;
                                                                                                                                                                                                                                                                                           N-PSDB; AAZ19310
                                W09942076-A2
                                                                                                   17-FEB-1999;
                                                                                                                                     05-MAY-1998;
18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1998;
18-FEB-1998;
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                                                                                                                                                                                                                       Campos-Neto
                                                                 26-AUG-1999
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                                                                                                                                                                                                                                       Lodes MJ,
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tuberculosis - are tuberculosis, also

Skeiky YAW;

vaccine;

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Gaps

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Indels

Length 80;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen. Th38-1. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a mon-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ien; immunogen; vaccine; tuberculosis; non specific adjuvant;
testing; M.tuberculosis.
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                                                                                                                                                                                                          Length 95;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                          1 QEAANKOKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF 42
                                                                                                                                                                                                                                                                                                           95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reed SG,
                                                                                                                                                                                                        Score 198; DB 18;
Pred. No. 1.4e-19;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                             54 qeaankqkqeldeistnirqagvqysradeeqqqalssqmgf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen Tb38-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                            AAW32376 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                960S-0680573.
950S-0523435.
950S-0532136.
960S-0620280.
                                                                                                                                                                                                        ch 96.1%;
1 Similarity 97.6%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 136; 190pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US14675.
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Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-192904/17.
N-PSDB; AAT91445.
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                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                       95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 AA;
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22-SEP-1995;
22-MAR-1996;
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                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW32376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  skin
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                                                                                                                                                                                                                                                                                                                                                                                      Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection {\sf L}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and for diagnosis, treatment and prevention of tuberculosis infection
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                Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to A, Dillon DC, Houghton R, Lodes MJ;
Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
                DB 18;
                                                                                                                  54 qeaankqkqeldeistnirqagvqysradeeqqqalssqmgf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 198; DB 19;
Pred. No. 1.4e-19;
0; Mismatches 1;
                                                                                            1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF
Score 198; DB 10, No. 1.4e-19;
                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis immunogenic polypeptide Tb38-1
                                    Pred. No. 1.46
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3b; Page 117; 230pp; English.
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              96.1%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US18293.
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ilarity 97.6%;
Conservative
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96US-0730510.
                                                                                                                                                                                                                              AAW81747 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                            (first entry)
                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 41; Conserv
                                Best Local Similarity Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9816646-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1997;
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                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW64321;
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                                                                                                                                                                                                              AAW81747
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Campos-Neto A;

99WO-US07717 98US-0056556 98US-0223040

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New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                               Tb38-1. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens such as Tb38-1, e.g. TbF-2 (see AAY32063) and a TbH9-Tb38-1 fusion. The new fusion proteins are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                     This sequence represents the Mycobacterium tuberculosis antigen
                                                                                                                                                                                                                                                                        Claim 1; Fig 4D; 83pp; English.
                                                                                                                                                                       Skeiky YAW, Alderson M,
                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                  WPI; 1999-601610/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 AA;
             WO9951748-A2
                                                                                               07-APR-1998;
30-DEC-1998;
                                                                    07-APR-1999;
                                         14-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                    components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY39118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1938-1. A DNA sequence (see AAV44384) coding for antigen Tb38-1 was isolated from a M. tuberculosis strain H37Rv expression library using sera from patients having pulmonary or pleural tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAM64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                        New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is an antigenic portion of Mycobacterium tuberculosis antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen; fusion protein; Tb38-1; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 95;
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                                                                   Tuberculosis; infection; diagnosis; antigen; Tb38-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis antigen Tb38-1 peptide.
                                                                                                                                                                                                                                                                                      Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 198; DB 19;
Pred. No. 1.4e-19;
); Mismatches 1;
                                                                                                                                                                                                                                                                                   DC, Houghton R, Lodes M. Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis antigen Tb38-1.
                                                                                               Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 123; 250pp; English.
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ilarity 97.6%;
Conservative
                                                                                                                                                                                   97WO-US18214.
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96US-0729622.
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           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                 Campos-Neto A, Dillon
Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                           WPI; 1998-251292/22.
N-PSDB; AAV44384.
                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; immunoqen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 AA;
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                                                                                                                          WO9816645-A2
                                                                                                                                                                                   07-OCT-1997;
                                                                                                                                                                                                              13-MAR-1997;
11-OCT-1996;
           09-NOV-1998
                                                                                                                                                       23-APR-1998.
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Gaps
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Length 95;
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                         1; Indels
                                                                                                                                                                                                           M. tuberculosis antigen Tb38-1 amino acid sequence.
                                                             1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF 42
96.1%; Score 198; DB 20; 97.6%; Pred. No. 1.4e-19; iive 0; Mismatches 1
                                                                                                                                    AAY39118 standard; Protein; 95
            Best Local Similarity 97.6%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                            99WO-US03268.
                                                                                                                                                                                                                                                                                                                                                                                  98US-0072967
                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto A,
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                                                                                                                                                                                                                                                                                                                                                           17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                   05-NOV-1999
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Gaps

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Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA – used
M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to develop products for the detection of \dot{M}, tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
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Pred. No. 1.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. tuberculosis immunogenic polypeptide Tb38-IN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 198; DB 19;
Pred. No. 1.5e-19;
                                                                                                                                                                                               1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF
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Reed SG, Skelky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                        0; Mismatches
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      AAW81706 standard; Protein; 100
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97.6%;
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96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis,
                                                                                             Query Match
Best Local Similarity 97.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                            AAW81706;
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                                                            Sequence
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                                                                                                                                               The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAY39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                      New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide comprising antigenic portions of M. tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M. tuberculosis recombinant antigen protein Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 198; DB 20;
Pred. No. 1.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 159; 323pp; English.
                                                                                                                Example 3; Page 113; 299pp; English.
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97.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
              WPI; 1999-527409/44
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Search completed: July 5, 2001, 11:45:43

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Gaps

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Length 100; Indels

Job time: 272 sec

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CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/420,976
FILING DATE: 10-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-112C-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEPAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,236 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                   July 5, 2001, 11:46:58 ; Search time 61.79 Seconds (without alignments) 13.693 Million cell updates/sec
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Appli
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Patent No. 5510466
Patent No. 5510466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 50,
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Sequence 4,
Sequence 4,
Sequence 4,
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                                                                                                                                                                                                                                   206
1 QEAANKQKQELDGISTNIRQ......VQXSRADEEDQQALSSQMGF
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Sequence
Sequence
Sequence
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Sequence
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Sequence
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: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-795-088A-2
US-08-416-756A-2
US-08-416-756A-5
US-08-562-535C-4
US-08-759-294-4
US-08-466-390-4
US-08-467-781-4
US-08-467-781-4
US-08-467-781-4
US-08-487-950-4
US-08-487-950-4
US-08-487-208-4
US-08-005-005C-4
US-08-005-005C-4
US-08-487-208-4
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US-07-955-905A-23
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5510466-2
5510466-4
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PCT-US95-16216-1
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                                                                                                                                                                                                                                                                                                                                                      193259 seqs, 20144635 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match
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Perfect score:
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Length 234;

Score 51.5; DB 3; Pred. No. 5.8;

25.0%; 37.8%;

Sequence 24, Appl Sequence 2, Appl1 Sequence 2, Appl1 Sequence 22, Appl1 Sequence 23, Appl1 Sequence 2, Appl1 Sequence 1, Appl1 Sequence 4, Appl1 Sequence 2, Appl1 Sequence 6, Appl1 Sequence 6	. IMMITIS OF HEARTWORM IN MAMMALS
US-08-556-419-24 US-08-659-16-2 US-09-109-273-2 US-09-556-419-22 US-08-556-419-23 US-07-707-367-2 US-07-707-367-2 US-08-716-897-2 US-08-781-891-77 US-08-781-891-77 US-08-781-891-77 US-08-781-190-2 US-08-785-190-2 US-08-785-190-2 US-08-785-190-2 US-08-785-190-2 US-08-785-10661A-2 US-08-728-323A-2 US-08-728-10661A-2 US-08-728-10661A-2	ALIGNMENTS  US/08836236 CLOTILDE K.S. FRANCINE B. OJANG NOVEL PROTEIN FROM DIROFILARIA AD METHOD FOR IMMUNODIAGNOSIS 13 SS: GLAND BIOLABS, INC. TTS  TTS  RM: RM: COMPATIBLE
2.8 126 3 2.8 4445 3 2.8 4445 3 2.8 4445 3 2.8 629 3 2.6 629 3 2.3 700 2 2.3	136-236-7  106-7  107  108-7  108-7  108-7  108-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-
288 47 222 30 47 222 31 47 222 33 4 47 222 33 4 46 .5 222 34 46 .5 222 40 46 222 40 46 222 41 46 222 41 46 222 42 45 222 43 45 .5 222 44 45 .5 222 45 45 5 222 45 45 .5 222	RESULT 1  US-08-836-236-7  Sequence 7, Application US/08836236  PARTENT NO. 6103484  GENERAL INFORMATION: APPLICANT: CARLOW, CLOTILDE K.S. APPLICANT: PERE, FRANINE B. APPLICANT: MEJIA, JHON S. TITLE OF INVENTION: AND METHOD NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: ADDRESSE: NEW ENGLAND BIOLAB STATE: MASSACHUSETTS COUNTRY: US COUNTRY: US ZIP: 01915 COMPUTER: IBAPEL FORM: MEDIUM TYPE: FLOPPY disk COMPUTER: IBM PC compatible

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APPLICANT: Orlicky, David
TITLE OF INVENTION: PROSTACLANDIN F2' RECEPTOR REGULATORY
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 KYKQSVQGAGTSYRNVLQAAIQKSLKDPSNNFRLHNGRSKEQRLKEQLG 218
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/795,088A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: 536
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group STREET: 75 Denise Drive CITY: Hillsborough STATE: California
                    APPLICANT: Sul, Hong-Bing
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: Regulators of Apoptosis
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 KOKQELDGIST --- NIRQAGVQYSRAD ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5747660
                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36,627
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TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.0%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (650) 343-4342 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 480 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Osman, Richard A
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 30.69
Matches 15; Conservative
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                                                                                                                                                                                                                     ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COMPUTER READABLE FORM:
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STATE: Californi
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APPLICANT: Orlick
    GENERAL INFORMATION:
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US-08-795-088A-2
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US-08-554-612C-50
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                                                                                                                                                                            Patent No. 5510466; MONTY; KODAMA, TATSUHIKO
TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 453;
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TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
Indels
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    14;
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                                                              EAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSS 38
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Pred. No. 13;
9; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51.5;
Pred. No. 9.0
                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302_00

FILING DATE: 16-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 997,113

FILING DATE: 24-DEC-1992

APPLICATION NUMBER: 391,486

FILING DATE: 09-AUG-1889

APPLICATION NUMBER: 272,002

FILING DATE: 15-NOV-1988

SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/307,400 FILING DATE: 16-SEP-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: 997,113
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Sequence 2, Application US/08795088A
Patent No. 6242569
  8;
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APPLICATION NUMBER: 391,486
FILING DATE: 09-AUG-1989
APPLICATION NUMBER: 22,002
FILING DATE: 15-NOV-1988
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30.2%;
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Best Local Similarity 30.2'
Matches 13; Conservative
  Conservative
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                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 12
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 349
5510466-2
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14;
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  Matches
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13;

15; Indels -----EEQQOALSSOMG 41

6; Mismatches

DB 4;

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DNA Encoding A Prostaglandin F2' Receptor, A Host Cell Transformed Therewith and An Expression
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DB 1; Length 369;
12;
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                                           Indels
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APPLICATION NUMBER: US/08/416,756A FILING DATE: 13-APR-1990 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE93/00789 FILING DATE: 01-OCT-1993 PRIOR APPLICATION NUMBER: SE 9202892-7
                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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Pred. No. 13;
7; Mismatches 14
  Score 51; DB 1
Pred. No. 12;
7; Mismatches
                                                                                                              337 ELSSIKNSLKVAAISESPAAEKENQQASSEAG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 ELSSIKNSLKVAAISESPAAEKENQQASSEAG 389
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                                                                                  10 ELDGISTNIRQAGVQYSRADEEQQQALSSQMG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New York Avenue, N. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 ELDGISTNIRQAGVQYSRADEEQQQALSSQMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALICATION APPLICATION APPLICATION APPLICATION UNBERN: SE 9202892-7 FILING DATE: 02-0CT-1992 ATTONEY ABENT INFORMATION: NAME: Cimbala, Michale A. REGISTRATION NUMBER: 33,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            Sequence 5, Application US/08416756A Patent No. 5750369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08562535C
Patent No. 5916791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 13
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Lake, Staffan
APPLICANT: Stjernschantz, JI
TITLE OF INVENTION: DNA Enc
TITLE OF INVENTION: HOST CE
TITLE OF INVENTION: HOST CE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                          Thereof
  24.8%;
34.4%;
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34.48;
  Query Match 24.85
Best Local Similarity 34.45
Matches 11; Conservative
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Best Local Similarity 34.4
Matches 11; Conservative
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COMPUTER READABLE FORM:
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ADDRESSEE: STERNE, K
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COUNTRY:
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APPLICANT: Lake, Staffan
APPLICANT: Lake, Staffan
APPLICANT: Stjernschantz, Johan
TITLE OF INVENTION: DNA Encoding A Prostaglandin F2' Receptor, A
TITLE OF INVENTION: Host Cell Transformed Therewith and An Expression Product
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                              Score 51; DB 1; Length 366; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOLDSTEIN & FOX P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,756A
FILING DATE: 13-APR-1990
                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE93/00789
FILING DATE: 01-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9202892-7
FILING DATE: 02-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1370.0070000
            REFERENCE/DOCKET NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELEPONNUNCATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                              10 ELDGISTNIRQAGVQYSRADEEQQQALSSQMG 41
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ADDRESSEE: STERNE, KESSLER, GOLDSTI
STREET: 1100 New York Avenue, N. W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08416756A Patent No. 5750369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTAL.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                            Query Match 24.8%;
Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                 TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 369 amino acids amino acids
                                                                                                                                                                 : 366 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-416-756A-2
                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-554-612C-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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US-08-416-756A-2
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                                                                                                                                                                 LENGTH:
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GENERAL INFORMATION:

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Gaps
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Joseph Hirschberg, Tamar Lotan and
APPLICANT: Mark Harker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Chicony NB5500/386SX
COMPUTER: CSYTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LISTEM: MS DOS VECSION 6.2,
OPERATING SYSTEM: Windows version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: CONVECTED to ASCI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/75
FILING DATE:
CLASSTORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 2
Pred. No. 20;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 EALKEKEKEVAGSSDVLRTWATQYSLPSEESDAA 50
  Word for Windows version 2.0,
                                                            APPLICATION NUMBER: US/08/742,605D FILING DATE: Oct. 28, 1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/562,535 FILING DATE: NO. 5967795. 24, 1995 ATTORREY/AGENT IRFORMATION: NAME: Friedmam, Mark M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/742,605
FILING DATE: Oct. 28, 1996
APPLICATION NUMBER: 08/562,535
FILING DATE: NO. 6218599. 24, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Virginia
COUNTRY: United States of America
                                                                                                                                                                                                                     NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 325/TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09259294 Patent No. 6218599
                    SOFTWARE: converted to ASCI CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.8%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.8 Best Local Similarity 35.3 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Friedmam, Mark M
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
TOPOLOGY:
US-08-742-605D-4
  SOFTWARE:
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                  TITLE OF INVENTION: Polynucieotide molecule from Haematococcus pluvialis encoding NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
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0
Joseph Hirschberg, Tamar Lotan and Mark Harker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
         ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
STREET: 2940 Birchtree space lane
CITY: Sllver Spring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Joseph Hirschberg, Tamar Lotan and APPLICANT: Mark Harker
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead Slimnote-890Tr.
COMPUTER: Twinhead Slimnote.890Tr.
COMPUTER: Twinhead Slimnote.800Tr.
COPERATING SYSTEM: Mindows version 3.11
SOFTWARE: Word for Windows version 2.0
CURRENY APPLICATION DATA:
CAPPLICATION NUMBER: US/08/562,535C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: 1.44 megabyte, 3.5" microdisk
Chicony NBS500/786SX
SYSTEM: MS DOS version 6.2,
SYSTEM: Windows version 3.11
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 325/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.8%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 1.44 me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Unit
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OPERATING SYSTEM:
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                              20906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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APPLICANT:
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Sequence 4, Application US/08467781
Patent No. 5780596
GENERAL INFORMATION:
APPLICANT: TOURGATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                          GENERAL INFORMATION:
APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.8%; Score 49; DB 1; Best Local Similarity 33.3%; Pred. No. 2.1e+02; Matches 10; Conservative 10; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
                                                                                                                                                                              STREET: 125 HIGH STREET
CITY: BOSTON
STATE: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/470,950 FILING DATE: 06-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: PITCHER ESQ, EDMUND R
RECISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
                                       Sequence 4, Application US/08470950 Patent No. 5698439
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-470-950-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                     RY: USA
02110
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                                                                                                                                                                                                                                                                                                     COUNTRY:
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                  -08-470-950-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08466390
Patent No. 5686562
GENERAL INFORMATION:
APPLICANT: TOURATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCE: 6
CORRESPONDENCE ADDRESS:
ADDRESSED: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.8%; Score 49; DB 1; Length 2101; 33.3%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                         DB 4; Length 329; 20;
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                                                                                                                                                                                                                                                                                                   16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,390
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                       Score 49; DB 4; Pred. No. 20; 6; Mismatches
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REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
                TELECOMMUNICATION INFORMATION TELEPHONE: 972-3-5625553 TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                         Query Match 23.8%;
Best Local Similarity 35.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                 INFORMATION FOR SEQ ID NO:
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Matches 10; Conserva
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                                                                                                                                                                                               US-09-259-294-4
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                                                                          TELEX:
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Gaps

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PatentIn Release #1.0, Version #1.25

SOFTWARE:

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Gaps
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                                                                                                                                                                                                                                                                                                                     APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                      Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.8%; Score 49; DB 2; Length 210 Best Local Similarity 33.3%; Pred. No. 2.1e+02; Matches 10; Conservative 10; Mismatches 10; Indels
                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,924
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: PITCHER ESQ. EDMUND R
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
                 23.8%; Score 49; DB 1; ilarity 33.3%; Pred. No. 2.1e+02; Conservative 10; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
                                                                                                                                    ::||:| : |::: : |:| : | : | 488
                                                                                                       6 KQKQELDGISTNIRQAGVQYSRADEEQQQA 35
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                                                                                                                                                                                                                                                           ; Sequence 4, Application US/08483924
; Patent No. 5882876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-483-924-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                      Query Match
Best Local Similarity
Matches 10; Conserv
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Job time: 313 sec
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                                                                                                                                                                                                                                       US-08-483-924-4
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Patent No. 5/83403
GENERAL INFORMATION:
GENERAL TOURATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                            23.8%; Score 49; DB 1; Length 2101; 33.3%; Pred. No. 2.1e+02; tive 10; Mismatches 10; Indels
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ZIP: 02109

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,487
                               FILING DATE: V. C. CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDWIND R
REGISTRATION NUMBER: 27,829
REFERENCE/DECKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
TELEFAX: (617) 248-7100
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KQKQELDGISTNIRQAGVQYSRADEEQQQA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,701
                 APPLICATION NUMBER: US/08/467,781
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2101 amino acids
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Matches 10; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-467-781-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-195-487-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-195-487-4
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model OM protein

Run on:

July 5, 2001, 11:48:31; Search time 79.63 Seconds (without alignments) 40.177 Million cell updates/sec

US-09-462-480-7 Perfect score:

1 QEAANKQKQELDGISTNIRQ......VQYSRADEEQQQALSSQMGF Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote myosin heavy chain myosin heavy chain nodulation protein preprotein translo hypothetical prote hypothetical prote ovtl protein - nem prote uroporphyrinogen I KIAA0640 protein phage antigenic de phycocyanin linker hypothetical prote uroporphyrin-III C male-enhanced anti hypothetical prote prote hypothetical prote conserved hypothet MG328 homolog P01\_ prote penicillin-binding lypothetical prote 42K membrane antig ipac protein - Shi isocitrate dehydro probable membrane DNA helicase II hypothetical hypothetical hypothetical Description S02185 G86066 T00379 T42722 C48943 B83947 F82150 % Query Match Length DB 54.5 54 54 53.5 Score 198 65 61 60 60 60 57 57 57 57 56 56 57 Result Š.

hypothetical prote	probable transport	myosin heavy chain	hypothetical prote	myosin heavy chain	giantin - human	giantin - human	ribosomal protein	22K zein precursor	biphenyl-2,3-diol	alpha/beta-gliadin	hypothetical prote	conserved hypothet	serine proteinase	serine proteinase	8.9K linker polype
G70803	A44458	S06117	T15496	B43402	152300	A56539	H75558	T02983	DAPSPC	A22364	B59103	F69121	F82734	H82826	A24691
7	7	7	7	Н	7	Н	7	7	Н	~	7	7	~	7	7
460	494	924	1263	2007	3225	3259	102	267	293	319	410	655	908	910	80
25.5	25.5	25.5	25.5	25.5	25.5	25.5	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.0
52.5	52.5	52.5	52.5	52.5	52.5	52.5	52	52	52	52	52	52	52	52	51.5
. 30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

Quely marchi
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Gaps ö Indels 1; Best Local Similarity 9/.0%; Pred. No. 1e-1/;
Matches 41; Conservative 0; Mismatches

RESULT

T10032

hypothetical protein MLCB628.13c - Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Accession: T10032
R; Eiglameier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993.
A; Title: Use of an ordered cosmid library to deduce the genomic organization of Mycob
A; Reference number: 216917; MUID:93188700

A; Accession: T10032

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-100 <EIG>

A;Residues: 1-100 <ELG> A;Cross-references: EMBL:Y14967; NID:g2370268; PIDN:CAA75210.1; PID:g2370280

ö Gaps ö 36.9%; Score 76; DB 2; Length 100; 36.6%; Pred. No. 0.014; 16; Indels Ouery Match 36.9%; Score 76; DB 2 Best Local Similarity 36.6%; Pred. No. 0.014 Matches 15; Conservative 10; Mismatches

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A;Cross-references: GB:AE000456; GB:U00096; NID:92367291; PIDN:AAC76806.1; PID:917902
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Riberra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May 11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A;Titler Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G86066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005174; NID:g12518667; PIDN:AAG58995.1; GSPDB:CN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X12614; NID:g41665; PIDN:CAA31134.1; PID:g41668
R;Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.
Science 277, 771-778, 1992
A;Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84. A;Teference number: S30660; MUID:92358234
A;Accession: S30693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: DNA
A Residues: 1-33 «CAN»
A Stresidues: 1-33 «CAN»
A Stresidues: 1-33 «CAN»
A Stresidues: 1-33 «CAN»
A Stresidues: 1-33 «CAN»
A Note: the nucleotide sequence was submitted to the EMBL Data Library, Novem
R Shattner, R R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley
Science 277, 1453-1462, 1997
A Stitle: The complete genome sequence of Escherichia coli K-12.
A Steference number: A64720; MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uroporphyrinogen III methylase [imported] - Bscherichia coli (strain 0157:H7) (S. Specias: Bscherichia coli (C. Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 (Accession: G86066
                                                                   PIDN:CAA31772.1; PID:941678
                                                                                                                                                    A;Title: The sequence of hemC, hemD and two additional E. coli genes. A;Reference number: S01693; MUID:89041586
A;Accession: S01693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 399;
6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.5;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                       A; Residues: 1-393 <SAS>
A; Cross-references: EMBL:X13406; NID:941677; P
R; Alefounder, P.R.; Abell, C.; Battersby, A.R.
Nucleic Acids Res. 16, 9871, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.6%;
Best Local Similarity 40.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                 A; Status: translation not shown
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-393 <BLAT>
                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-393 <ALE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-399 <STO>
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A; Residues: 1-393 <B
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                                                                                                                                                                                                                                                       N'Alternate names: myosin-like antigen
C:Species: Onchocerca volvulus
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Jun-2000
C;Accession: T43214; A44939, A54513; S27825
R:Triteeraprapab, S: Richie, T.L.: Tuan, R.S.; Shepley, K.J.; Dinman, J.D.; Neubert, T
Mol. Biochem. Parasitol. 69, 161-171, 1995
A;Title: Molecular cloning of a gene expressed during early embryonic development in Ond
A;Reference number: 222341; MUID:95287898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Escherichia coli
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 05-May-2000
C;Accession: SO189; S01693; S36693; D65184
R;Sasarman, A.; Echelard, Y.; Letowski, J.; Tardif, D.; Drolet, M.
Nucleic Acids Res. 16, 11835, 1988
A;Title: Nucleotide sequence of the hemx gene, the third member of the uro operon of Esc
A;Reference number: S02185; MUID:89098348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: the sequence is revised in GenBank entry ONGANTML, release 115, (PIDN:AAA29413.1 R; Donelson, J.E.; Duke, B.O.L.; Moser, D.; Zeng, W.; Erondu, N.E.; Lucius, R.; Renz, A.; Mol. Biochem. Parasitol. 31, 241-250, 1988
A; Title: Construction of Onchocerca volvulus cDNA libraries and partial characterization A; Reference number: A54513; MUID:89127417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues: 733-874,'E',876-916,'S',918-1038,1040-1047,'S',1049-1283,'E',1285-1363 <EROX
Cross-references: GB:M30398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: mRNA
Residues: 733-874,'E',876-916,'S',918-1038,1040-1047,'S',1049-1283,'E',1285-1347,'E'
Cross-references: EMBL:M30398; NID:g159876; PIDN:AAA29413.1; PID:g159877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description: Characterization of a myosin-like antigen from Onchocerca volvulus. Reference number: 827825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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12. Blochem. Parasitol. 40, 213-224, 1990
Title: Characterization of a myosin-like antigen from Onchocerca volvulus.
Reference number: A44939, MUID:90301142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-20.2 <rrr>
A;Cross-references: EMBL.U12681; NID:9530824; PID:9530825; PIDN:AAA80009.1
A;Experimental source: specific_host Homo sapiens
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Residues: 733-866 <DON>
Cross-references: GB:J03995; NID:g159874; PIDN:AAA29412.1; PID:g159875
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   EAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF
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Pred. No. 8.6;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ngozi, E.; Erondu, N.E.; Donelson, J.E. submitted to the EMBL Data Library, April 1990
                                                                                                                                                                                                                               protein - nematode (Onchocerca volvulus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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C;Keywords: leucine zipper
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C; Accession: B83947
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A; Reference number: A83650; MUID: 20263314
A; Accession: B83947
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-521 <STO>
A; Residues: 1-521 <STO>
A; Residues: 1-521 <STO>
A; Experimental source: strain C-125
C; Genetics:
A; Experimental source: strain C-125
C; Genetics:
A; Genetics:
C; Superfamily: hypothetical protein ymdA
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R;Saez, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990
A;Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through alt
A;Reference number: A34876; MUID:90138958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          My Sin heavy chain nonmuscle form A - human
My Sin heavy chain nonmuscle form A - human
My Alternate names: cellular myosin heavy chain; myosin type 9; NWMHC-A
My Contains: myosin ATPase (EC 3.6.1.32)
C; Species: Homo sapiens (man)
C; Date: 12-May-1994 # sequence_revision 14-Jul-1994 # text_change 19-Jan-2001
C; Accession: A61231; A34876; I52562; I61692
R; Simons, M; Wang, M; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.;
Circ. Res. 69, 530-539, 1991
A; Title: Human nonmuscle myosin heavy chains are encoded by two genes located
A; Reference number: A61231; MUID:91316803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein BH2378 [imported] - Bacillus halodurans (strain C-125)
                                                     A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-109 <SCH->
A, Cross-references: GB:S44859; NID:9254472; PIDN:AAB49318.1; PID:9254473
A, Cross-reference extracted from NCBI backbone (NCBIN:114554, NCBIP:114555)
A, Note: host Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                              Gaps
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A, Molecule type: mRNA
A, Residues: 715-1961 < SAE>
A, Cross-references: GB:M31013; NID:9189035; PIDN:AAA36349.1; PID:9189036
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Pred. No. 19;
7; Mismatches 14
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2.6;
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A; Reference number: A48943; MUID:92384563
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Best Local Similarity 40.0%;
Matches 14; Conservative
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Best Local Similarity 37.5%;
Matches 15; Conservative
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                                                                                                                                                                                                                                               C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C; Accession: T00379
R; Shikawa, K; Nagase, T; Suyama, M; Miyajima, N; Tanaka, A; Kotani, H; Nomura, N; DNA Res; 5, 169-176, 1998
A; Title: Prediction of the coding sequences of unidentified human genes. X; The complete A; Reference number: 214142; MUID: 98403880
A; Accession: T00379
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         male-enhanced antigen-2 - mouse
C;Species: Mus musculus (house mouse)
C;Accession: T42722
F,Kondo, M.; Sutou, S.
DNA Seq. 7, 71-82, 1997
A,Title: Cloning and molecular characterization of cDNA encoding a mouse male-enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T42722
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 1-1325 < KON-
A; Residues: 1-1325 < KON-
A; Residues: 1-1325 < KON-
A; Reperimental source: EMBL:D78270; NID:d1096175; PID:d1020389; PIDN:BAA19612.1
A; Experimental source: strain CD-1
C; Function: supposed to play some role for spermatogenesis
C; Keywords: leucine zipper
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C;Date: 28-Mar-1994 #sequence_revision 25-Apr-1997 #text_change 05-Nov-1999
C;Accession: C48843
R;Schouler, C.; Bouet, C.; Ritzenthaler, P.; Drouet, X.; Mata, M.
Appl. Environ. Microbiol. 58, 2479-2484, 1992
A;Title: Characterization of Lactococcus lactis phage antigens.
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                                                              267 QEKAELQAQ-LAALSTRL-QAQVEHSHSSQQKQDSLSSEV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                             1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQM 40
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Pred. No. 9.5;
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40.0%;
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Best Local Similarity 40.09
Matches 16; Conservative
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Best Local Similarity
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preprotein translocase chain secD [validated] - Escherichia coli
N.Alternate names: protein-export membrane protein secD; secretion protein secD
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: H64769; J00696; S12301
R;Blatther, Fx.P; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A;Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Recence number: A64720; MUID: 97426617
A;Science 277, 1453-1463
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for two classes of fumarase in Bacillus
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A; Residues: 1-615 - CBLAT>
A; CTOSS-references: GB:AE000147; GB:U00096; NID:91786603; PIDN:AAC73511.1; PID:917866
A; EXPERIMENTAL SOURCE: strain K-12, substrain MG1655
R; Gardel, C.; Johnson, K.; Jacq, A.; Beckwith, J.
EMBO J. 9, 3209-3216, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The secD locus of E.coli codes for two membrane proteins required for protein A;Reference number: JQ0693; MUID:91006014
A;Accession: JQ0696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Bacillus stearothermophilus
C;Date: 19-Dec-1993 #sequence_revision 27-Jan-1995 #text_change 11-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: var. non-diastaticus, DSM 2334
A;Note: sequence extracted from NCBI backbone (NCBIN:129946, NCBIP:129948)
C;Superfamily: nodulation protein nodB; nodB homology
                                                                                                                                                                                                                      F:1277-1999/Region: light meromyosin
F:125/Modified site: N6.N6.N6-trimethyllysine (Lys) #status predicted
F:185/Modified site: ATP (Lys) #status predicted
F:180/Aninding site: Cys #status predicted
F:693,703/Active site: Cys #status forced to the covalent (Spingle Site: phosphate (Ser) (covalent) #status predicted
F:1943/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1999;
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    nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;541-575/Region: actin binding #status predicted
F;653-675/Region: actin binding #status predicted
F;836-1999/Domain: coiled coil #status predicted
F;836-1276/Region: S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ANKOKOELDGISTNIRQAGVQYSRADEEQQQALSSQ 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: B47692
C,Accession: B47692
R;Reaney, S.K.; Bungard, S.J.; Guest, J.R.
J. Gen. Microbiol. 139, 403-416, 1993
J-Title: Molecular and enzymological evidence
A;Reference number: A47692; MUID:9332761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.7%; Score 57;
36.1%; Pred. No. 8
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Matches 16; Conserv
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Matches 13; Conserv
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A; Residues: 1-265 <REA>
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N'Contains: myosin APPase (EC 3.6.1.32)
C'Species: Rattus norvegicus (Norway rat)
C'Species: Rattus norvegicus (Norway rat)
C'Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C'Accession: S21801; PN0013; S18134
R'Sun, W.; Chantler, P.D.
A'Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain A'Reference number: S21801; MUID:92235856
A'Accession: S21801
                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mNS
A;Molecule type: mSS
A;Molecule type: mNS
A;Mole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: GDB:120216; OMIM:160775
A;Map position: 22q12.3-22q13.1
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP: coiled coil; hydrolase; methylated amino acid; nucleotid
F;84-764/Domain: myosin motor domain homology <AMOT>
F;174-181/Region: nucleotide-binding motif A (P-loop)
F;552-565/Region: actin binding #status predicted
F;626-640/Region: actin binding #status predicted
F;837-1938/Domain: coiled coil #status predicted <COI>
F;837-1277/Domain: S2 #status predicted <NOS>
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C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotid
F; 84-763/Domain: myosin motor domain homology <MMOT>
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A;Title: A unique cellular myosin II exhibiting differential expression in the cerebral
A;Reference number: PN0013; MUID:91151356
R;Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.A.
                                                                                            5' cDNA clones,
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                                                Blood 78, 1826-1833, 1991
A/ritle: Cellular myosh heavy chain in human leukocytes: isolation of
A/Reference number: 152562, MUID:92003925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1278-1961/Domain: light meromyosin #status predicted <LAM>
F;1278-1961/Domain: carboxyl-terminal <CBT>
F;1257Modified site: N6.N6.N6-trimethyllysine (Lys) #status predicted
F;1257Modified site: ATP (Lys) #status predicted
F;694,704/Active site: Cys #status predicted
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36.18;
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A; Residues: 1-1999 <SUN>
A; Cross-references: EMBL:X62659
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A; Residues: 1914-1998, 'I' <SU2>
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Best Local Similarity 36.1:
Matches 13; Conservative
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A; Residues: 182-218 <BEM>
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R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lem submitted to the Protein Sequence Database, June 1999
A;Reference number: 216991
                                                                                                                                                                                                 hypothetical protein F21C20.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T10623
A;Molecule type: DNA
A;Residues: 1-416 <BEV>
A;Cross-references: EMBL:AL080254; GSPDB:GN00062; ATSP:F21C20.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: cultivar Columbia; BAC clone F21C20 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 4
A;Introns: 41/2; 81/3; 109/3; 146/2; 258/3; 326/3; 389/1
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Search completed: July 5, 2001, 11:48:32 Job time: 371 sec
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Best Local Similarity
Matches 12; Conserv
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AjStart codon: GTG
C;Complex: heterohexamer; chains secY (PIR:QQECSY), secE (PIR:VXECSE), secG (PIR:S40402)
ded trimeric complex of secY, secE and secG and the peripheral secA protein; the protein
ssociated to form SecYEGDEPajC, the hexameric integral membrane domain of the pre-protein
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K.; Apodaca,
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A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Itile: Genetic and molecular characterization of the Escherichia coli secD operon and A:Reference number: A36969; MUID:94131960
A:Contents: annotation; membrane topology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: the secD protein is a transmembrane component of the protein export compl
C; Superfamily: protein export membrane protein secD
C; Keywords: inner membrane; protein export; transmembrane protein
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C.Accession: G85536
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                  A; Residues: 1-77, 'S', 79-154, 'A', 156-615 <GAR>
A; Cross-references: GB:X56175; NID:942929; PIDN:CAA39634.1; PID:9581230
R; Gardel, C.; Johnson, K.; Jacq, A.; Beckwith, J.
EMBO J. 9, 4205-4206, 1990
A; Reference number: S12298; MUID:91065354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.2%; Score 56; DB 2; Length 615; 29.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-77,'S',79-154,'A',156-615 <GA2>
A; Cross-references: EMBL:X56175; NID:g42929; PID:g581230
R; Pogliano, R.J.; Beckwith, J.
J. Bacteriol. 176, 804-814, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F.31-455/Domain: periplasmic #status predicted <PPI>F.456-472/Domain: transmembrane #status predicted <TM2>F.497/Domain: transmembrane #status predicted <TM2>F.497/Domain: transmembrane #status predicted <TM3>F.498-501/Domain: periplasmic #status predicted <PP2>F.502-518/Domain: transmembrane #status predicted <TM4>F.564-580/Domain: transmembrane #status predicted <TM5>
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A; Molecule type: DNA
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5, 2001, 11:51:42; Search time 41.8 Seconds (without alignments) 34.419 Million cell updates/sec
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	Description	P21249 onchocerca	P09127 escherichia				P19673 escherichia		P75310 mycoplasma				P53838 saccharomyc	P45958 mycoplasma	042130 gallus gall	shigel		cricetul		PO4725 triticum ae	P57679 homo sapien		P11396 mastigoclad		_						P43117 mus musculu	8	47	P73625 synechocyst
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KINH_SYNRA	CLCA_BOVIN	AP50_HUMAN	VP33_BPAPS	DNK3_SYNY3	41_HUMAN	AG17 ARATH	NCB1_MOUSE	NCB1 RAT	MPIP YEAST	CLCA MOUSE	CLCA_HUMAN	ALIGNMENTS			PRT; 2022		g)	sequence update)	annotation update)				a; Chromador					70081;	T.L., Tuan R.S.,		e expressed	olvulus.";	69:161-171(1995)			54764;
935	243	435	462	771	831	227	455	459		235	248				STANDARD;		18, Creat	32, Last	39, Last			ılus.	Eukaryota; Metazoa; Nematoda; Chromadorea;	Onchocercidae; Onchocerca.			.A.	MEDLINE-95287898; PubMed-7770081;	Triteeraprapab S., Richie T	Neubert T.A., Scott A.L.;	ing of a gen	development in Onchocerca volvulus.	Mol. Biochem. Parasitol. 69		SEQUENCE OF 733-866 FROM N.A.	MEDLINE=89127417; PubMed=2464764;
							.5 24.0	۲,	5	67	, o						1991 (Rel.	_	2000 (Rel.	NTIGEN.		Onchocerca volvulus.	ta; Metaz	rcidae; (	NCBI_TaxID=6282;		SEQUENCE FROM N.A.	-95287898	aprapab (	T.A., Sc	lar clon	ment in (	ochem. Pa		E OF 733	-8912741
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151 251 COILED COIL (POTENTIAL).
327 384 COILED COIL (POTENTIAL).
417 1879 COILED COIL (POTENTIAL).
2022 AA; 237341 MW; B7132AACF1520317 CRC64; EMBL; U12681; AAA80009.1; -. EMBL; J03995; AAA29412.1; -. PIR; A54513; A54513. Antigen; Coiled coil HSSP; P02633; 31CB SEQUENCE DOMAIN 

Donelson J.E., Duke B.O.L., Moser D., Zeng W., Erondu N.E., Lucius R., Renz A., Karam M., Flores G.Z.; "Construction of Onchocerca volvulus cbNA libraries and partial characterization of the cbNA for a major antigen."; Mol. Biochem. Parasitol. 31.241-250(1988).
--- FUNCTION: MAY BE A MYOFIBRILLAR PROTEIN.

Gaps ö Length 2022; Indels 15; DB 1; 12; Mismatches 31.6%; Score 65; 30.8%; Pred. No. Query Match 31.6% Best Local Similarity 30.8% Matches 12; Conservative

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STRAIN=KIZ / MG165;
STRAIN=KIZ / MG165;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K.12.";
Electrophoresis 18:1259-1313(1997).
-!- CATALYTIY: 2 S-ABRIGGYL-L-METHIONINE + UROPORPHYRIN III
- 2 S-ADENOSYL-L-HOMOCYSTELIME + SIROHYDROCHLORIN.
-!- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF SIROHEME AND COBALAMIN.
                                                                                                                                                   01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel.: 37, Last annotation update)
PUTATIVE UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) (UROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                         Sasarman A., Echelard Y., Letowski J., Tardif D., Drolet M.; "Nucleotide sequence of the hemX gene, the third member of the Uro operon of Escherichia coli K12.";
                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteríaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alefounder P.R.; "The sequence of hemC, hemD and two additional E. coli genes."; Nucleic Acids Res. 16:9871-9871(1988).
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Porphyrin biosynthesis; Transferase; Methyltransferase.
SEQUENCE 393 AA; 42963 MW; 9D272C6401D0E354 CRC64;
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1811 QLTHKQREEYDKFAQNMRTEKIQIERIIENRERSLKSRI 1:849
                                                                                                                393 AA
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                                                                                                                PRT;
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STRAIN-K12 / CS520;
MEDLINE-89041586; PubMed-3054815;
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MEDLINE=97443975; PubMed=9298646;
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EMBL; X12614; CAA31134.1; -.
EMBL; M87049; AAA67599.1; -.
EMBL; AEO00456; AAC76806.1; -.
PIR; S02185; S02185.
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                                                                                                                STANDARD;
                                                                                                                                                                                                                               METHYLASE) (ORF X).
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                                                                                                                                                                                                                                                                      Escherichia coli
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=CD-1; TISSUE=Testis; STRAIN=CD-1; TISSUE=Testis; STRAIN=CD-2717683; PubMed=9063644; Kondo M., Sutou S.; "Cloning and molecular characterization of cDNA encoding a mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            male-enhanced antigen-2 (Mea-2): a putative family of the Golgi
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Score 61, DB 1, Length 393, Pred. No. 2.6, 8, Mismatches 12, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN 201 204 POLY-ALA.
SEQUENCE 1325 AA; 149880 MW; 3230636962C687B0 CRC64;
                                                                                                                                   267 QEKAELQAQ-LAALSTRL-QAQVEHSHSSQQKQDSLSSEV 304
                                                                                                      1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQM 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.1%; Score 60; DB 1; 40.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GOLGIN-160 (MALE-ENHANCED ANTIGEN-2) (MEA-2).
                                                                                                                                                                                                                                                                                        1325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYSN_HUMAN STANDARD; PRT; 1960 AA P35579; 060805; 01-JUN-1994 (Rel. 29, Created) 15-DEC-1998 (Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatogenesis; Developmental protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPPING:
SUBNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY
CHAIN SUBNITS (MIC), 2 ALEALI LIGHT CHAIN SUBNITS (MIC) AND 2
REGULATORY LIGHT CHAIN SUBNITS: (MIC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28 RESIDUE REPERT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

MISCELLANEOUS: BACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-715 FROM N.A.
MEDILINE-91316803; PubMed=1860190;
Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K.,
Gdula D., Adelstein R.S., Walr L.;
"Human nonmuscle myosin heavy chains are encoded by two genes located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         through alternative polyadenylylation.";
Proc. Natl. Acad. Sci. U.S.A. 87:1164-1168(1990).
-1- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST
                                                                                                                                                                                                                                                         SEQUENCE OF 1-1337 FROM N.A.

PUDDLINE-22003925; Pubmed-1912569;
Toothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M., Arnaout M.A., Clayton L.K., Tenen D.G.;
"Cellular myosin heavy chain in human leukocytes: isolation of 5'
Cobn clones, characterization of the protein, chromosomal localization, and upregulation during myeloid differentiation.";
  01-OCT-2000 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYOSIN HEAVY CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 714-1960 FROM N.A.
BEDLINE-20138958; PubMed-1967836;
Saez C.G., Myers J.C., Shows T.B., Leinwand L.A.;
"Human nonmuscle myosin heavy chain mRNA: generation of diversity
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                       Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO OTHER NONMUSCLE MYOSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 282215; CAB05105.1; -. EMBL; M81105; AAA59888.1; -. EMBL; M69180; AAA61765.1; -. EMBL; M31013; AAA36349.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on different chromosomes.";
Circ. Res. 69:530-539(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P08799; 1MND.
MIM; 160775; -.
InterPro; IPR00048; -.
InterPro; IPR001609; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR002928; -.
                                                                            Homo sapiens (Human)
                                      TYPE A) (NMMHC-A).
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                    Lloyd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 30.6 KDA PROTEIN IN FUMA 3'REGION PRECURSOR (EC 3.5.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL 30.6 KDA PROTEIN IN FUMA 3' REGION (ORF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular and enzymological evidence for two classes of fumarase in Bacillus stearchermophilus (var. non-diastaticus).";
J. Gen. Microbiol. 139:403-416(1993).
-: SIMILARITY: TO GTHER POLYSACCHARIDE DEACETYLASES.
-: SIMILARITY: TO B. SUBTILIS YLXY.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                          SIMILARITY).
                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                        ö
                       GLOBULAR HEAD (S1).
RODLIKE TAIL (S2 AND LAM DOMAINS)
COILED COIL (POTENTIAL).
ATP.
                                                                                                        CALMODULIN-BENDING (BY SIMILARITY
CALMODULIN-BINDING (BY SIMILARITY)
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
EAI -> KGH (IN REF. 3).
T -> M (IN REF. 3).
T -> M (IN REF. 4).
C -> Y (IN REF. 4).
C -> Y (IN REF. 4).
C -> Y (IN REF. 4).
T -> A (IN REF. 2).
       Myosin; Coiled coil; Actin-binding; Alkylation; ATP-binding;
Multigene family; Calmodulin-binding.
                                                                                                                                                                                                                                                                                                                           DB 1; Length 1960;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                  588F84BB8C106E6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus.
Bacteria; FirmLoutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                               1858 AEQYKDQADKASTRLKQLKRQLEEAEEEAQRANASR 1893
                                                                                                                                                                                                                                                                                                                                                                                    4 ANKOKOELDGISTNIRQAGVQYSRADEEQQQALSSQ 39
                                                                                                                                                                                                                                                                                                                          Score 57; DB ]
Pred. No. 45;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 AA
                                                                                               ACTIN-BINDING
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Hypothetical protein; Hydrolase; Signal.
SIGNAL 1 23 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=VAR. NON-DIASTATICUS / DSM 2234,
MEDLINE-93232761; PubMed-8473853;
Reaney S.K., Bungard S.J., Guest J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30583 MW;
                                                                                                                                                                                                                                                                                                                          Query Match 27.7%;
Best Local Similarity 36.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                  226531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                     836
1960
1960
181
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829
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660
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1764
1771
                                                                                                                                                                                                                                                                                   AA;
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Q04729;
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                                                                 DOMAIN
NP_BIND
DOMAIN
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MOD_RES
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                                                                  'n
                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gardel C., Johnson K., Jacq A., Beckwith J.;
The secD locus of E.coli codes_thr two membrane proteins required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAIN=K12 / MG1655;
STRAIN=K12 / Partial for the form of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
Submitted (JAN-1997): to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                     .
8
                   Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                        Indels
                                                                                                               3 AANKOKOELDGISTNIR----QAGVOYSRAD----EEQQQALSSQMGF 42
                                                                15;
                      1;
                                                                                                                                                                                                                                                                              SECD_ECOLI STANDARD; PRT; 615 AA. P19673; P77531; P72348; 01-FEB-1991 (Rel. 17, Created) 01-NOY-1997 (Rel. 35, Last sequence update) 01-NOY-2000 (Rel. 40, Last annotation update) PROTEIN-EXPORT MEMBRANE PROTEIN SECD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91065354; Pubmed-2249673;
Gardel C., Johnson K., Jacq A., Beckwith J.;
EMBO J. 9:4205-4206(1990).
                      DB
                                                                  Mismatches
                   Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91006014; PubMed=2170107;
                                                                6
                   27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 9:3209-3216(1990).
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein export.
                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-K12
                   Query Match
Best Local S
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ERRATUM.
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                                               Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: BELONGS TO THE SECD/SECF FAMILY. SECD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS WHICH COMPRISE SECA, SECB, SECB, SECE, SECF, SECG AND SECY
                                                                                                                  Protein transport; Translocation; Transmembrane; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella cholerae-suis (Salmonella enterica).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuhn F.C., Gies A.J., Smeltzer M., Crupper S.S., Sobieski R.J.; "Identification of secD gene from Salmonella choleraesuis."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein transport; Translocation; Transmembrane; Inner membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                               27.2%; Score 56; DB 1; Length 615; 29.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                1099E6A9CC988EBE CRC64;
                                                                                                                                                                                           CYTOPLASMIC (PROBABLE). PROBABLE.
                                                                                                                                                                                                                               PERIPLASMIC (PROBABLE).
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CYTOPLASMIC (PROBABLE).
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R -> A (IN REF. 1).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROTEIN-EXPORT MEMBRANE PROTEIN SECD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
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EMBL; AE00014; AAC73511.1; --
EMBL; U82664; AAB40164.1; --
EMBL; S68715; AAC60469.1; --
PIR; JQ00696; JOACOC
                                                                                                                                                                                                                                                                                                                                                                                66632 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 29.0
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                PIR; JQ0696; JQ0696.
PIR; S12301; S12301.
EcoGene; EG10938; secD.
                                                                                                                                                                455
472
476
497
501
518
563
580
605
                                                                                                                                                                                                                                                                                                                                               78
155
615 AA;
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ID SECD_SALCH
AC Q9ZFF8;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 9
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; ...
InterPro; ...
InterPro; ...
InterPro; IPR001241; -..
InterPro; IPR001241; -..
InterPro; IPR002204; DNA_topoisoII; 1.
DR Pfam; PF00204; DNA_topoisoIV; 1.
DR PRINTS; PR00415B; TPIZFAMILY.
DR PRINTS; PR00415B; TOPISMEASEII:
DR PRINTS; PR00115B; TOPISMEASEII:
DR RINTS; PR0115B; TOPISMEASEII:
DR RINTS; PR0115B; TOPISMEASEII:
DR RINTS; PR0115B; TOPISMEASEII:
DR RINTS; PR0115B; TOPISMEASEII:
DR PRINTS; PR0115B; TOPISMEASEII:
DR PROTES TOPISMEASEII
SEQUENCE FROM N.A.

Niimi A., Harata M., Mizuno S.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).

-! CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-87246520; PubMed-3109890; MEDLINE-87246520; PubMed-3109890; Belknap W.R., Haselkorn R.; "Cloning and light regulation of expression of the phycocyanin operon
                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NEGATIVE AND POSITIVE SUPERCOLLS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOLLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1988 (Rel. 07, Created)
01-APR-1998 (Rel. 07, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
PHYCOBILISOME 8.9 KDB LINKER POLYPEPTIDE, PHYCOCYANIN-ASSOCIATED,
                                                                                                                                                                                                                                                                                     -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: NUCLEAR; GENERALLY LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB007446; BAA22540.1; -. HSSP; P06786; 1BGW.
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Best Local Similarity
Thes 13; Conserve
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                                                                                                                                                                                                                                                                                                                                                           NUCLEOPLASM.
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P07124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
Himmelrelch R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                              Length 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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1033 AA; 118078 MW; B32A330BEA4869BA CRC64;
   POTENTIAL.
81370B11EFC983F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MRY-2000 (Rel. 39, Last annotation update)
DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3).
                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN MG328 HOMOLOG (P01_ORF1033).
MPN474 OR MP367.
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                                                                                                                                              Score 56; DB 1;
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                                                                                                                    27.2%; Score 29.0%; Pred. No. 17; 29.0%; Pred. No. 17; 4.ve 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1627 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1033 AA
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                                                                                                                                                                                                                                                                                                                              147 QEQNIDSLRSDLREKGIPYTTVRKENNYGLS 177
                                                                                                                                                                                                                                                                                  7 QKQELDGISTNIRQAGVQYSRADEEQQQALS 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                    66632 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma pneumoniae.
       564 :
615 AA;
                                                                                                                                                                               Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 13; Conserv
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O42131;
15-JUL-1998 (
15-JUL-1998 (
30-MAY-2000 (
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P75310;
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       TRANSMEM
SEQUENCE
                                                                                                                                              Query Match
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TP2B\_CHICK

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of the cyanobacterium Anabaena.";

6:871-884(1987

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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Messenguy F., Dubois E., Vierendeels F., Scherens B., Pierard A.,
Glansdorff N.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROFEIN (POTENTIAL).
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN IN MET2-SEC2 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Entomoplasmataceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4EA3FFC89F66307A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anion exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
DNAK PROTEIN (HEAT SHOCK 70 KDA PROTEIN) (HS970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCO3_cotransp; 1.
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MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 271551; CAA96183.1; -. SGD; S0005219; YNL275W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.7%;
36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003020; -
Pfam; PF00955; HCO3_cot
Hypothetical protein; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma capricolum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496
519
576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 13; Conserv
                                                                                                         01-0CT-1996 (Rel.
                                                                                                                                                                                   YNL275W OR N0626.
                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNAK_MYCCA
P45958;
                                                                       YN15_YEAST
P53838:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
DNAK_MYCCA
                                                      YN15_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial
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the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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or send an email to license@isb-sib.ch).
                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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ک
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                                                                                                                                                                                                                                                                                                                            DB 1; Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 468;
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 54.0 KDA PROTEIN C32A3.1 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-! - SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIT GLN.
B50E623F5AB4D7DB CRC64;
                                                                                                                                                                                                                                                                        52DF2D7DEF5444D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                            Score 53.5; DE Pred. No. 3.8; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  6 KOKOELDGISTNIROAG-----VOYSRADEEQQQ 34
                                                                                                                                                                                                                                                                                                                                                                                                                                    28 ROSSETDKNKYNIRNSGSVFITVPYSRMNEEYQR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                 InterPro; IPR001685; -. Pfam; PF01383; CpcD; 1. Phycobilisome; Photosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54008 MW;
                                                                                                                                                                                                                                                                                                                            26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 248241; CAA88284.1; -. WormPep; C32A3.1; CE01505.
                                                                                                                                                                             EMBL; X05239; CAA28865.1; -. PIR; D29674; D29674.
                                                                                                                                                                                                                                                                         8895 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.7%;
                                                                                                                                                                                                                                                                                                                            Query Match 26.0
Best Local Similarity 41.2
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormPep; C32A3.1; CE(
Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥,
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                                                                                                                                                                                                                                                                           80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
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YQC1\_CAEEL

RESULT 11 YQC1\_CAEEL

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SEQUENCE

Thomas K.;

Query Match Best Local S Matches 14

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DOMAIN DOMAIN

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Gaps

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Mol. Microbiol. 5:2217-2221(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174880 MW;
                                                                                                                                                                                                                                                           EMBL; AB007445; BAA22539.1; -. HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                            InterPro; IPR000947; -.
                                                                                                                                                                                                                                                                                                                           InterPro; IPR001241; -. InterPro; IPR002205; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yao R., Palchaudhuri S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             806 80
1552 AA;
                                                                                                                                                                                                                                                                                                               InterPro; IPR001154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigella dysenteriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid Invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dysenteriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPAC_SHIDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
IPAC_SHIDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Niimi A., Harata M., Mizuno S.;

Niimi A., Harata M., Mizuno S.;

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CONTROL OF TOPOLOGICAL.STATES OF DNA BY TRANSIENT

BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS, TOPOISOMERASE II

MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING

OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                     Gaps
                                                                          Falah M., Gupta R.S.; "Phylogenetic analysis of mycoplasmas based on Hsp70 sequences: cloning of the dnaK (hsp70) gene region of Mycoplasma capricolum."; Int. J. Syst. Bacteriol. 47:38-45(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.7%; Score 53; DB 1; Length 591; 30.8%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B962340066F52343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 ELKNKAENYINIIETSLLQAGDKISAEQKEQSQKMIDEI 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EAANKOKQELDGISTNIRQAGVQYSRADEEQQQALSSQM 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1552 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIMTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Chaperone; ATP-binding; Heat shock.
SEQUENCE 591 AA; 63869 WW; B965
                         SEQUENCE FROM N.A.
STRAIN-ATCC 25416;
MEDLINE-97148974; Pubmed-8995799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U51235; AAB09430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z33106; CAA83764.1; -.
HSSP; P04475; 1DKX.
                                                                                                                                                             SEQUENCE OF 1-227 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001023; -. Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TP2A_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the "EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: ASSOCIATED WITH THE ENTRY OF THE BACTERIA INTO COLONIC EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00204; DNA_topoisol1; 1.
Pfam; PF00521; DNA_topoisolV; 1.
PRINTS; PR00418; TP12FAMILY.
PRINTS; PR00418; TOPISMEMASIL.
PROSITE; PR001158; TOPISMEMASELII; 1.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
ISOMerase; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.
                                                                           NUCLEOPLASM.

-!- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
RELAX ONLY NEGATIVE SUPERCOILS.
-!- SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of the ipaBCD structural genes of Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR; GENERALLY LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
DNA CLEAVAGE (BY SIMILARITY).
M; B9E27657024A91D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.7%; Score 53; DB 1; Best Local Similarity 31.7%; Pred. No. 1.1e+02; Matches 13; Conservative 11; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
42 KDA MEMBRANE ANTIGEN PRECURSOR.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - protein search, using sw model
Run on: July 5, 2001, 11:50:47 ; Search time 123.78 Seconds (without alignments) 44.893 Million cell updates/sec
Title: US-09-462-480-7 Perfect score: 206 Sequence: 1 QEAANKQKQELDGISTNIRQVQYSRADEEQQQALSSQMGF 42
Scoring table: BLOSUM62 Gapext 0.5
Searched: 425026 segs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026
Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database : SPTREMBL_16:*  1: SP_archea:* 2: Sp_bacteria:* 3: Sp_fung1:* 4: Sp_invertebrate:* 5: Sp_invertebrate:* 6: Sp_manmal:* 7: Sp_mhc:* 8: Sp_organelle:* 9: Sp_phage:* 10: Sp_phage:* 11: Sp_rodent:* 12: Sp_unclassified:* 13: Sp_vertebrate:* 14: Sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	069739 mycobacteri	033084 mycobacteri	Q9uh65 homo sapien	Q9p0z8 homo sapien	075135 homo sapien	Q9qyt3 mus musculu	Q9qyt2 mus musculu	Q38554 lactococcus	Q38234 bacteriopha	Q38305 lactococcus	Q9kab2 bacillus ha	088443 mus musculu	002717 bos taurus	Q9x624 bacillus st	Q63731 rattus norv	09xbn2 enterobacte	Q9rn19 citrobacter	Q9h1k0 homo sapien	Q91j60 arabidopsis
	ID	069739	033084	Ф301165	Q9P0Z8	075135	Q9QYT3	Q9QYT2	Q38554	038234	Q38305	Q9KAB2	088443	002717	Q9X624	063731	Q9XBN2	Q9RNL9	Q9H1K0	Q9LJ60
	DB	. ~	~	4	4	4	;	1	σ	σ	σ	7	11	و	~	11	7	~	4	10
	Query Match Length DB	100	100	585	585	603	1447	1487	109	620	106	521	585	625	729	1999	615	615	784	2756
dР	Query Match	96.1	36.9	29.1	29.1	29.1	29.1	29.1	28.5	28.2	28.2	27.7	27.7	27.7	27.7	27.7	27.2	27.2	27.2	27.2
	Score	198	76	9	09	09	9	9	28	58	58	57	57	57	57	57	26	26	26	26
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O9svg6 arabidopsis O9stw1 arabidopsis O96stw1 arabidopsis O96s0 Spisula sol O27991 bos taurus O9kq24 vibrio chol O91644 salmonella O9ppy9 ureaplasma O62812 rattus norv O9swy9 lithospermu O15413 homo sapien O9plt3 homo sapien O95718 synechocyst O9sn02 arabidopsis O9wam 3 drosophila O92614 homo sapien O43241 homo sapien O43241 homo sapien O9100 rattus norv O9rbt1 pseudomonas	Q9ncw7 drosophila Q9hqs9 halobacteri
10 Q9SVG6 10 Q9STW1 2 Q96580 2 Q96604 2 Q9PE04 2 Q9PE04 2 Q9PE13 11 Q62812 10 Q9SXV9 4 Q9PIT3 4 Q9PIT3 4 Q9PIT3 4 Q9PIT3 4 Q9FE1 5 Q9WGS2 5 Q9WGS2 3 Q9WGS2 3 Q9WGS2 3 Q9WGS2 5 Q9WGS2 3 Q9WGS2 5 Q9WGS2 3 Q9WGS2 5 Q9WGS2 5 Q9WGS2 7 Q9WGS2	5 Q9NCW7 1 Q9HQS9
478 670 1976 1976 224 389 743 1961 1976 1976 1976 1976 1977 1978 1978 1978 1978 1978 1978 1978	2501 253
00000000000000000000000000000000000000	25.7 25.5
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# ALIGNMENTS

RESULT 1 069739	069739 PRELIMINARY; PRT; 100 AA.	01-AUG-1998	01-AUG-1998 (TrEMBLrel. 07, Last	01-JUN-2000	HYPOTHETICAL 10.8 KDA PROTEIN.								MEDLINE=9829981; PUDMOCH903423) Colo C H Brocch D Darkhill I Carnior H Churchor C Harrie D	Gordon S.V., Eiglmeier K., Gas S.,				Oliver S.,				Nature 393:537-544(1998).				Berthet FX., Birk Rasmussen P., Andersen P., Gicquel B.;				EMBL; ATO22120; CAR1966.1;		Hypothetical protein.	SEQUENCE 100 AA; 10/94 MW; Z85F4FC96F55D194 CKC64;
RE O6	A B	D	D	D I	DE C	5 6	200	8	ö	RN	RP 2	ξ;	X Y	RA	RA	RA	RA	RA	KA G	A F	: E	R.	RN	RP	R	RA	RŢ	R	R.	D. C.	Z Z	KW	S

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585 AA

Length 585; Indels

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DB 11;

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Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monz D.W., Comtesse N.E., Heckel D.;
"Human SWAP-70 homolog.";
Submittad (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO EF-HAND FAMILY.
EMBL; AF134894; AAF61403.1; --.
    B42B63CF033E612F CRC64;
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345 QAANESKQQELEAVRKILEEAA---SRAAEEEKKRLQTQV 381
                                                                                                                                                           2 EAANKOK-QELDGISTNIRQAGVQYSRADEEQQQALSSQM 40
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Pred. No.
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    68997 MW;
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37.5%;
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                                                                                                                   Conservative
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  585 AA;
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    SEOUENCE
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EMBL: Y14967; CAA75210.1; -.. SEQUENCE 100 AA; 10964 MW; 460EE12F876EC383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Association of SWAP-70 with the B cell antigen receptor complex."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO EF-HAND FAMILY.
EMBL; AF210818: AAF24486.1; -.
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Score 198; DB 2; Length 100;
Pred. No. 2.7e-18;
0; Mismatches 1; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
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                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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                                                                                       1 QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQMGF 42
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; Pred. No. 0.014;
10; Mismatches 1
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01-MAY-2000 (TrEMBLrel, 13, Last sequ
01-MAR-2001 (TrEMBLrel, 16, Last-pnnc
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MEDLINE=93188700; Pubmed=8446027;
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SMART; SM00233; PH; 1.
Calcium-binding.
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96.18;
97.68;
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Pfam; PF00169; PH; 1.
                                            41; Conservative
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Best Local Similarity
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                         Best Local Similarity
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Query Match

**090YT3** 

RESULT **090YT3** 

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Natsukuma S.;
Wea2/Golga3 Gene Product is Indispensable for Spermatogenesis in the
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE=92384563; Pubmed=1514794;
Schouler C., Bouet C., Ritzenthaler P., Drouet X., Mata M.;
"Characterization of Lactococcus lactis phage antigens.";
Appl. Environ. Microbiol. 58:2479-2484(1992)..
EMBL, S44859; AAB49318.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5BADF716C251FBFF CRC64;
                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11900 MW; D8F90EB62539DF7B CRC64;
                                                          01-MAY-2000 (TrEMBLrel. 13, 'Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MEA2/COLGA3 PROTEIN.
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Last annotation update)
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                              PRT; 1487 AA.
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Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEWBLrel. 08, Last annot
PHAGE ANTIGENIC DETERMINANT (FRAGMENT)
Lactococcus lactis phage phi 197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
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37.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAA86890.1;
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                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                         Submitted (JUL-1999)
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Best Local Similarity
                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=C57BL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12427;
                                                                                                                                                                                NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109
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                                                                                                                                                                                                                                                                                                                                   AB029522;
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                                                                                                                      MEA2/GOLGA3
                                                                                                                                                                                                                                              Matsukuma S
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SEQUENCE
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Q38554;
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                            Q9QYT2
                                             Q9QYT2;
                                                                                                                                                                                                                                                                                                         EMBL;
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 RESULT
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"Mea2/Golga3 Gene Product is Indispensable for Spermatogenesis in the
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TFEMBLrel. 13, Last sequence update)
01-WAY-2000 (TFEMBLrel. 13, Last annotation update)
WALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 2
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                                                                                                                                                                                                                             Length 603,
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                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                    1 1
603 AA; 71020 MW; 83C1677AAC5CCFC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 QAANESKQQELEAVRKKLEEAA---SRAAEEEKKRLQTQV 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches 11;
                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                           29.1%; Score 60; DB 4; 37.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1447 AA.
                                                                                                                                                                                                                                        Best Local Similarity 37.5%; Pred. No. 11;
Matches 15; Conservative 11; Mismatches
       EMBL, ABO14540; BAA31615.1; -1. SIMILARITY: TO EF-HAND FAMILY.
EMBL, ABO14540; BAA31615.1; -1. InterPro; IPR001849; -1. InterPro; IPR002048; -1. Prem: PF00036; efhand; 1. Pr6m: PF00169; Pt. I. PROSITE: PS50003; PH_DOMAIN; 1. SMART; SM00233; PH; 1. Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
DNA Res. 5:169-176(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1999)
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE
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EMBL;

EMBL; EMBL;

Mouse.

EMBL; EMBL; EMBL; EMBL; EMBL;

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MBL; EMBL; EMBL:

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"Sequencing," and analysis of the prolate-headed lactococcal bacteriophage c2 genome and identification of the structural genes.", Appl. Environ. Microbiol. 61:4348-4356(1995).
-! SIMILARITY: TO EF-HAND FAMILY.
EMBL; L48605; AAA92189.1; -.
InterPro; IPR002048; -.
Pfam; PF00036, efhand; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
Calcium-binding.
SEQUENCE 706 AA; 75263 MW; E53B1E6C3A92CBD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                              Length 706
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
Takami H., Nakassone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001515; BAB06097.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
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Last sequence update)
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Last annotation update)
                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group;
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6
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                                                                                                                                                                                                Score 58; DB Pred. No. 24;
                                                                                                                                                                                                                            8; Mismatches
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NCBI_TaxID=86665;
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Best Local Similarity 37.5%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00013; KH-domain; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus halodurans.
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Best Local Similarity
Matches 14; Conserv
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   Gaps
                                                                                                                                                                                                              Bacteriophage blig7.
Viruses; dsDNA viruses, no RNA stage; Talled phages; Siphoviridae.
NCBL_TaxID=36343;
                                                                                                                                                                                                                                                                                                   MEDLINE-95111629; PubMed-7812447;
Schouler C., Ehrlich S.D., Chopin M.C.;
"Sequence and organization of the lactococcal prolate-headed bIL67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95115663; PubMed=7816023;
Lubbers M.W., Ward L.J., Beresford T.P., Jarvis B.D., Jarvis A.W.;
"Sequencing and analysis of the cos region of the lactococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus bacteriophage c2.
Vituses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
NCBL_TaxID=31537;
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MEDLINE-96086019; PubMed-8534101;
Lubbers M.W., Waterfield N.R., Beresford T.P., Le Page R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 620;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                620 AA; 66192 MW; 44E946A684064F3B CRC64;
                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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Last sequence update)
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 15;
                             QEAANKQKQELDGISTNIRQAGVQYSRADEEQQQALSSQM 40
                                             8; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 9;
 Mismatches
                                                                                                                                    620 AA.
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                                                                                                                                                                                                                                                                                                                                            Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Can. J. Microbiol. 39:767-774(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterlophage c2.";
Mol. Gen. Genet. 245:160-166(1994).
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                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2001 (TrEMBLrel: 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel, 01, 01-MAR-2001 (TrEMBLrel, 16,
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Matches 15; Conservative
Conservative
                                                                                                                                  PRELIMINARY;
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SEQUENCE FROM N.A.
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01-NOV-1996
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
NEURONAL MYOSIN HEAVY CHAIN.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Neuroryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                Sun W., Chantler P.D.; "Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain and its differential expression within the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 729;
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                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 NKQKLPNGLEGLAKNINQMGMQFGLWVEPEMVSVDSEL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 NKQK -- QELDGISTNIRQAGVQYSRADEEQQQALSSQM 40
                                                         729 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1999 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.7%; Score 57; DB 34.2%; Pred. No. 34; iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system[see comments].";
J. Mol. Biol. 224:1185-1193(1992).
HSSP; P10587; 1BR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92235856; PubMed=1569576;
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InterPro; IPR001609; ...
InterPro; IPR002017; ...
InterPro; IPR002928; ...
Pfam; PF00063; myosin_head; 1.
Pfam; PF00612; IQ; 1.
Pfam; PF001576; Myosin_tail; 2.
PRINTS; PR00193; MYOSINHEAVY.
Probom; PD000355; .; 1.
                                                                                                                                                                                                  Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 34.29
Matches 13; Conservative
                                                                                                                                                         ALPHA-GALACTOSIDASE AGAN.
                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              NCBI_TaxID-1422;
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SEQUENCE
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                                                       Q9X624
Q9X624;
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                    RESULT 14
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                                         29x624
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"Novel characteristics of a myosin isolated from mammalian retinal pigment epithelial and endothelial cells.";
J. Biol. Chem. 272:8759-8763(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.7%; Score 57; DB 11; Length 585; Best Local Similarity 35.0%; Pred. No. 27; Matches 14; Conservative 12; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                  585 AA; 68995 MW; 3FFD1B671976782C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EC9E5A8CE9BB71B5 CRC64;
                                                         Jessberger R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-12000 (TrEMBLrel. 15, Last annotation update)
NON-WUSCLE MYOSIN HEAVY CHAIN (FRAGMENT).
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EAANKOK-QELDGISTNIRQAGVQYSRADEEQQQALSSQM 40
                                                 Borggrefe T., Wabl M., Akhmedov A.T., Jessberg "A B-cell-specific DNA recombination complex." J. Biol. Chem. 273:17037(1998).

EMBL: AIMILARITY: TO EF-HAND FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ANKOKOELDGISTNIRQAGVQYSRADEEQQQALSSQ 39
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Cell Motil. Cytoskeleton 39:191-194(1998).
EMBL, U870ES, AAC19403.1; -.
InterPro; IPR000533; -.
InterPro; IPR002928; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                   MEDLINE-98307943; PubMed-9642267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98178721; PubMed-9519899;
                                                                                                                                                                                                                                   Pfam; PF00036; efhand; 1.
Pfam; PF00169; PH; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          625 AA; 72370 MW;
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PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                         MGD; MGI:1298390; Swap70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                     InterPro; IPR002048; -
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                            InterPro; IPR002017
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                               Calcium-binding
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SEQUENCE

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Gaps

5;

Thu Jul

0; Gaps Query Match 27.7%; Score 57; DB 11; Length 1999; Best Local Similarity 36.1%; Pred. No. 1e+02; Matches 13; Conservative 8; Mismatches 15; Indels C

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Search completed: July 5, 2001, 11:50:48 Job time: 471 sec

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5, 2001, 11:45:42; Search time 130.35 Seconds (without alignments) 22.789 Million cell updates/sec
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247
I MAEMKTDAATLGQEAGNFER.....DQVESTAGSLQGQWRGAAGT 49
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/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412676 segs, 60623988 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\* /SIDS8/gcgdata/geneseg/genesegp/AA1999.DAT: /SIDS8/gcgdata/geneseg/genesegp/AA2000.DAT:

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Description	M. tuberculosis LH	M. tuberculosis LH	M. tuberculosis im	Mycobacterium tube	M. tuberculosis an	M. tuberculosis re	M tuberculosis Rv3	Mycobacterium tube	M. tuberculosis fu	Mycobacterium anti	Mycobacterium tube
SUMMARIES	AAY03706	AAY03705	AAW81706	AAW64339	AAY39136	AAY38993	AAB35218	AAB19845	AAW81746	AAW64379	AAY32063
DB	20	20	19	19	20	20	22	22	19	19	20
% Query e Match Length DB	49	100	100	100	100	100	100	100	802	802	802
% Query Match	100.0	100.0	97.6	97.6	97.6	97.6	97.6	97.6	95.5	95.5	95.5
Score	247	247	241	241	241	241	241	241	236	236	236
Result No.	1	7	m	4	S	9	7	80	O	10	11

New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis - useful in vaccines, for diagnosis, and for expression of heterologous proteins

WPI; 1999-132249/11.

M. tuberculosis fu M. tuberculosis fu M. tuberculosis fus M. tuberculosis fus	4 .		Mycobacterium tube M. tuberculosis an M. tuberculosis re	ycobacterium tu		3	M. tuberculosis an M. tuberculosis re	2	M. tuberculosis		tuberculos	=	tuberculosis	M. tuberculosis an	Mycobacterium tube		tuberculosis	M. tuberculosis LH	M tuberculosis Rv3	GB	СВ	GB	tis GB
AAY39224 AAY39176 AAY39081 AAY39033			AAX3209/ AAX39118 AAX38981		AAW8170	AAW6434	AAY38994	AAW3245	AAW8169		AAY0370	AAW3245	AAW8169	AAY3912	AAW3245/	AAV3912	AAY0370	AAY03710	AAB3523	AAR8245	AAB0947	AAB09	
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## ALIGNMENTS

RESULT AAY03706

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The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open readilatory expression signals of the ESAT-6 protein as well as an open readilar for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the wtuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two provide a synergistic increase in ability to induce a protective immune provide a synergistic increase in ability to induce a protective immune reponse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 247; DB 20;
Pred. No. 7.2e-26;
                   Claim 21; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY03705 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M. tuberculosis LHP polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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Gaps

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Indels

Mismatches

Length 49;

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Mycobacterium
for expression
                                                              ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis;
immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic;
                                                                                                                                                                                                                                              New nucleic acid containing regulator and LHP gene of tuberculosis - useful in vaccines, for diagnosis, and
                                                                                                                                                                                                        Rasmussen PB;
                                                                                                                                                                                                       Gicquel B,
                                                                                                                                                                                                                               N-PSDB; AAX29168, AAX29171.
                                                                                                                                                                               (INSP ) INST PASTEUR.
(STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                               of heterologous proteins
                                                                                                                                                                                                        Berthet F,
                                                                                                                                                                                                                      WPI; 1999-132249/11
                                                                                                                                                                                                        Andersen P,
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DB 19; Length 100;

97.6%; Score 241;

Query Match

The present invention is directed to a polynucleotide carrying the regulatory expression signals of the BSAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium

Claim 17; Page 64; 88pp; English.

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                         can pe
tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can bused as immunogens and vaccines, to protect against bacteria of the M. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, portier other immunogenic proteins of the bacteria or their fragments, pecifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynucleotide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to proved a synergistic increase in ability to induce a protective immune response. The present sequence represents the LHP polypeptide.
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;
vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a methor for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunishing against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
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                                                                                                                                                                                                                                                                                           Length 100;
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n R, Lodes MJ;
Vedvick TS;
                                                                                                                                                                                                                                                                                         100.0%; Score 247; DB 20;
100.0%; Pred. No. 1.7e-25;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis immunogenic polypeptide Tb38-IN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3B; Page 138-139; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o A, Dillon DC, Houghton R, Skeiky YAW, Twardzik DR, Ved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW81706 standard; Protein; 100
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96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-261042/23.
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                       100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW81706;
                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW81706
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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or cytokine secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAY39083 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                          Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.6%; Score 241; DB 20; Length 100; 98.0%; Pred. No. 1.1e-24; 1.ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton R;
, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. tuberculosis recombinant antigen protein Tb38-IN.
                                                                                                         M. tuberculosis antigen Tb38-IN amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC, Hendrickson RC, Ho
SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 133-134; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY38993 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                       99WO-US03268
                                                                                                                                                                                                                                                                                                                                                                                            98US-0025197
                                                                                                                                                                                                                                                                                                                                                                            98US-0072967
                                                                                                                                                                                   immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto.A,
Lodes MJ, Reed
                                                                                                                                                                                                                                                           WO9942076-A2
                                                                                                                                                                                                                                                                                                                                     17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1998;
18-FEB-1998;
                                                                        05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1999
                                                                                                                                                                                                                                                                                                  26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY38993;
                                     AAY39136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY38993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This polypeptide comprises a partial sequence of Mycobacterium tuberculosis antigen Tb38-IN. It is encoded by genomic DNA isolated from an tuberculosis strain H37Rv genomic library using a probe derived from clone Tb38-1 (see AAV44384). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAV44391-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                    Indels
                                     Indels
                                                                                                                                                                                                                                                                                                                                                         Tuberculosis; infection; diagnosis; antigen; Tb37-FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dillon DC, Houghton R, Lodes MJ; YAW, Twardzik DR, Vedvick TS;
Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 241; DB 19; Pred. No. 1.1e-24; O; Mismatches 1;
                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis antigen Tb38-IN.
                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis strain H37Rv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 145; 250pp; English.
                                                                                                                                                                                                   AAW64339 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY39136 standard; Protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.6%;
98.0%;
               98.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US18214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0818111
96US-0729622.
                                                                                                                                                                                                                                                                             (first entry)
           Best Local Similarity 98.0 Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 98.0 ses 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-251292/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                             09-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                 W09816645-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed SG,
                                                                                                                                                                                                                                        AAW64339;
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Gaps

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AAY39136 ID AAY3 RESULT

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The present invention provides the protein and coding sequences for members of the esat-6 gene family from Mycobacterium tuberculcosis. These proteins include Rv0287, Rv1036c, Rv1037c, Rv2346c, Rv2348c, Rv253c, Rv2654c, Rv3000c, Rv3444c, Rv3445c, Rv3890c, Rv3891c, Rv3900c, Rv3800c, Rv3800c, Rv300c, Rv3000c, Rv300c, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of the Mycobacterium tuberculosis MTBN4 protein. This is 1 of 8 proteins, i.e. MTBN1-8 (see AAB19642-49), encoded by 8 open reading frames (see AAA89035-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. WTBN1-8 represent reagents that are useful in discriminating between MTBN1-8 represent reagents that are useful in discriminating between which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these MTBN polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic (vaccine) methods, including genetic vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTBN4; tuberculosis; BCG; vaccine; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.6%; Score 241; DB 22; 98.0%; Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis protein MTBN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥
                               Example 2; Page 65; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB19845 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000; 2000WO-US12257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-007153/01.
N-PSDB; AAA89038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
48; Conserv
                                                                                                                                                                                                                                                                                                                                                                    100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200066157-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gennaro ML;
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB19845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nethods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB19845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide encoded by a member of the esat-6-gene family for immunizing against and diagnosis of tuberculosis ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           esat-f, gene family; Rv0287; Rv1036c;
Rv2653f; Rv2654c; Rv3020c; Rv3444c;
Rv3904c; Rv3905c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 100;
                                                                                                                                                                                                                                                                                                                                                                    Houghton R;
, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 241; DB 20;
Pred. No. 1.1e-24;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                 Campos-Neto A, Dillon DC, Hendrickson RC, Ho.
Lodes MJ, Reed SG, Skelky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 179; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35218 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M tuberculosis Rv3874 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.6%;
Best Local Similarity 98.0%;
Matches 48; Conservative
                                                                                                                                99WO-US03265
                                                                                                                                                                                              98US-0072596
98US-0024753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99DK-0001020.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuberculosis; TB; vaccine;
Rv1037c; Rv2346c; Rv2348c;
Rv3445c; Rv3890c; Rv3891c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-091923/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 AA;
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W09942118-A2
                                                                                                                                                                                                 05-MAY-1998;
18-FEB-1998;
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                                                                                                                                17-FEB-1999;
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                                                              26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB35218;
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Query Match Best Local Matches 4

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composed of Mycobactaium tuberculosis antigens TDRA3 (see AAW64295), composed of Mycobactaium tuberculosis antigens TDRA3 (see AAW64295), 38 kpa antigen (see AAW64364), TDS8-1 (see AAW64321) and DPEP (see AAW64322). It was produced by PCR amplification (see AAV6450-57) of the appropriate antigen DNA sequences, cloning into an expression vector, and expression in E. coli. TDF-2 can be used for serodiagnosis of tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising antigenic or liminunogenic portions of M. tuberculosis antigens, or fusion proteins, DNA sequences encoding such polypeptides, recombinant expression vectors and host cells. Also claimed are methods and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                  Tuberculosis; infection; diagnosis; 38 kDa antigen; TDRa3; DPEP;
TD38-1; TDF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises a fusion protein, designated TbF-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kits for detecting M. tuberculosis infection in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis antigen fusion protein TbF-2.
                                                                                                                                                                                                                                                                                                                                                                                                        DC, Houghton R, Lodes M
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 236; DB 19;
Pred. No. 6.3e-23;
0; Mismatches 1;
                                                                     Mycobacterium antigen TbF2 protein fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page 223-226; 250pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY32063 standard; Protein; 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.58;
                                                                                                                                                                                                                                                                                97WO-US18214.
                                                                                                                                                                                                                                                                                                                97US-0818111.96US-0729622.
                                                                                                                                                           Mycobacterium tuberculosis.
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.5
Best Local Similarity 97.9
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A, Dillon
Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
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                                                                                                                                                                                                            W09816645-A2
                                                                                                                                                                                                                                                                              07-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                    11-0CT-1996;
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                                  09-NOV-1998
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                                                                                                                                                                             Synthetic.
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AAW64379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the fusion protein TbF-2 which is composed of immunogenic polypeptides from Mycobacterium tuberculosis (MT). This protein is used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of TB.
                                                                                                                                                                                                                                                                                                                                                                     TB;
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                   Tuberculosis; immunogenic; soluble; antigen; protective immunity; vaccine; pharmaceutical; infection; diagnosis.
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                                  Length 100;
                                                                                                                      1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                   Indels
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Pred. No. 6.3e-23;
                                Score 241; DB 22;
Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O A, Dillon DC, Houghton R, Lodes Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.36
0, Mismatches
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 208-211; 230pp; English.
                                                                                                                                                                                                                                                                                                                                 M. tuberculosis fusion protein TbF-2.
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                                                                                                                                                                                                                           AAW81746 standard; Protein; 802
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97.9%;
                                  97.6%;
98.0%;
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96US-0730510.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 97.9
nes 47; Conservative
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
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                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     802 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV64567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-0CT-1997;
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11-OCT-1996;
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                                                                                                                                                                                                                                                                                                27-JAN-1999
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Reed SG,

Synthetic.

AAW81746;

AAW81746 RESULT

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Gaps

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Indels

Length 802;

Tuberculosis; antigen; fusion protein; TbF-2; TbRa3; 38kD; Tb38-1; DPEP; diagnosis; therapy; vaccine; immunogen.

AAW64379 standard; Protein; 802 AA.

RESULT 10

AAW64379 ID AAW64

Seguence

Query Match

Matches

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. Bor natural killer cells and/or macrophages in tuberculosis-immune subjects. AA119249 to AA219460 and AAY39033 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                             New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                 on DC, Hendrickson RC, Houghton R;
Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 aemktdaatlaqeagnferisgdlktqidqvestagslqgqwrgaagt 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 236; DB 20;
Pred. No. 6.3e-23;
0; Mismatches 1;
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 37; Page 271-273; 299pp; English.
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ID AAX39176

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AC AAX39176;

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AY39176;

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DT 05-NOV-1999 (first entry)

XX

Wycobacterium tuberculosis; M. tubn immunotherapy; diagnosis; immunisal im
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Best Local Similarity 97.9%;
Matches 47; Conservative
                                 98US-0025197
                                                                                                                                                                 Dillon DC,
                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                               WPI; 1999-527409/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 802 AA;
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                                                                                                                                                                 Campos-Neto A,
Lodes MJ, Reed
05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                      Lodes MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a recombinant Mycobacterium tuberculosis tetra-antigen fusion protein, terhed TbF-2, composed of the antigens TbR3 38kD, Tb88-1 and DBEP. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AA220198) comprising the 4 coding sequences. The invention provides fusion proteins (see AAY20099-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 6.3e-23;
0; Mismatches 1;
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Best Local Similarity 97.9%;
Matches 47; Conservative (
                                                                                                                                                                                                                                                                                          98US-0056556.
98US-0223040.
                                                                                                                                                                                                                          99WO-US07717
                                 Mycobacterium tuberculosis.
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Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-601610/51.
N-PSDB; AAZ20198.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      802 AA;
                                                                                              WO9951748-A2
                                                                                                                                                                                                                          07-APR-1999;
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30-DEC-1998;
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Houghton R; ;, Vedvick TS;

Length 802;

802 AA;

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                                                                                                                                                                                The present invention describes polypeptides comprising an immunogenic are vaccines and fusion protein containing M. Luberculosis Aq's. Also described are vaccines and fusion protein containing M. Luberculosis Aq's. MAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. Bo natural killer cells and/or macrophages in tuberculosis-immune subjects. AAX19249 to AAX19460 and AAX39033 to AAX39225 are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                           New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
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Skeiky YAW, Twardzik DR,
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                                                                                                                         Disclosure; Page 205-208; 299pp; English
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Lodes MJ, Reed SG, Skeiky
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18-FEB-1998;
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Reed SG, Skeiky YAW, Twardzik DR, Vedvick
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Pred. No. 6.3e-23;
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Search completed: July 5, 2001, 11:45:42 Job time: 271 sec

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                                                                                                                                                                                                                                                                      APPLICANT: Smith, Daniel S.
APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
TITLE OF INVENTION: Glycine and Phaseolus
TITLE OF INVENTION: alpha-D-Galactosidases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard & Perry
STREET: P.O. Box 4390
CITY: Troy
STREET: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,961
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US-09-020-467-5
US-09-020-467-5
US-08-756-317-13
US-08-486-099-107
US-08-484-2238-107
US-08-484-2238-107
US-08-41-25-668A-107
US-08-485-551A-107
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US-08-627-873-7
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ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-320 (UMO)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      US-00-37
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Patent No. 5606042
GENERAL INFORMATION:
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TELEFAX: (810) 689-4071
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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COMPUTER READABLE FORM:
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/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-188-582-9

US-08-452-5928-7

US-08-452-5928-7

US-08-655-647-3

US-08-655-647-3
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US-08-488-961-7
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 59.5; DB 5; Length 3 Pred. No. 1.8; 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 DPATWAKSVGNSWRTTGDIQDKWDSMISRA-DLNDKWASYAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  κανικέSSEE: Reising, Ethington, Barnard & Perry STREET: P.O. Box 4390 CITY: Troy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERRAL INFORMATION:
APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
TITLE OF INVENTION: Glycine and Phaseolus
TITLE OF INVENTION: alpha-D-Galactosidases
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Reising, Ethington, Barnard &
                                                         CLASSIFICATION:
NAME: ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REPERENCE/POCKET UNMBER: 0994.00050
TELECOMMUNICATION:
TELEPHONE: (810) 539-5050
                     PCT/US96/06511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: KOHN, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET UNMBER: 9-32/
TELEPHONE: (810) 689-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08488961 Patent No. 5606042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                 TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.9%;
33.3%;
                                                                                                                                                                                                                                                              LENGTH: 363 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 363 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.13
Best Local Similarity 35.73
Matches 15; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity
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                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
PCT-US96-06511-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-08-488-961-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                             ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6184017thwestern Hwy., Suite 410
STRIT: Farmington Hills
STATE: Michigan
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 DAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1_0, Version #1.30
                                                   Sequence 4, Application US/08973297
Patent No. 6184017
GENERAL INFORMATION:
APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
TITLE OF INVENTION: alpha-D-Galactosidases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 Northwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59.5; DB; Pred. No. 1.8; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
PCT-0596-06511-4
Sequence 4, Application PC/TUS9606511
SGENERAL INFORMATION:
APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
TITLE OF INVENTION: alpha-D-Galactosidases
TITLE OF INVENTION: alpha-D-Galactosidases
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1_0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KÖIN, KENECH I.
REGISTRATION NUMBER: 30,955
REFERENCE/POCKET NUMBER: 0994
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 363 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-973-297-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                               48334
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Gaps
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Sequence 8, Application US/08452592B

Patent No. 5712366

GENERAL INFORMATION:

APPLICANT: McGrath, Kevin P.

APPLICANT: Kaplan, David L.

TITLE OF INVENTION: Fabrication of Nanoscale Materials Using

TITLE OF INVENTION: Fabrication of Nanoscale Materials Using

TITLE OF INVENTION: Fabrication of Nanoscale

NUMBER OF SEQUENCES: 11

CONRESPONDENCE ADDRESS:

ADDRESSEE: U.S. Army Soldier Systems Command

STREET: AMSCC-CC (Patent Counsel)

COUNTRY: United States of America

STATE: Massachsuetts

COMPUTER: Readable Forms

MEDIUM TYPE: Ibs PC Compatable

COMPUTER: IBM PC Compatable

COMPUTER: SYSTEM: DOS 6.22

SOFTWARRE: WordPerfect Version 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/452,592B

FILING DATE: 25 May 1995

PRICING DATE: 25 May 1993

ATTORNEY/AGRENT INFORMATION:

NAMF: Donahue RICHAIG IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56.5; DB 5; Length 363; Pred. No. 4.7;
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                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CUBRENT APPLICATION DATA: APPLICATION NUMBER: PCI/US96/06511 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kennerh I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 0994.00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 22,062 (Donahue)
REGISTRATION NUMBER: 34,857 (Lamming)
REGISTRATION NUMBER: 29,579 (Ranucci)
REFERENCE/DOCKET NUMBER: NA-1096D
TELECOMMONICATION INFORMATION:
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Donahue, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamming, John H.
Ranucci, Vincent J.
                                                                                                                                                                                                                                                                                                                                                                                                                    363 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.99
Best Local Similarity 33.39
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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TOPOLOGY:
PCT-US96-06511-7
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  Gaps
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19; Indels
                                                                                                                                                                                                                                                                                                                                  STREET: Michigan STATE: Michigan STATE: US
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                                                                 168 DPATWAKSVGNSWRTTGDIEDKWESMISRA-DLNDEWASYAG 208
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                                          7 DAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application PC/TUS9606511
; GENERAL INFORMATION:
   APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
   TITLE OF INVENTION: alpha-D-Galactosidases: NUMBER OF SEQUENCES: 11
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STRET: 30500 Northwestern Hwy., Suite 410
CITY: Farmington Hills
COUNTRY: US
Mismatches
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
TITLE OF INVENTION: Glycine and phaseolus
TITLE OF INVENTION: alpha-D-Galaftosidases
UNMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: KODI, Kenneth 1.
ERGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 0994.00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFERX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,297
                                                                                                                                                                                           Sequence 7, Application US/08973297
Patent No. 6184017
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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amino acid
14; Conservative
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CLASSIFICATION: 530
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                  RESULT 5
US-08-973-297-7
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Matches
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508-233-4510

TELEPHONE:

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APPLICANT: TUCKER, KENNETH
APPLICANT: PLOSILA, LAURA
TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                  APPLICANT: McGrath, Kevin P.
APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using TITLE OF INVENTION: Self-Assembling Proteins
CORRESPONDENCE: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READALE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage COMPUTER: TBM PC Compatable COMPUTER: TBM PC COMPATABLE OPERATING SYSTEM: DOS 6.25 SOFTWARE: WORDPERFECT Version 6.1 CURRENT APPLICATION DATA: FLLING DATE: 25 May 1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 AELKQEVSRLENEIEDLKAKIGDLENEVAQLEREVRSLEDE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQ 42
                                                                                                                                                                                                                                                                                                           ADDRESSEE: U.S. Army Soldier Systems Command STREET: AMSCC-CC (Patent Counsel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB
Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,579 (Ranucci)
REFERENCE/DOCKET NUMBER: NA-1096D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-233-4510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachsuetts
COUNTRY: United States of America
ZIP: 01760-5035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,948
FILING DATE: 25 May 1993
ATTORNEY/AGENT INFORMATION:
NAME: Donahue, Richard J.
NAME: Lamming, John H.
NAME: Ranucci, Vincent J.
REGISTRATION NUMBER: 22,062 (Done REGISTRATION NUMBER: 34,857 (Lamm
                                                                                             Sequence 10, Application US/08452592B Patent No. 5712366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08968685A Patent No. 6214981 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 22.3%
Best Local Similarity 29.3%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508-233-5167
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                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
TITLE OF INVENTION: Self-Assembling Proteins
CORRESPONDENCE 3.11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 84;
                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Massachsuetts
CUTY: Massachsuetts
COUNTRY: United States of America
ZIP: OTOTRY: United States of America
COMPUTER: Lab Rocket, 3.50 inch, 2.0 MB storage
COMPUTER: DAN COMPARIE: DO S 6.2
SOFTWARE: WordPerfect Version 6.1
CURRENT APPLICATION NUMBER: US/08/452,592B
FILING DATE: 25 May 1993
ATTORNEY/AGENT INFORMATION:
NAME: North APPLICATION NUMBER: 08/068,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                           2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQ 40
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: U.S. Army Soldier Systems Command STREET: AMSCC-CC (Patent Counsel)
                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                              Score 56; DB 1;
Pred. No. 0.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.2;
6; Mismatches
                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Donahue, Richard J.
NAME: Lamming, John H.
NAME: Ranucci, Vincent J.
REGISTRATION NUMBER: 22,062 (Donahue)
REGISTRATION NUMBER: 34,857 (Lamming)
REGISTRATION NUMBER: 29,579 (Ranucci)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08452592B Patent No. 5712366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 508-233-4510
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                                                                                                                                                                                                    Ouery Match
Best Local Similarity 33.38
Matches 13, Conservative
TELEFAX: 508-233-5167
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.3
Best Local Similarity 34.1
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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                                                                                             amino acid
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TOPOLOGY:
US-08-452-592B-8
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Gaps

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APPLICANT: Wang, Edith
APPLICANT: Wang, Edith
APPLICANT: Weinzlerl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROFEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                        5 KTDAATLGQEAGNFERI ----SGDLKTQIDQVESTAGSLQGQWRGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Sulte 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
NAME: Osman, Richard A REGISTRATION NUMBER: 36,627 REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                  Score 53.5; DI
Pred. No. 8.7;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08646715 Patent No. 5637686
                                                               TELEFAX: (415) 781-1989
TELEFAX: (415) 781-1989
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comai, Lucio
Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
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Best Local Similarity 26.9%;
Matches 14; Conservative 9
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TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                   : 278 amino acids amino acid
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LENGTH: 278 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                    US-08-188-582-9
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APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Slegfried
APPLICANT: Tanese, Naoko
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 4; Length 2123;
Pred. No. 73;
5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 KTDAATLGQEAGNFERISGDLKTQID -- QVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                          COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSFWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,685A
FILING DATE: No. 6214981ember 12, 1997
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7969-060
TELECOMMUNICATION INFORMATION:
TELEPONE: (212) 790-9090
TELEFX: (611 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08188582
Patent No. 5534410
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Best Local Similarity 38.3'
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-968-685A-10
                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Tjian,
                                                               10036-2711
                                                                                                                                                                                                                                                                CLASSIFICATION:
                                               USA
                                                                                                            MEDIUM TYPE:
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                                             COUNTRY:
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Query Match
Best Local Similarity
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                         INFORMATION:
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STREET: A...
TTV: Natick
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US-08-452-592B-7
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US-08-665-647-3
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                                                                                                             7;
                                                                                                                                                                                                                                                        Sequence 6, Application US/08452592B
Patent No. 5712366
GENERAL INFORMATION:
APPLICANT: McGrath, Kevin P.
APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using TITLE OF SEQUENCES: 11
                                                                                                                                                                    196 KTVGSSGGGGGGGEVKSESTGAGGDLKMEVDSDAAAVGSIAGASGSGAGS 247
                                                                                                                                         DB 1; Length 278;
                                                                                                           22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America
ZIP: 01760-5035
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: IBM PC Compatable
OPERATING SYSTEM: DOS 6.22
SOFTWARE: WordPerfect Version 6.1
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/452,592B
FILING DATE: 25 May 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: U.S. Army Soldier Systems Command
STREET: AMSCC-CC (Patent Counsel)
                                                                         Score 53.5; DE Pred. No. 8.7; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 21.5%; Score 53; DB 3 Similarity 23.8%; Pred. No. 2.2; 10; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Donahue)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 (Ranucci)
NA-1096D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,948
FILING DATE: 25 May 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-452-592B-7
; Sequence 7, Application US/08452592B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 22,062
REGISTRATION NUMBER: 34,857
REGISTRATION NUMBER: 29,579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELECOMMUNICATION INFORMATION:
                                                                         21.7%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Donahue, Richard J.
Lamming, John H.
Ranucci, Vincent J.
                                                                 Query Match
Best Local Similarity 26.98
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508-233-5167
; MOLECULE TYPE: protein US-08-646-715-9
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Natick
STATE: Massachsuetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-452-592B-6
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                    US-08-452-592B-6
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Gaps
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APPLICANT: McGrath, Kevin P.
APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using TITLE OF INVENTION: Self-Assembling Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dayler, Nicki J.
APPLICANT: Dorit
APPLICANT: Ron, Dorit
APPLICANT: Nonova, Anna F.
APPLICANT: Nopolitano, Eugene W.
TITLE OF INVENTION: WETHOOS TO IDENTIFY IMMUNOMODULATORS
TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE : 89
CORRESPONDENCE : MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage COMPUTER: IBM PC Compatable OPERATING SYSTEM: DOS 6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches 17;
                                                                                                                                                            ADDRESSEE: U.S. Army Soldier Systems Command STREET: AMSCC-CC (Patent Counsel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQ 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AELKQEVSRLENEIEDLKAKIGDLKNKVAQLKRKVRSLK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; D
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Donahue, Richard J.

NAME: Lamming, John H.

MAME: Ranucci, Vincert J.

REGISTRATION NUMBER: 22,062 (Donahue)

REGISTRATION NUMBER: 34,857 (Lamming)

REGISTRATION NUMBER: 29,579 (Ranucci)

REFERENCE/DOCKET NUMBER: NA-10960
                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS 6.22
SOFTWARE: WordPerfect Version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,592B
FILING DATE: 25 May 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                     STATE: Massachsuetts
COUNTRY: United States of America
ZIP: 01760-5035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,948
FILING DATE: 25 May 1993
ATTORNEY AGENT INFORMATION:
NAME: Donahue, Richard J.
NAME: Lamming, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08665647
Patent No. 5935803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
TELEPHONE: '508-233-4510
TELEFAX: 508-233-5167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 508-233-5167
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20006-1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D
COUNTRY:
ZIP: 200
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us-09-462-480-6.rai
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEBM PC compatible
COMPUTER: IEBM PC compatible
COMPUTER: TEBM PC compatible
COMPUTER: TEBM PC compatible
COMPUTER: TEBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
COMPUTER: DatentIn Release #1.0, Version #1.30
APPLICATION NOTABLE: US/08/665,647
FILING DATE: 18-JUN-1996
CLASSIFICATION: 435
ACCIASSIFICATION: 435
AUTORNEY/ACEWT INNORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 22550-20025.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 3:
SEDUBENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: TERPER TYPE: protein
US-08-665-647-3
```

Search completed: July 5, 2001, 11:46:58 Job time: 312 sec

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1;

Gaps ;

Query Match 21.1%; Score 52; DB 2; Length 334; Best Local Similarity 31.7%; Pred. No. 18; Matches 13; Conservative 8; Mismatches 18; Indels

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Thu Jul

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 5, 2001, 11:48:30; Search time 79.63 Seconds (without alignments) 46.874 Million cell updates/sec Run on:

US-09-462-480-6 247 Perfect score:

1 MAEMKIDAATLGQEAGNFER.....DQVESTAGSLQGQWRGAAGT Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_68:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote				keratin, 47K type	probable ligand-ga	alpha-galactosidas	hypothetical prote	3C3.10 protein - S	probable G-box bin	hypothetical prote	serotype-1-specifi	hypothetical prote	probable sensory h	pre-mRNA splicing	hypothetical prote	biotin synthase bi	alpha-galactosidas	probable chromosom	gas-vesicle protei	hypothetical prote	aconitate hydratas	aconitate hydrase	tail tip fiber pro	alpha-galactosidas	flagellin A - Camp	NH(3)-dependent NA	hypothetical prote	fcrA protein precu
SUMMARIES	QI	H70802	T10032	B70600	D83205	A25145	T02742	T06388	G70367	T10919	T03373	C86181	н81020	F96673	T35681	T45158	T24225	D83868	T10860	T35661	S28115	S77042	G64875	E85759	T13107	T50781	A39228	G72277	H85071	783
	DB	~	~	~	~	7	7	7	7	7	7	7	7	~	7	7	7	7	7	7	7	~	7	~	7	7	~	7	7	7
	Query Match Length	100	100	103	702	429	934	. 422	119	124	360	1001	1082	1313	1829	906	248	333	425	1186	381	417	891	891	1061	378	576	576	168	387
ð	Query	97	37	25.5	25	25	54	7	23	23	23	2	23	23	23	23	23	23	5	5	22	5	2	5	22.	22.	22.		22.	
	Score	241	92	63	63	62	60.5	59.5	58	28	28	58	58	58	58	57.5	57	57	56.5	56.5	26	99	26	26	26	55.5	55.5	55.5	52	22
	Result No.	-	7	Э	4	2	9	7	80	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	53

fcrA 15 protein -	Fc gamma (IgG) rec	kinesin heavy chai	hypothetical prote	hypothetical prote	mucin 2 precursor,	hypothetical prote	flagellin B - Camp	probable mmpL7 pro	probable transport	SLH family protein	hypothetical 46.9	probable membrane		prophage ps3 prote	myosin heavy chain
552536	A33939	A31497	T22976	S48385	A43932	S20527	B39228	C70668	F83119	C75434	C65174	F86056	в96667	G86867	833068
~	~	-	7	~	7	~	~	7	7	~	~	7	~	7	7
388	405	975	1133	1679	3020	147	576	920	414	423	445	445	476	489	527
22.3	22.3	22.3	22.3	22.3	22.3	22.1	22.1	22.1	21.9	21.9	21.9	21.9	21.9	21.9	21.9
55	55	55	55	55	55	54.5	54.5	54.5	54	54	54	54	54	54	54
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

Cyaccession: H70802
R;Cole, S.T.; Brosch, R.; Parthill, J.; Garnier, T.; Churcher. C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA.

A; Residues: 1-100 <COL>
A; Residues: 1-100 <COL>
A; Cross-references: GB:AL022120; GB:AL123456; NID:g3261558; PIDN:CAA17966.1; PID:g296
A; Experiental source: strain H37Rv
C; Genetics:
A; Gene: Rv3874

ó Length 100; Indels Query Match 97.6%; Score 241; DB 2; L Best Local Similarity 98.0%; Pred. No. 2.3e-22; Matches 48; Conservative 0; Mismatches 1;

Gaps

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hypothetical protein MLCB628.13c - Mycobacterium leprae

C; Species: Mycobacterium leprae
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jul-2000
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jul-2000
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jul-2000
R;Edjmeler, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol, 7, 197-206, 1993
A;Title: Use of an ordered cosmid library to deduce the genomic organization of Mycob A;Reference number: 216917; MuID:93188700
A;Accession: T10032

A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA

A;Residues: 1-100 <EIG> A;Cross-references: EMBL:Y14967; NID:92370268; PIDN:CAA75210.1; PID:92370280 1-100 <EIG>

Gaps ö Score 92; DB 2; Length 100; Pred. No. 0.00029; 9; Mismatches 20; Indels Query Match 37.2%; Best Local Similarity 40.8%; Matches 20; Conservative

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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-934 <ROU>
A;Residues: 1-934 <ROU>
A;Cross-references: EMBL:AC005315; NID:g3461834; PID:g3482941
A;Cross-references: EMBL:AC005315, NID:g3461834; PID:g3482941
A;Experimental source: cultivar Columbia
B;Lin, X.; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402, 761-768, 1999
Aftitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: G84692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Y.; Mason, T.M.; Shen,
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: GB:AE002093; NID:g3482941; PIDN:AAC33239.1; GSPDB:GN00139 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N'Alternate names: hypothetical protein 1914.20
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Date: 4-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C'Accession: T02742; G84692
R'Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Ssupmitted to the EMBL Data Library, August 1998
A'Description: Arabidopsis thaliana chromosome II BAC T914 genomic sequence.
A'Reference number: 214710
s: Xenopus laevis (African clawed frog)
22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ligand-gated ion channel protein [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                    Figure 2.1. Sargent, T.D.; Dawid, I.B.
Proc. Natl. Acad. Sci. U.S.A. 82, 5413-5417, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 5413-5417, 1985
A; Reference number: A25145; MUD:85270534
A; Accession: A25145
A; Molecule type: mRNA
A; Residues: 1-429
A; Cross-references: GB:M11940; NID:g214565; PIDN:AAA49894.1; PID:g214566
C; Superfamily: cytoskeletal keratin
C; Keywords: coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --AGNFERISGDLKTQIDQVESTAGS---LQGQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                       18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 ELQSQLAMKQSVEGNLNELQGFYSSQLQQIQNTIGSLEEQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
;
                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 6.8;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60.5; 1
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                        Score 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
T06388
alpha-galactosidase (EC 3.2.1.22) - soybean
                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 2
A; Introns: 69/1; 514/3; 617/1; 748/3
                                                                                                                                                                                                                                                                                                                                                                     25.1%;
30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.5%;
ilarity 29.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: T914.20; At2929120
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-934 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary A; Molecule type: DNA
                      C; Date: 22-Jul-1987
C; Accession: A25145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: T02742
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K.; Lim,
                                                                                                                                                                                                                                                                                                         Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Majandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE004773; GB:AE004091; NID:g9949672; PIDN:AAG06922.1; GSPDB:GN001A;Experimental source: strain PAO1C;Genetics: A;Gene: PA3534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:294121; GB:AL123456; NID:g3261736; PIDN:CAB08096.1; PID:e312272; A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable oxidoreductase PA3534 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, L.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                      hypothetical protein Rv3905c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                    Length 103;
                           1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            keratin, 47K type I cytoskeletal, larval - African clawed frog
N;Alternate names: XK81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 23.9%; Score 63; DB Similarity 23.9%; Pred. No. 1; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 GNLDRVGGALCTSPALDLVASTSGGHFGRWR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 GNFERISGDLKTQ--IDQVESTAGSLQGQWR 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.5%;
45.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-103 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-702 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                        C; Accession: B70600
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Best Local Simi
Matches 11;
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hudres, B.; Hudzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: C86181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T03373
R;Nakagawa, H.; Ohmiya, K.; Hattori, T.
Plant J. 9, 217-227, pote
A;Title: A rice bZIP protein, designated OSBZ8, is rapidly induced by abscisic acid.
A;Reference number: Z14906; WUID:96417817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-360 <NAK>
A;Cross-references: EMBL:042208; NID:91147631; PIDN:AAB40291.1; PID:91147632
A;Experimental source: cv. Nipponbare
C;Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE005172; NID: 97211984; PIDN: AAF40455.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein [imported] - Arabidopsis thallana
C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                   --- AGNFERISGDLKTQIDQVESTAGSLQGQWRGAAG
                                                                                                                                                                                                                                                                                                                          5 TSASEEGQETMSVDYSDQDLTDLADKIRTFHTDVSSRVTSLNAVVDMIQGGWQGAAG
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                                                                                                                                                 DB 2; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 DGATVSTGSGNSEKTSGDC-----SLEGSSDGNNQKASGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 DAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AEMKIDAAILGQEAGNFERISGDLKTQIDQVESTAGSLQ 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 2;
Pred. No. 17;
5; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
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A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 2,
Pred. No. 55;
7; Mismatches
                                                                                                                                             Score 58; DB 2
Pred. No. 5;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable G-box binding factor 8 - rice
A; Experimental source: strain A3(2) C; Genetics: A; Gene: 3C3.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.5%;
35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.5%;
Best Local Similarity 37.2%;
Matches 16; Conservative :
                                                                                                                                                 Query Match 23.5%;
Best Local Similarity 24.6%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.55
Best Local Similarity 35.99
Matches 14; Conservative
                                                                                                                                                                                                                                                                   6 TDAATLGQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: C86181
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A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein aq_771 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-Sep-2000
C;Accession: G70367
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666 A;Accession: G70367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                       C. Accession: T06388
R. Davis, M.O.; Walker, J.C.; Smith, D.
Submitted to the EMBL Data Library, August 1994
A; Description: Cloning and expression of a soybean alpha galactosidase gene.
A; Reference number: 215645
A; Accession: T06388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3C3.10 protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: T10919
C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                        A: Description: catalyzes hydrolysis of melibiose into galactose and glucose C; Superfamily: alpha-galactosidase C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U12926; NID-9927574; PIDN:AAA73963.1; PID:9927575
A;Experimental source: strain williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AL031231; NID: e1315070; PID: e1315080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: aq_771
C;Superfamily: Aquifex aeolicus hypothetical protein aq_771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAG
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                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-422 <DAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59.5; DE
Pred. No. 13;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1998 A;Reference number: 217215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.1%;
Best Local Similarity 35.7%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 26.33 nes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-119 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T10919
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Best Local Si
Matches 10;
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Indels

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Gaps

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Indels

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pre-mRNA splicing factor prpl - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 21-3an-2000 #text_change 18-Feb-2000
C; Accession: T45158; T40648
R; Urushiyama, S:; Tani, T.; Ohshima, Y.
submitted to the EMBL Data Library, February 1996
A; Description: The prpl+ gene of Schizosaccharomyces pombe encodes a protein with PW A; Reference number: 222934
A; Reference number: 222934
A; Molecule type: DNA
A; Residues: 1-906 <URU>A; Residues: 1-906 <URU>A; Residues: 1-906 <URU>A; Residues: 1-906 <URU>A; Rajandream, M.A.; Barrell, B.G.; Hamlin, N.; Churcher, C.M.
Submitted to the EMBL Data Library, February 1998
A; Reference number: 221943
                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL031031; PIDN:CAA19849.1; GSPDB:GN00070; SCOEDB:SC7C7.03 A;Experimental source: strain A3(2) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL021838; PIDN:CAA17050.1; GSPDB:GN00067; SPDB:SPBC6F
A;Experimental source: strain 972h-; cosmid c6B1
                     1 MAEMKTDAATLGQEAG--NFERISGDLKTQIDQVESTAGSLQGQWRGAA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AATLGQEAGNFERISGDLKTQIDQVESTAGSLQ-GQWRGAA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB 2;
Pred. No. 1.1e+02;
5; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 56;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.5%;
Best Local Similarity 34.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
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A;Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: SCOEDB: SC7C7.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-906 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T40648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
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                                                                                                                                                                                                   C)Date: 31.Mar-2000 #sequence_revision 31.Mar-2000 #text_change 19-Jan-2001
C;Accession: H81020
R;Tettellin, H:; Saunders, N.J.; Heidelberg, J:; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1889-1815, 2000
A;Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755
                                                                                                                                                    serotype-1-specific antigen, probable NMB1969 [imported] - Neisseria meningitidis (strai
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 A.Status: preliminary
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-1082 <TET>
A.Residues: 1-1082 <TET>
A.Residues: 1-1082 <TET>
A.F. Cross-references: GB:AE002545; GB:AE002098; NID:g7227229; PIDN:AAF42298.1; PID:g722723
A.F. Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ritheologis, A.; Ecker, J.R.; Palm, Q-1.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ransen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Hiller, Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: F96673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F13011.30 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision_02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.5%; Score 58; 26.1%; Pred. No.
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Best Local Similarity 26.15
Matches 12; Conservative
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Best Local Similarity
Matches 15; Conserv
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: F96673
R; Theologis, A.; Eck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-1313
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A;Map position: 1
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Gaps

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Length 1829;

5, 2001, 11:48:31 Search completed: July Job time: 370 sec

> | : |: | : | : | : | : | 456 ESQVDSLKLASKETNEKYEKMLEDARNEIDSLKSTVDSIQNEFENS 501 3 EMKTDAATLGQEAGN--FERISGDLKTQIDQVESTAGSLQGQWRGA 46

RESULT 14

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Gaps

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Indels

Length 906;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 5, 2001, 11:51:41; Search time 41.8 Seconds (without alignments) 40.156 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-462-480-6 247 1 MAEMKTDAATLGQEAGNFER.....DQVESTAGSLQGQWRGAAGT 49

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 segs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q46114 campylobact P50176 r poly-beta	P79955 xenopus lae P03815 escherichia	P05659 acanthamoeb P23467 homo sapien	028475 archaeoglob P74330 synechocyst	P14251 sendai viru	Q01401 oryza sativ	P29693 xenopus lae	P43800 haemophilus
FLB3_CAMJE PHBC_RHIME	CTK2_XENLA CLPB_ECOLI	MYSN_ACACA PTPB_HUMAN	YH99_ARCFU SYC_SYNY3	RRPP_SEND6	GLGB_ORYSA	EF1D_XENLA	GLPB_HAEIN
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574 611	643 857	1509	226 483	268	820	265	432
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51 51	21	51 51	50.5 50.5	50.5	50.5	20	20
34 35	36	8 6 3 8	<b>4</b> 0	42	43	44	45

## ALIGNMENTS

ARD; PRT; 429 AA.	<pre>, Created) , Last sequence update) , Last annotation update)</pre>	TYPE I CYTOSKELETAL 47 KDA.	Kenopus laevis (African clawed frog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;			SEQUENCE FROM N.A. Meditine-87057649: Dubbach-2430981.	t T.D., Dawid I.B.;	"Stage-specific keratins in Xenopus laevis embryos and tadpoles: the	sı gene tamııy."; Cell Biol. 103:1957-1965(1986).		hWed=2410923.	David T R .	"Epidermal keratin gene expressed in embryos of Xenopus laevis.";	1-5417(1985).	SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS. MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND	MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC)	(40-55 AND 56-70 KILODALTONS, RESPECTIVELY).		This SWISS-PROT entry is copyright. It is produced through a collaboration	.nstitute of Bioinformatics and the EMBL outstation -	institutions as long as its content is in no way	modified and this statement is not removed. Usage by and for commercial	license agreement (See http://www.isb-sib.ch/announce	or send an email to licenseelsD-sid.on).	196.1;	74.1;				NEDIC; ↓. PRIKERATIN		ıt; Coiled coil; Heptad repeat pattern; Keratin. 69		TAIL.
STANDARD;	(Rel. 09, C; (Rel. 09, L; (Rel. 29, L;	E I CYTOSKE	is (African letazoa; Cho	trachia; An	Xenopus.		M N.A.	Winkles J.	fic keratin	103:1957		M N.A.	report T D	eratin gene	Acad. Sci.	HETEROTETRANEOUS: THER	BRILLAR KERA	AND 56-70 KI		PROT entry i	between the Swiss Institute	profit in	this state	quires a lic	email to lic	EMBL; X04804; CAA28496.1;	X04668; CAA28374.1;	A25145: A25145.	IPR001664;	IPR002957;	PEOUO38; IIIAMENE; I PEOUO38; IIIAMENE; I	0226; IF; 1			382 429
KICL_XENLA ID KICL_XENLA	PUB///; 01-NOV-1988 01-NOV-1988 01-JUN-1994	KERATIN, TYP XK81A1.	Xenopus laev Eukaryota; M	Amphibia; Ba	Xenopodinae; Xen NCBI TaxID=8355;	[1]	SEQUENCE FROM N.A.	Miyatani S.,	"Stage-speci	J. Cell Biol	[2]	SEQUENCE FROM N.A.	Tonas F Ca	"Epidermal k	Proc. Natl.	-!- SUBUNIT:		(40-55 P		This SWISS-1	the European	use by nor	modified and	entities rec	or send an	EMBL; X04804		PIR: A25145:	Pro;	InterPro; IF	PRINTS: PRODO	PROSITE; PS00226; IF; 1.	intermediate filament;	DOMAIN	DOMAIN
KIC1_X ID K	DI DI	C N	s ၁၀	8	S S	RN	RP px	RA .	RT	R.F.	RN	RP	4 6	RT	RL	នូខ	88	ပ္ပ မ	ខ្លួ	ပ္ပ	ညှင့်	ງ ຍ	ည	ပ္ပင္ပ		DR	DR	ž 2	DR	DR	¥ 6	S S	X E	FT	FT

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MEDLINE-9126010; PubMed-8098333;
MCCOllum D., Monosov E., Subramani S.;
"The pas8 mutant of Picha pastoris exhibits the peroxisomal protein import deficiencies of Zellweger syndrome cells -- the PAS8 protein binds to the COOH-terminal tripeptide peroxisomal targeting signal, and is a member of the TPP protein family ";
J. Cell Biol. 121:761-774(1993).
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gould S.J., Kalish J.E., Morrel J.C., Bjorkman J., Urguhart A.J.,
Crane D.I.;
                                                                                                                                                                                                                    P33292; 001967;
01-FEB-1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEROXISOMAL TARGETING SIGNAL RECEPTOR (PEROXISOMAL PROTEIN PAS8)
PEROXIN-5) (PTS1 RECEPTOR).
                                                                                                                                                                                                                                                                                                    Pichia pastoris (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 7 TPR REPEATS.
SIMILARITY: STRONG, TO OTHER PEROXISOMAL TARGETING SIGNAL
RECEPTORS.
                                                                            Score 62; DB 1; Length 429;
Pred. No. 2.6;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                 STUTTER.
4248E12440B45D2D CRC64;
                                                                                                                                          18;
                                                                                                                            3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQ 42
                                                                                                                                                                                                           576 AA
                                                                                                        Mismatches
          LINKER 12
                        COIL 2.
                                                                                                                                                                                                           PRT;
                                                                            25.1%; Scoi
30.0%; Pred
tive 10;
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                                               MM;
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                                              47241
                                                                                                      Conservative
                                                                                                                                                                                                            STANDARD;
                        381
128
220
243
323
429 AA;
                                                                              Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                      12;
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PEX5_PICPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Urushiyama S., Tani T., Ohshima Y., "The prp1+ gene required for pre-mRNA splicing in Schizosaccharomyces pombe encodes a protein that contains TPR motifs and is similar to Profe of budding yeast.";

Genetics 147:101-115(1997).
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood V., Rajandream M.A., Barrell B.G., Hamlin N., Churcher C.M.;
Submitted (FEB-1998) to the EMBL/Genbank/DDBA databases.
-!- FUNCTION: INVOLVED IN PRE-MRNA SPLICING. INTERACTS WITH PRE6 AND
PRP13. MAY ALSO BE INVOLVED IN THE REGULATION OF THE GO-G1/G2
                                                                                                                                                                                     DOFOAOWEKDFAQYAEG -> RPVSGSMGERFCPIRRR
                                                                                                                                                                                                                                                                                                         ;
;
InterPro; IPR001440; -. Pfan. Pro515; TPR; 4. Percoxisome; Repeat; TPR repeat; Transport; Protein transport. DOMAIN 19 232 GLN-RICH.
                                                                                                                                                                                                                                                                                                       23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF LEU-616
                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND MUTAGENESIS OF PRO-875.
Okazaki K., Okayama H.,
"Fission yeast TPR gene involved in GO transition.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-1- SIMILARITY: TO SOME OTHER PRE-MRNA SPLICING FACTORS.
-1- SIMILARITY: CONTAINS 19 TPR REPEATS.
                                                                                                                                                                                                       (IN REF. 1).
C249FBE50FDE5247 CRC64;
                                                                                                                                                                                                                                                                                                                                                           206 MINSKTQEPKTKQQEQNTFEQVWDDIQVSYADVELTNDQFQAQW 249
                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                      1 MAEMKT-DAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQW
                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
PRPI OR ZERI OR SPBC6BI.07.
                                                                                                                                                                                                                                                                      Score 59.5; Di
Pred. No. 7.3;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
                                                                  TPR 1.
TPR 3.
TPR 4.
TPR 5.
TPR 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                       65083 MW;
                                                                                                                                                                                                                                                                       24.1%;
34.1%;
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                    3311
345
4421
523
523
                                                                                                                                                                                                                   576 AA;
                                                                                                                                                                                                                                                                                    1 Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                  278
3312
346
4422
4456
243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR01_SCHP0
Q12381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-972;
                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDIJINE-92174916; PubMed-1541275;
Prodromou C., Artymluk P.J., Guest J.R.;
Prodromou C., Artymluk P.J., Guest J.R.;
Prodromitase of Escherichia coli. Nucleotide sequence of the aconitase gene and amino acid sequence similarity with mitochondrial aconitases, the iron-responsive-element-binding protein and isopropylmalate isomerases.";
Eur. J. Blochem. 204:599-609(1992).
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattene F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemcto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kashimoto K., Kim S., Kiimura S., Kitagawa M., Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                    .;
6
                                                                                                                                                                       7 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACOL_ECOLI STANDARD; PRT; 890 AA.
P25516; P78060; P78148;
01-MAY-1992 (Rel. 22, Lost sequence update)
01-NAY-1997 (Rel. 32, Lost sequence update)
01-NOY-1997 (Rel. 35, Lost annotation update)
ACONITATE HYDRATASE 1 (EC 4.2.1.3) (CITRATE HYDRO-LYASE 1)
                                                                                                                                                                                                                                                                                                                                                      Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                           ASP/GLU-RICH (ACIDIC).
9FB48199D0305921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      47
                                                                                                                                                                                                                                                                                                                                                                                                                    6 TDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAA
                                                                                                                                                                                                                                                                                                                                                      ; DB 1;
: 12;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                        Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                           MM.
                                                                                                                       EMBL; X64701; CAA45944.1; -. PIR; S28115; S28115. Gas vesicle; Repeat.
                                                                                                                                                                                                                                                                                                                                                        22.7%;
38.1%;
                                                                                                                                                                                                                                                                                                           42653
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                122
160
192
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22
22
60
85
123
161
193
233
246
381 AA;
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ACONITASE 1).
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REPEAT
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"Three different but related gene clusters encoding gas vesicles in halophilic archaea.";
J. Mol. Biol. 227:586-592(1992).
-!- FUNCTION: MAY CONFER STABILITY TO THE GAS VESICLE MEMBRANES. GAS VESICLES ARE SMALL, HOLLOW, GAS FILLED PROTEIN STRUCTURES THAT ARE FOUND IN SEVERAL PROKARYOTIC PLANKTONIC MICROORGANISMS. THEY ALLOW THE POSITIONING OF THE BACTERIA, AT THE FAVORABLE DEPTH FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halobacterium mediterranei (Haloferax mediterranei).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloferax.
NCBI_TaxID=2252;
                                                                                                                                                                                                                                                                                                                                                                                                                                 P->L: IN ZER1-C5; TEMPERATURE SENSITIVE GROWTH ARREST SHOWING GO STATE LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                          mRNA processing; mRNA splicing; TPR repeat; Repeat; Nuclear protein. DOMAIN 56 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: BINDS TO THE EXTERNAL SURFACE OF THE GAS VESICLE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                      L->I: DEFECT IN POLY(A)+ RNA NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF CYANOBACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57.5; DB 1; Length 906; Pred. No. 21; 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4690EDBCA9F1AA3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 AARLEEQQGNVSRVEKIMARGVSELQATGGMLQRDQWLSEA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AATLGQEAGNFERISGDLKTQIDQVESTAGSLQ-GQWRGAA 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
12-JUL-1998 (Rel. 36, Last annotation update)
GAS VESICLE PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   EXPORT.
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MEDLINE=93021102; PubMed=1404376;
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TPR
TPR
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 EMBL; D83743; BAA12094.1; -.
EMBL; D83659; BAA12033.1; -.
EMBL; AL021838; CAA17050.1; -.
InterPro; IPR001440; -.
Pfam; PF00515; TPR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               906 AA; 103003 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.3%;
Best Local Similarity 31.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                         2296
3326
3326
3326
4418
4451
4451
663
663
764
802
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                                                                                                         875
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Q02228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                      -!- FUNCTION: PREFERENTIALLY CLEAVES ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDE LINKAGES. INVOLVED IN THE HYDROLYSIS OF THE GALACTOMANNAN, IT SPATHS ALPHA-LINKED GALACTOSE MOTETIES. IT IS PARTICULARLY SUITABLE FOR THE HYDROLYSIS OF GUAR GUM TO A GUM WITH IMPROVED GELLING PROPERTIES. CAN CLEAVE FERMINAL ALPHA-1,3-LINKED GALACTOSE RESIDUES RESPONSIBLE FOR BLOOD GROUP B SPECIFICITY FROM THE SURFACE OF ERYTHROCYTES THEREBY CONVERTING THESE CELLS SEROLOGICALLY TO GROUP O.

-!- CATALYTIC ACTIVITY: MELIBIOSE + H(2)O - GALACTOSE + GLUCOSE.
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Gentianales; Rubiaceae; Coffea.
NCBI_TaxID=13443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                "Cloning and functional expression of a cDNA encoding coffee bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuijten P.J., van Asten F.J., Gaastra W., van der Zeijst B.A., "Structural and functional analysis of two Campylobacter jejuni
                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 16-34; 215-231 AND 373-378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9FC7610BFD760AE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 DAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA-GALACTOSIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.5%; Score 55.5; DB 1; 33.3%; Pred. No. 14;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             575 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00740; GLHYDRLASE27.
PROSITE; PS00512; ALPHA_GALACTOSIDASE; 1.
Hydrolase; Glycosidase; Signal.
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                                                                                                                                                                            MEDLINE=94193002; PubMed=8144030;
Zhu A., Goldstein J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=81116;
MEDLINE=91009243; PubMed=2211662;
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378
                                                                                                                                                                                                                                                                                     Gene 140:227-231(1994)
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InterPro; IPR002241; -
InterPro; IPR002287; -
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                                                                                                                                                                                                                                                            alpha-galactosidase
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Best Local Similarity
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ID FLA2_CAMJE
AC P22251;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last annotation update)
ALPHA-GALACTOSIDASE PRECURSOR (EC 3.2.1.22) (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE).
Coffea arabica (Coffee).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                Seki Y., Tagami H., Takemoto K., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 1; Length 890;
Pred. No. 31;
6; Mismatches 11; Indels
                                         Yamamoto Y., Yano M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON (IRON-SULFUR CLUSTER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> S (IN REF. 2).
B3961D6052970BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyase; Tricarboxylic acid cycle; Iron-sulfur; 4Fe-4S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 DAVTL----DYMRLSGRSEDQVELVEKYA-KAQGMWR 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWR 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 AA
                                                                                                                                                   MEDLINE-92148368; PubMed-1838390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00450; ACONITASE_1; 1. PROSITE; PS01244; ACONITASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AE000225; AAC74358.1; --
BMBL, D90765; BAA14828.1; --
EMBL, D90765; BAA14830.1; --
PIR, S22375; S22375.
ECGENE, EGIRS, ESTANO, ENTREPRO, ENTREPOST, ENTREPS, EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00694; Aconitase_C; 1. Pfam; PF00330; aconitase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X60293; CAA42834.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.7%;
39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00415; ACONITASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.7
Best Local Similarity 39.5
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            521
             Saito N., Sampei G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521 5
890 AA;
                                                                                                                       SEQUENCE OF 1-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOCITRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAL_COFAR
Q42656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INIT_MET
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AGAL_COFAR
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                                                                                      FIGR; TM1253; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                              KINH_DROME
                                                                                                                                                                    NP_BIND
ACT_SITE
SEQUENCE
                     entities
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            KINH_DROME
       à
                                                                                                                                                                                                                                                                                                                                                             g
                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hidkey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                 FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO FORM THE FILAMBRYS OF BACTERIAL FLAGELLA.
SUBUNIT: HETEROPOLYMER OF FLABA AND FLAB.
SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
PROBABLE GLUTAMINE-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1) (NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE (BY SIMILARITY).
-1- CATALITIC ACTIVITY: ATP + DEAMIDO-NAD(+) + L-GLUTAMINE + H(2)O
AMP + DIPHOSPHATE + NAD(+) + L-GLUTAMATE.
-1- PATHWAY: DE NOVO BLOSYNTHESIS OF NAD.
-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE NAD SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CAN USE BOTH GLUTAMINE OR AMMONIA AS A NITROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 AALKTTAANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AEMKTDAATLGQEAGNFERISGDLK-----TQIDQVESTAGSLQGQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                            71F192EFD0AF0DC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55.5; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome sequence of Thermotoga maritima."; Nature 399:323-329(1999).
Chem. 265:17798-17804(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MSB8 / DSM 3109;
MEDLINE-99287316; Pubmed-10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNTHASE [GLUTAMINE-HYDROLYSING])
                                                                                                                                                                                                                                                                                                                                                                             ΒY
                                                                                                                                                                                                                                                                                                     Pfam; PF00700; Flagellin_C; 1.
Pfam; PF00669; Flagellin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                           59398 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              22.5%;
28.0%;
                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00207; FLAGELLIN
                                                                                                                                                                                                                                     EMBL; J05635; AAA23024.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                         PIR; A39228; A39228.
InterPro; IPR001029; -.
                                                                                                                                                                                                                                                                                          IPR001492; -
                                                                                                                                                                                                                                                                                                                                                                                           575 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADE2 OR TM125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAE2_THEMA
Q9X0Y0;
                                                                                                                                                                                                                                                                                                                                                                           INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                             Flagella.
   Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAE2_THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHC OR KIN.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-
TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF
KINESIR (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL
ALPHA-HELICAL COLLED CALL DOMAIN THAT MEDIATES THE HEAVY CHAIN
DIMERIZATION; AND A SWALL GLOBULAR C-TERMINAL DOMAIN WHICH
INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS),
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPAGATION AND NEUROTRANSMITTER RELEASE AT NEUROMUSCULAR JUNCTIONS, BUT ARE STILL CAPABLE OF TRANSPORTING CERTAIN MEMBRANES, INCLUDING SYNAPTIC VESICLES, TO THE NEWE FERMINAL. SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 258:313-316(1992).
-!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
-!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE.
-!- SUBUNIT: OLICOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: MUTANT FLIES DISPLAY IMPAIRED ACTION POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang J.T., Laymon R.A., Goldstein L.S.B.;
"A three-domain structure of kinesin heavy chain revealed by sequence and microtubule binding analyses.";
Cell 56:889(1989).
                                                                                                                                                                                                                                                                                                                         DB 1; Length 576;
                                                                                                                                                                                                           ATP (BY SIMILARITY).

BY SIMILARITY.

208FDC77964C957F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gho M., McDonald K., Ganetzky B., Saxton W.M.; "Effects of kinesin mutations on neuronal functions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 SEMATGYATLYGDMAGGFAVIKDVYKTDVYRI----GRWYNSWRG 472
                                                                                                                                                                                                                                                                                                                                                                                                              2 AEMKTDAATL-GQEAGNFERISGDLKTQIDQVESTAGSLQGQWRG
                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
KINESIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                975 AA
                      (See
                                                                                                                      Pfam; PF00795; CN_hydrolase; 1.
PROSITE; PS00920; NITRIL_CHT_1; UNKNOWN_1.
Ligase; NAD; ATP-binding.
                                                                                                                                                                                                                                                                                                                         Score 55.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VESICLES AND MEMBRANOUS ORGANELLES.
                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                        agreement
                                                                                                                                                                                              LIGASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93030741; PubMed=1384131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89168428; PubMed=2522352;
                                                                                                                                                                                                                                                          64919 MW;
                                                                                                                                                                                                                                                                                                                         22.5%;
                    requires a license
                                                                                  EMBL; AE001780; AAD36328.1;
                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 37.8 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                321
323
576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                    ö
 and for commercial
               (See http://www.isb-sib.ch/announce/
                                                                                                                                                      PRINTS; PR00380; KINESINHEAVY.
PR0SITE; PS00411; KINESIN MOTOR_DOMAIN1; 1.
PR0SITE; PS5067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; Colled coil.
DOMAIN 1 334 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Walsh S.V., Whitehead S., Rowley N., Skelton J., Smith V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
HYPOTHETICAL 195.1 KDA PROTEIN IN DNA43-UBI1 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                    Length 975;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l protein.
1679 AA; 195141 MW; 298950CC52202D8F CRC64;
 ρλ
                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
; 9966CBC35BA74FD6 CRC64;
 Usage
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                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  618 ISKMKTEAKNIAQRCSNMETQQADSNKKISEYEKDLG 654
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 modified and this statement is not removed.
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                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                    Score 55;
Pred. No.
                  entities requires a license agreement
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                                                                                                                                                                                                                                                                                                     110429 MW;
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                                                             EMBL; M24441; AAA28652.1; -.
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29.7%;
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                                                                            PIR; A31497; A31497.
HSSP; P56536; 2KIN.
FlyBase; FBgn0001308; Khc.
                                                                                                                         InterPro; IPR001752; -. Pfam; PF00225; kinesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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975 AA;
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                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
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SEQUENCE 16
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01-FEB-1995
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P40457;
                                                                                                                                                                                                                                                                     DOMAIN
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: THE N-TERMINAL DOMAIN SHOWS SOME SIMILARITY TO THAT OF SIMILARITY: CONTAINS. SIMILARITY: CONTAINS 2 WWFC DOMAINS. SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The human MUC2 intestinal mucin has cysteine-rich subdomains located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and polymorphism.";
J. Clin. Invest. 88:1005-1013(1991).
-!- FUNCTION: COATS THE EPITHELIA OF THE INTESTINES, AIRWAYS, AND OTHER MUCUS MEMBRANE-CONTAINING ORGANS. THOUGHT TO PROVIDE A PROTECTIVE, LUBRICATING BARRIER AGAINST PARTICLES AND INFECTIOUS AGENTS AT MUCOSAL SURFACES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.; "Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the amino terminus and overall sequence similarity to prepro-von Willebrand factor.", J. Biol. Chem. 269:2440-2446(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W., Petersen G.M., Kim Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "MUC-2 human small intestinal mucin gene structure. Repeated arrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93016075; PubMed=1400449;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe E.-M., Lagace R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: MULTIMERIC.
SUBCELLULAR LOCATION: SECRETED.
SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: COLON, SMALL INTESTINE, COLONIC TUMORS,
BRONCHUS, CERVIX AND GALL BLANDER.
FTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
INTERCHAIN DISGLETIDE BONDS (BY SIMILARITY).
POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND
VARIES AMONG DIFFERENT ALLELES.
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        both upstream and downstream of its central repetitive region.";
J. Biol. Chem. 267:21375-21383(1992).
                        778 AKIKELENNLERLRSDLQSKIQEIESIRSCKDSQLKWAQNT
9 ATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT
                                                                                                                                                                                UCTON-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1343-1895 AND 4176-4195 FROM N.A.
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                                                                                                                                                 5179 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Intestine;
MEDLINE=94132002; PubMed=8300571;
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                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Q02817; Q14878;
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                                                                                                                         MUC2_HUMAN
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Gaps

; 0

Indels

20;

9; Mismatches

Conservative

Best Local Similarity Matches 12; Conserv

Query Match

22.3%; Score 55; 29.3%; Pred. No.

DB 1; Length 1679; 83;

2;

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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                            Length 5179;
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                                                       N-LINKED (GLCNAC. . .) (POTER N-LINKED (GLCNAC. . .) (POTER H -> L (IN REF. 3).
T -> S (IN REF. 3).
L -> P (IN REF. 3).
M -> T (IN REF. 3).
M -> T (IN REF. 2).
W, 85CD7571F89A5663 CRC64;
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Pred. No. 2.8e+02;
4; Mismatches 19; Indels
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D0531AF308A7BF1D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
FLAGELLIN B.
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Pfam; PF00669; Flagellin_N; 1.
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575 AA; 59728 MW;
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Best Local Similarity 35.7%;
Matches 15; Conservative
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Best Local Similarity 28.0'
Matches 14; Conservative
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InterPro; IPR001029; -.
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FLB2_CAMJE
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InterPro; IPR001051; -
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InterPro; IPR001007; -
InterPro; IPR001007; -
InterPro; IPR001046; -
InterPro; IPR002400; -
Pfam; PF00009; vwd; -
Pfam; PF00094; vwd; -
PR0SITE; PS00122; EGF_1; UNKNOWN_1, PROSITE; PS01185; CTCK_1; 1, PROSITE; PS01125; CTCK_1; 1, PROSITE; PS01125; CTCK_2; 1, PROSITE; PS01208; VWFC; 2, 1, PROSITE;
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VWFC 2.
CTCK.
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EMBL; M94132; AAA59164.1;
MIM; 158370; -.
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Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=K12 / MG1653.
STRAIN=K12 / MG1658.
BMEDLINE=93315143; PubMed=7686882;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coli genomics organizational symmetry around the origin of replication.";
Genomics 16:551-561(1993).
                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
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027272; 09VX16;
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
10-CCT-2000 (Rel. 40, Last encotation update)
10-CCT-2000 (Rel. 40
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MEDLINE=94150630; PubMed=7545910;
Kokubo T., Gong D.W., Wootton J.C., Horikoshi M., Roeder R.G.,
Nakatani Y.,
"Molecular cloning of Drosophila TFIID subunits.";
Nature 367:484-487(1994).
    01-JUL-1993 (Rel. 26, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 46.9 KDA PROTEIN IN TNAB-BGLB INTERCENIC REGION.
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EMBL; AE000448; AAC76737.1; -
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les 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elgimeler K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares J., Taylor K., Whitehead S., Barrell B.G., Taylor K., Whitehead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence.";
Nature 393:537-544(1998).
-1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-1 - SIMILARITY: BELONGS TO THE MMPL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 23;
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463 AALKTTAANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQ 512
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PUTATIVE MEMBRANE PROTEIN MMPL7.
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Hypothetical proteir
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920 AA;
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Best Local Similarity
Matches 18; Conserv
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RESULT 14 YIEG\_ECOLI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Proinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I-FUNCTION: TAFS ARE COMPONENTS OF THE TRANSCRIPTION FACTOR IID (TFIID) COMPLEX THAT ARE ESSENTIAL FOR MEDIATING REGULATION OF
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the basal transcription factor TFIIB.";
Cell 75:519-530(1993).
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                                                                                                                   MEDLINE-20196006; PubMed-10731132;
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                                                                   SEQUENCE FROM N.A.
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DOMAIN SEQUENCE

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Gaps
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                                                                                       196 KTVGSSGGSGGGGGEVKSESTGAGGDLKMEVDSDAAAVGSIAGASGSGAGS 247
                                                           49
 Length 278;
                                                            5 KIDAAILGQEAGNFERI-----SGDLKTQIDQVESTAGSLQGQWRGAAGT
                               Indels
                               22;
   DB 1;
                               9; Mismatches
   Score 53.5; I
Pred. No. 18;
 21.7%;
26.9%;
Query Match
Best Local Similarity 26.99
Matches 14; Conservative
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Search completed: July 5, 2001, 11:51:42 Job time: 501 sec

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247
1 MAEMKTDAATLGQEAGNFER......DQVESTAGSLQGQWRGAAGT
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Post-processing: Minimum Match 0%
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sp\_unclassified:\*
sp\_vertebrate:\*
sp\_virus:\* sp\_invertebrate:\*
sp\_mammal:\*
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sp\_bacteria:\*
sp\_fung1:\* sp\_organelle:\* sp\_rodent:\* sp\_plant:\* SPTREMBL\_16:\* sp\_phage: \* sp\_human:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	O69739 mycobacteri	033084 mycobacteri	005440 mycobacter1	Q9hy76 pseudomonas	Q96898 hepatitis q	081080 arabidopsis	039811 glycine max	O9vd64 drosophila	рошо	076037 homo sapien	Omor	homo	omor	ошоц	Omor	Omor	Q9h484 homo sapien	Omor	Q9h482 homo sapien
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	55.5 55.5

## ALIGNMENTS

	PRT; 100 AA.	07, Created)	07, Last sequence update) 14. Last annotation update)	)	.60	Mycobacterium tuberculosis. Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.				=9634230;				Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,	Hornsby T., Jagels K., Krogn A., McLean J., Moule S., Murpny L., Oliver S., Osborne J., Obail M.A., Rajandream M.A., Rogers J.,	Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,	Taylor K., Whitehead S., Barrell B.G.;	"Deciphering the biology of Mycobacterium tuberculosis from the						"Promoter analysis of the M. tuberculosis offic gene encourng the parly secreted antidenic target 6 kDa (RSAT-6).":	Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.	.1,			4 MW; 285F4FC96F55D194 CRC64;
	PRELIMINARY;	(TrEMBLrel.	(TrEMBLrel.		LHP OR RV3874 OR MTV027.09.	Mycobacterium tuberculosis Bacteria: Firmicutes: Acti	tales, Coryneb	-1773;	r a Mod	RV:	MEDLINE=98295987; PubMed=9634230;	Cole S.T., Brosch R., Parkhill J.,	Gordon S.V., Eiglmeier K., Gas	, Basham D., B	Devlin K., Fe	Osborne I. O	Seeger K., Sk	Whitehead S.,	ng the biology	complete genome sequence.	(OCCT) **C-/CC:	ROM N.A.	RV;	-X., Birk Rasm	analysis of the	(MAY-1997) to	EMBL; AL022120; CAA17966.1;	EMBL; AF004671; AAC83445	L; RV36/4;	. 0
LT 1	069739	01-AUG-1998	01-AUG-1998 01-TIIN-2000	HYPOTHETIC	LHP OR RV3	Mycobacter Racteria:	Actinomyce	NCBI_TaxID=1773;	[1]	STRAIN=H37RV:	MEDLINE-98	Cole S.T.,	Gordon S.V	Badcock K.	Davies R.,	Oliver S.	Rutter S.,	Taylor K.,	"Decipheri	complete g	[2]	SEQUENCE FROM N.A.	STRAIN=H37RV;	Berthet F.	Parly secri	Submitted	EMBL; AL02	EMBL; AF00.	Hypothetical	SEQUENCE
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EMBL; 294121; CAB08096.1;
           Tuberculist; Rv3905c;
Hypothetical protein.
SEQUENCE 103 AA; 10
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Best Local Similarity
Matches 14; Conserv
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01-MAR-2001 (
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Nature 393:537-544(1998).
                           Gaps
                                                                                                                                                                                                                                                                                                                                         MEDLINE=93188700; PubMed-8446027;
Biglinneier K., Honoren N., Woods S.A., Caudron B., Cole S.T.;
Biglinneier K., Honoren N., Woods S.A., Caudron B., Cole S.T.;
"Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae.";
Mol. Microbiol. 7197-206(1993).
BEMBL: Y14067; CAA715710.1;
SEQUENCE 100 AA: 10964 MW; 460EE12F876EC383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1769;
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NCBL_TaxID=1773;
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Score 241; DB 2; Length 100;
Pred. No. 9.8e-22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 100;
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                                                              1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 92; DB 2; Length 100
Pred. No. 0.00075;
9; Mismatches 20; Indels
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                                                1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT
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WYSJOSC OR MICK15F10.06.
                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                        PRT; 100 AA
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MEDLINE-98295987; PubMed-9634230;
 97.6%;
98.0%;
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Best Local Similarity 40.8%;
Matches 20; Conservative 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
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         Best Local Similarity
Matches 48; Conserv
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MEDLINE-20437337; PubMed-10984043; Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L. Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulenen I.T., Reizer J., Saler M.H., Hancock R.E., W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                    Gaps
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
NCBL_TaxID=39112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB 2; Length 702;
Pred. No. 20;
                                                                          25.5%; Score 63; DB 2; Length 103; 23.9%; Pred. No. 2.3;
                                                                                                                              15; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                   4 MKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00384; molybdopterin; 1.
Pfam; PF01568; Molydop_Linding; 1.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
SEQUENCE 702 AA; 76766 MW; C9B769830479F047 CRC64;
                                                                                                                                                                                                                                    7 LRVEPAVMQGFAASLDGAAEHLAVQLAELDAQVGQMLGGWRGASGS 52
10460 MW; 3994E272A7BDFF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         702 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 GNLDRVGGALCTSPALDLVASTSGGHFGRWR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 GNFERISGDLKTQ--IDQVESTAGSLQGQWR 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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MEDLINE=95241511; PubMed=7724574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE004773; AAG06922.1; -.
InterPro; IPR000194; -.
InterPro; IPR001467; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.5%;
illarity 45.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TremBLrel, 16, (TremBLrel, 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02,
02,
16,
                                                                  Query Match 25.5%
Best Local Similarity 23.9%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE OXIDOREDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
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21; Gaps

agent.

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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                 ----AGNFERISGDLKTQIDQVESTAGS---LQGQW 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max (Soybean).

Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Glycine.

NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 422;
                                                                               Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Davis M.O., Walker J.C., Smith D.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U12926; AAA73963.1; -.
Mendel; B332; Glyma;1501;8332.
InterPro; IPR000111; -.
InterPro; IPR000111; -.
         SMART; SM00079; PBPe; 1.
SEQUENCE 934 AA; 105052 MW; 6A325C48CF4E2B4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR002287; -.
Pfam; PF02065; Melibiase; 2.
PRINTS; PR00740; GLHYDRLASE27.
PRODOM; PD002572; -; 1.
PROSTE; S800512; ALPHA_GALACTOSIDASE; 1.
SEQUENCE 422 AA; 46395 MW; 9281B25EAD6940A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                   17;
                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59.5; DB
pred. No. 30;
pred. Nismatches
                                                                               Score 60.5; DB
Pred. No. 56;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created) 01-WAY-2000 (TrEMBLrel. 13, Last seq) 01-WAR-2001 (TrEMBLrel. 16, Last ann CG6560 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.1%;
Best Local Similarity 35.7%;
Matches 15; Conservative 7
                                                                               24.5%;
29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2000 (TrEMBLrel. 14, ALPHA GALACTOSIDASE.
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                               Query Match
Best Local Similarity
                                                                                                                                                          5 KTDAATLGQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                      390 RPSNG 394
                                                                                                                                                                                                                                 44 RGAAG 48
                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                  039811;
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                                                                                                                       Matches
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Q39811
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Simons J.N., Pilot-Matias T.J., Thary T.P., Dawson G.J., Desai S.M., Schlauder G.G., Muerhoff A.S., Erker J.C., Buijk S.L., Chalmers M.L. van Sant C.L., Mushahwar I.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Bubryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicoryledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M., Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.; "Arabidopsis thallana chromosome II BAC T914 genomic sequence."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AC005315; AAC33239.1; -.
                                                             'Identification of two flavivirus-like genomes in the GB hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBITE; FSYCLE; FSYCLE; BENDC; 1.
SMART; SM00487; DEXDC; 1.
NONSETUCTURAL PROTEIN; Polyprotein; RNA-directed RNA polymerase.
REPORTED 2954 AA; 318835 MW; 4A0C35FC2ED283B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.1%; Score 62; DB 14; Length 2954; ilarity 34.8%; Pred. No. 1.4e+02; Conservative 4; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2357 DGHQLFDERGPIEVSTPICEVIGDIRLQCDQIEETPTSYSYIWSGA 2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 DAATLGQEAGNFE-----RISGDLKTQIDQVESTAGSLQGQWRGA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Pfan; PF01094; ANF_receptor; 1.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
                                                                                                Proc. Natl. Acad. Sci. U.S.A. 92:3401-3405(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00998; HCV_RGRP; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF01538; HCV_NS2; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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PUTATIVE LIGAND-GATED IONIC CHANNEL.
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081080;
01-NOV-1998 (TEMBLrel. 08,
01-NOV-1998 (TEMBLrel. 08,
01-MAR-2001 (TEMBLREL. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [nterPro; IPR001311; -.
InterPro; IPR001320; -.
                                                                                                                                                                                                                                                                                                                          InterPro; IPR000255; -.
InterPro; IPR000745; -.
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001410; -.
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001490; -. InterPro; IPR002166; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002518; -. InterPro; IPR002868; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001395; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                             MEROPS; S29
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RESULT 081080

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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39.0%;
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                                                                                                                                                                                                                                                                                                                                                                                     Biol. Reprod. 60:58-64(1999)
EMBL; AF058803; AAC34750.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, MUC4 PROTEIN SPLICE VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUCIN PRECURSOR (FRAGMENT).
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Best Local Similarity 39.07
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        944
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944 AA; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
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SEQUENCE
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Q9H4D6
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                  Adams N.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R.A. Adams N.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R.A. Adams N.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R.A. George R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
R.A. Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
R.A. Ball J.F., Apbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayrakerproglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayrakerproglu L., Beasley E.M.,
Baltis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chadra I.,
R.A. Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chadra I.,
R.A. Burtis R.C., Busam D.A., Bahlke C., Davenport L.B., Davies P., Onn P.,
R.A. Gong F., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Gong F., Gorrell J.H., Gu Z., Gelbart M.M., Glasser R.,
R.A. Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser R.,
Alostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
R.A. Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Hockhum K.A.,
Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Merkulov G., Milshina N.V., Mobarry C., Morberson D.,
Retazolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
R. Reinert K., Reinington K., Sunders R., Paciel J.M.,
R. Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
R. Spier E., Spradling A.C., Stapleton M., Strong R., Smith H.,
Wallems E., Whyers R., Woodage T., Worley K., Wu D., Yang S., Yao Q., A.,
Wallams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q., A.,
Wallams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q., A.,
Wallams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q., A.,
Wallams S.M., Woodage T., Worley S., Shang G., Shang S., Shang S., Shang S., Shang S., Shang S., Sha
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SEQUENCE 203 AA; 23017 MW; 1A75678FA9BD6185 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              944 AA.
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8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 DAATLGQEAGNFERISGDLKTQIDOVESTAG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
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01-MAY-2000 (TrEMBLrel. 13, Last anno
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MEDLINE=20196006; PubMed=10731132;
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PRINTS; PRO0328; SARIGTBP.
PROSITE; PS01019; ARF; 1.
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Best Local Similarity 27.8%;
Matches 15; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0038916; CG6560
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HSSP; P32889; 1RRF.
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Q9UP82;
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"Human mucin gene MUC4: organization of its 5'-region and polymorphism of its central tandem repeat array."; Biochem. J. 332:739-748(1998). EMBI. AJ000281; CAA039985.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SEQUENCE FROM N.A. MEDLINE-99077625; PubMed-9858486; Gipson I.K., Spurr-Michaud S., Moccia R., Zhan Q., Toribara N., Ho S.B., Gargiulo A.R., Hill J.A. III.; MuC4 and MUC5B transcripts are the prevalent mucin messenger
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                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 944;
                                                                                                                                                                                                                                                                                                                                                                                                                          19; Indels
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28 >1045 MUCIN.
1045 1045
1045 AA, 106737 MW, 26F12DF28E6D60A0 CRC64;
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Last sequence update)
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SV11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGT 49
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                                                                                                                                       ribonucleic acids of the human endocervix.";
Biol. Reprod. 60:58-64(1999).
                                                                                                                                                                                                                                                                                                                                                                ; Score 58.5; DB
; Pred. No. 99;
5; Mismatches
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MEDLINE-98285542; Pubmed-9620877;
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Q9UPB2 ID Q9 AC Q9 DT 01 DT 01 DT MU GN MU OS HC

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Gaps

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SEQUENCE FROM N.A.
TISSUB-PANCREATIC TUMOUR;
TISSUB-PANCREATIC TUMOUR;
Choudhury A., Moniaux N., Hollingsworth M.A., Aubert J.P., Batra S.K.;
Choudhury A., Moniaux N., Hollingsworth M.A., Aubert J.P., Batra S.K.;
"Human MUC4 mucin splice variants in pancreatic adenocarcinoma.";
submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ400852; CAC14137.1; -..
EMBL; AJ400852; CAC14137.1; -..
SEQUENCE 1199 AA; 123130 MW; 13EC88F6977EF11B CRC64;
                                      SEQUENCE FROM N.A.
MEDLINE-2038L033; Pubmed=10920259;
Choudhury A., Moniaux N., Winpenny J.P., Hollingsworth M.A.,
Aubert J.P., Batra S.K.;
"Human, MUC4 mucin cDNA and its variants in pancreatic carcinoma.";
J. Biochem. 128:333-243(2000).
EMBL; AJ400851; CAC14136.1; -.
EMBL, AJ400851; CAC10062.1; -.
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TISSUE-PANCREATIC TUMOUR;
Choudhury A., Moniaux N., Hollingsworth M.A., Aubert J.P., Batra S
"Human MIC4 mucin splice variants in pancreatic adenocarcinoma.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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  Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
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SV15.
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SV16.
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                     23.7%; Score 58.5; DB 4.39.0%; Pred. No. 1.3e+02
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                                                                                                                                                                                                                                                                                           Pred. No. 1.3e-5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                         1187 AA; 121926 MW;
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39.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, MUC4 PROTEIN SPLICE VARIANT
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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Best Local Similarity 39.09
Matches 16; Conservative
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Best Local Simi
Matches 16;
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Q9H487;
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29н486;
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TISSUE-PANCREATIC TUMOUR;
Choudhury A., Moniaux N., Hollingsworth M.A., Aubert J.P., Batra S.K.;
"Human MUC4 mucin splice variants in pancreatic adenocarcinoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Batra S.K.;
                                                                                                                                                                                                                                                                                                              Gaps
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Last sequence update)
Last annotation update)
SV13 (MUC4 PROTEIN SPLICE VARIANT SV12).
                                                                                                                      Choudhury A., Moniaux N., Ringel J., Aubert J.P., Batra S.K.;
"Human MUC4 mucin splice variants in pancreatic adenocarcinoma.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ277505; CAC14885.1; -.
SEQUENCE 1107 AA; 113576 MW; 2669ADBF5DA53721 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-PANCREATIC TUMOUR;
Choudhury A., Moniaux N., Hollingsworth M.A., Aubert J.P., Batra & Choudhury A., Moniaux N., Hollingsworth M.A., Aubert J.P., Batra & Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ400850; CAC14135.1; -.
EMBL; AJ400849; CAC14134.1; -.
SEQUENCE 1157 AA; 118925 MW; F46F039320969A9C CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                     Length 1107;
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Last sequence update)
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SV14 (MUC4 PROTEIN VARIANT VII).
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                                                                                                                                                                                                                                                                   Score 58.5; DB 4;
Pred. No. 1.2e+02;
5; Mismatches 19;
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39.0%;
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Best Local Similarity 39.0
Matches 16; Conservative
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                                                                                                       SEQUENCE FROM N.A.
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                                                            NCBI_TaxID=9606;
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Q9GZM2;

Q9GZM2

RESULT 12

ò g Q9GZM2

Query Match

Matches

ð a

09GZV6; 9AZS60

13

RESULT 9AZS60

Gaps

EMBL; AJ400853; CAC14138.1; -. SEQUENCE 1201 AA; 123504 MW; 8C635BEAB245C5DC CRC64; SQ SQ

1; Gaps Query Match 23.7%; Score 58.5; DB 4; Length 1201; Best Local Similarity 39.0%; Pred No. 1.3e+02; Matches 16; Conservative 5; Alsmatches 19; Indels 1;

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Search completed: July 5, 2001, 11:50:47 Job time: 470 sec

us-09-462-480-5.rag

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Gencore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2002, 21:27:53 ; Search time 58:34 Seconds

(without alignments)
190:390 Million cell updates/sec
10S-09-462-480-5
190:390 Million cell updates/sec
1 MAEMKTDAATLGGEAGNER......VQYSRADEEQQQALSSQMGF 100
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574
Minimum DB seq length: 0
Maximum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
No.	Score	Match	Match Length DB	DB	a	Description
П	492	100.0		20	AAY03705	M. tuberculosis LH
7	486	98.8		19	AAW81706	M. tuberculosis im
m	486	98.8		19	AAW64339	Mycobacterium tube
4	486	98.8		20	AAY39136	M. tuberculosis an
ស	486	98.8		20	AAY38993	M. tuberculosis re
9	486	98.8	100	22	AAB35218	M tuberculosis Rv3
7	486	98.8		22	AAB19845	Mycobacterium tube
æ	481	97.8		19	AAW81746	M. tuberculosis fu
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## ALIGNMENTS

RESULT

AAXU3/U5 ID AAY03705 standard; Protein; 100 AA.		AC AAY03705;	XX	DT 07-JUN-1999 (first entry)		DE M. tuberculosis LHP polypeptide.	:		KW immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic;				PN W09904005-A1.	XX	PD 28-JAN-1999.		16-JUL-1998;		16-JUL-1997;		(INSP)	(STAT-)		PI Andersen P, Berthet F, Gicquel B, Rasmussen PB;	XX				New nucleic acid containing regulator and LHP gene of		PT tuberculosis - useful in vaccines, for diagnosis, and for expression	AAYO XXX ACX XXX ACX XXX XXX XXX XXX XXX XXX	03705 standard; Protein; 100 AA. 03705; JUN-1999 (first entry) tuberculosis LHP polypeptide. T-6 protein; antigenic protein; LHP; Mycobacterium unogen; vaccine; bacteria; tuberculosis; regulatory une response. 004005-A1. JAN-1999. JUL-1998; 98WO-IB01091. SP) INST PASTEUR. AT-) STATENS SERUM INST. ersen P, Berthet F, Gicquel B, Rasmussen PB; 1999-132249/11. SDB; AAX29171.
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WO9816645-A2
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                                                                                                                                                                                                                                                                                                                         The present invention is directed to a polynucleotide carrying the regulatory expression signals of the ESAT-6 protein as well as an open reading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprising the polynucleotide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the CM. tuberculosis complex in humans or animals (the vaccines may include other immunogenic proteins of the bacteria or their fragments, specifically ESAT-6); and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The requilatory region present in the polynucleotide may be used to express almost any heterologous protein in grobacteria, particularly as a fusion with polyhistidine. The two proteins encoded by the polynucleotide, LHP and ESAT-6, are expected to provide a synergistic increase in ability to induce a protective immune conservative and processed to response. The present sequence represents the LHP polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                        1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
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                                                                                                                                                                                                                                                                        ; Score 492; DB 20; Length 100;
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0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. tuberculosis immunogenic polypeptide Tb38-IN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW81706 standard; Protein; 100 AA.
                      Claim 17; Page 64; 88pp; English.
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                                                                                                                                                                                                                                                                          100.08;
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960S-0730510.
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nes 100; Conservative
of heterologous proteins
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                                                                                                                                                                                                                                       100 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-1997;
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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises a partial sequence of Mycobacterium tuberculosis antigen Tb38-IN. It is encoded by genomic DNA isolated from a M. tuberculosis strain H37Rv genomic library using a probe derived from clone Tb38-1 (see AAV44384). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAV64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or kransfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                    Score 486; DB 19;
Pred. No. 1.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis antigen Tb38-IN.
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 145; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW64339 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                 98.88;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US18214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0729622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0818111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                     100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-1997;
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The same

Similarity

Matches , 99;

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Sednence

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This invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 maemktdaatlaqeagnferisgdlktgidqvestagslqgqwrgaagtaaqaavvrfqe 60
detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 486; DB 20; Length 100;
Pred. No. 1.8e-45;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton R;
, Vedvick
                                                                                                                                                                                                                                                                                      M. tuberculosis recombinant antigen protein Tb38-IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campos-Neto A, Dillon DC, Hendrickson RC, Hc
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 179; 323pp; English.
                                                                                                                                                                               Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                               AAY38993 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35218 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.8%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US03265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0072596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0024753
                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.0
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                            Antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  WO9942118-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                     05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-AUG-1999
                                                                                                                                                                                                                   AAY38993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB35218
                                                                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB35218
                                                                                                                                                               AAY38993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                            AREMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                           Gaps
                                                                                                                         1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antigens from Mycobacterium tuberculosis useful in diagnostic skin itests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 486; DB 20; Length 100;
Pred. No. 1.8e-45;
0; Mismatches 1; Indels
                                                        Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton R;
R, Vedvick TS;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               M. tuberculosis antigen Tb38-IN amino acid sequence.
                                                                                                                                                                                                61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                   Score 486; DB 19;
Pred. No. 1.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on DC, Hendrickson RC, Hc
Skeiky YAW, Twardzik DR,
                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 133-134; 299pp; English
                                                                                                                                                                                                                                                                                                                            ¥
                                                                                                                                                                                                                                                                                                                          AAY39136 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.8%;
99.0%;
                                                    98.8%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US03268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0072967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 99.0 99; Conservative
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI*) CORIXA CORP.
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Campos-Neto A, Lodes MJ, Reed

W09942076-A2

05-NOV-1999

AAY39136;

17-FB-1999; 05-MAY-1998; 18-FEB-1998;

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Gaps

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100 AA;

Sequence

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99US-0132505
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96US-0730510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                WPI; 2001-007153/01.
N-PSDB; AAA89038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                             100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
Mycobacterium
           04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-1996;
                                               Gennaro ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1998
                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW81746;
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW81746
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                         one of
                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences for members of the esat-6 gene family from Mycobacterium tuberculosis. The proteins include Rv0287, Rv1036c, Rv1037c, Rv2346c, Rv2346c, Rv23653c, Rv2654c, Rv34020c, Rv3444c, Rv3444c, Rv34940c, Rv3890c. These can be used to produce vaccines against, and in the diagnosis of, tuberculosis (TB) infection. The present sequence is one
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide encoded by a member of the esat-6-gene family for immunizing against and diagnosis of tuberculosis -
                                    esat-6 gene family, Rv0287; Rv1036c; Rv2653c; Rv2654c; Rv3020c; Rv3444c; Rv3904c; Rv3905c.
                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                              Length 100;
                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTBN4; tuberculosis; BCG; vaccine; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                            Score 486; DB 22;
Pred. No. 1.8e-45;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis protein MTBN4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB19845 standard; Protein; 100 AA
                                                                                                                                                                                                                                                       Example 2; Page 65; 80pp; English.
                 M tuberculosis Rv3874 protein.
                                                                                                                                                                                                                                                                                                                               the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                          98.88;
                                    vaccine; e
Rv2348c; F
Rv3891c; F
                                                                                                                           13-JUL-2000; 2000WO-DK00398
                                                                                                                                             99DK-0001020
                                                                                                                                                       99US-0144011
                                                                      Mycobacterium tuberculosis
                                                                                                                                                                        (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000; 2000WO-US12257
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.0°
Matches | 99; Conservative
                                                                                                                                                                                          Skjot R;
                                                                                                                                                                                                           WPI; 2001-091923/10.
                                  Tuberculosis; TB;
Rv1037c; Rv2346c;
Rv3445c; Rv3890c;
                                                                                                                                                                                                                                                                                                                                                 100 AA;
                                                                                        WO200104151-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200066157-A1.
                                                                                                                                             13-JUL-1999;
15-JUL-1999;
24-APR-2001
                                                                                                                                                                                          Andersen P,
                                                                                                          18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB19845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB19845
g
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The present sequence is that of the Mycobacterium tuberculosis MTBN4 protein. This is 1 of 8 proteins, i.e. MTBN1-8 (see AABB942-49), encoded by 8 open reading frames (see AAAB8935-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. MTBN1-8 represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these MTBN polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic (vaccine) methods, including genetic vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                           Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.8%; Score 486; DB 22; 99.0%; Pred. No. 1.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
(PUBL-) PUBLIC HEALTH RES INST NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. tuberculosis fusion protein TbF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW81746 standard; Protein; 802 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Fig 1; 35pp; English.
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Gaps

; 0

Length 802; Indels

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TAX SAME

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composed of Mycobacterium tuberculosis antigens TSBA3 (see AAW64295), 38 kDa antigen (see AAW64364), Tb38-1 (see AAW6431) and DPEP (see AAW64322). It was produced by PCR amplification (see AAV4450-57) of the appropriate antigen DNA sequences, cloning into an expression vector, and expression in E. coli. TbF-2 can be used for serodiagnosis of tuberculosis. The invention relates to compositions and methods foor diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising antigens or liminuogenic portions of M. tuberculosis antigens, or fusion proteins, DNA sequences encoding such polypeptides, recombinant expression vectors and host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis - \,
                                                                                                                                                                                                                                                                                                                                                   This sequence represents a recombinant Mycobacterium tuberculosis tetra-antigen fusion protein, termed TbF-2, composed of the antigens TbRa3, 39KD, Tb38-1 and DBEP. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AAZ20198) comprising the 4 coding sequences. The invention provides fusion proteins (see AAX32059-71) containing at least 2 M. tuberculosis
                                                                                                                                                                                                                                                                                                                                   2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculosis; antigen; fusion protein; TbF-2; TbRa3; 38kD; Tb38-1; DPEP; diagnosis; therapy; vaccine; immunogen.
               polypeptide comprises a fusion protein, designated TbF-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis antigen fusion protein TbF-2.
                                                                                                                                                                                                                                                                       97.8%; Score 481; DB 19;
99.0%; Pred. No. 8.1e-44;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                 62 ANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                             Campos-Neto A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY32063 standard; Protein; 802 AA
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98US-0223040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.0
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW, Alderson M,
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                                                                                                                                                                                                                                802 AA;
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30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-1999;
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                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                             This sequence represents the fusion protein TbF-2 which is composed of immunogenic polypeptides from Mycobacterium tuberculosis (MT). This protein is used fin a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of TB.
                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                               2 AEMKTDAATLGDEAGNFERISGDLKTQIDQVESTAGSLOGGWRGAAGTAAQAAVVRFQEA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Mycobacterium tuberculosis polypeptides and DNA - .used to develop products for the detection of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculosis; infection; diagnosis; 38 kDa antigen; TbRa3; DPEP;
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                                                                                                                                                                                                                                                                                                                                  Score 481; DB 19; Length 802;
Pred. No. 8.1e-44;
); Mismatches 1; Indels (
   R, Lodes MJ;
Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DC, Houghton R, Lodes M. Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium antigen TbF2 protein fusion.
                                                                                                                                                    Disclosure; Page 208-211; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 223-226; 250pp; English
Campo's-Neto A, Dillon DC, Houghton
Reed (SG, Skeiky YAW, Twardzik DR, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW64379 standard; Protein; 802
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                                                                                                                                                                                                                                                                                                                                  97.8%;
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96US-0729622.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Reed SG, Skeiky YAW,
                                            WPI; 1998-261042/23.
N-PSDB; AAV64567.
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N-PSDB; AAV55801.
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Matches 98; Conserv
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                                                                                                                                                                                                                                                                                         802
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                                                                                                                                                                                                                                                                                         Sequence
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M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other, polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                            NEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61
antigns. The new fusion proteins and polynucleotides encoding them pre useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antigens from Mycobacterium tuberculosis useful in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
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                                                                                                                                                                                DB 20; Length 802;
                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                        Score 481; DB 20;
Pred. No. 8.1e-44;
0; Mismatches 1;
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Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 37; Page 271-273; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY39,224 standard; Protein; 802 AA
                                                                                                                                                                             97.8%;
99.0%;
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98US-0025197
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Reed SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                             Query Match 97.8
Best Local Similarity 99.0
Matches, 98; Conservative
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                                                                                                                              802 AA;
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18-FEB-1998;
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                                                                                                components.
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                                                                                                                                Sednence
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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAX19249 to AAX19460 and AAX39083 to
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61
AAY39225 are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antigens from Mycobacterium tuberculosis useful in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
immunotherapy; diagnosis; immunisation; vaccine; infection;
immune response; skin test.
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                                                                                                                                       Length 802;
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;, Vedvick TS;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis fusion protein TDF-2 amino acid sequence.
                                                                                                                                     ; DB 20; I
8.le-44;
ches 1;
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                     Score 481; DB
Pred. No. 8.1e
0; Mismatches
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                                                                                                                                       97.8%;
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                                                                                                                                       Query Match 97.8
Best Local Similarity 99.0
Matches 98; Conservative
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                                                        802 AA;
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Length 802;

Score 481; DB 20;

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AAY39033 standard; Protein; 802 AA
    AAY39033
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                                                             ABMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen; diagnosis; detection; infection; antibody; immunisation;
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Pred. No. 8.1e-44;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dillon DC, Hendrickson RC, Houghton R;
SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ANKOKOELDEISTNIRQAGVOYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANKOKOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
    Pred. No. 8.1e); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Page 316-318; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       M tuberculosis fusion protein TbF-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.8%; Scur-
99.0%; Pred
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                     ;
99.08;
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98US-0024753.
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Best Local Similarity 99.0
Matches 98; Conservative
                     Conservative
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  Best Local Similarity
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Lodes MJ, Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9942118-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FIB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                    425
                                                                                                                                          62
                                                                                                                                                                                  485
                     Matches
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invention describes novel recombinant antigens and their encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA
                                                                                               Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TbF15; antigen; vaccine; tuberculosis; AIDS; His tag; Ra3; 38kD; 38-1; FL TbH4; acquired immunodeficiency disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.8%; Score 481; DB 20;
99.0%; Pred. No. 8.1e-44;
ive 0; Mismatches 1;
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Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Page 251-253; 323pp; English.
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                                              M. tuberculosis fusion protein TbF-2.
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                                                                                                                                                                                                                                                                                                                     99WO-US03265
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98US-0024753.
                                                                                                                                                                       Mycobacterium tuberculosis
(first entry)
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N-PSDB; AAZ19156.
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Matches 98; Conserv
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18-FEB-1998;
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05-NOV-1999
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Mycobacterium tuberculosis.

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The sequence represents Mycobacterium fusion protein antigen TbF15 consisting of a His tag for purification, antigens Ra3, 38tD, 38-1 and FL-TbH4 (full-length TbH4). Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the scrological sensitivity of individuals infected with tuberculosis, a disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requently affecting patients with acquired immunodeficiency disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AEMKTDAATLGDEAGNFERISGDLKTQIDQVESTAGSLQGGWRGAAGTAAQAAVVRFQEA 61
                                                                                                                                                                                                                                                                                                                                                        Lodes ML;
                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
                        Location/Qualifiers
3.88
/label Histidine_tag
/loce= "Nickel chelating region used for purifying the fusion protein"
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                                                                                                                                          426..524
/label= 38-1_region
525..983
/label= FL_TbH4_region
                                                                                       9.74
/label= Ra3_region
75.425
/label= 38kD_region
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99US-0158425.
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Best Local Similarity 99.0
Matches 98; Consprvative
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N-PSDB; AAS03795.
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07-0CT-1999;
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Search completed: July 22, 2002, 01:11:37 Job time: 13424 sec

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Sequence 3, 1 Sequence 2, 1 Sequence 4, 1 Sequence 4, 1 Sequence 4, 1 Sequence 4, 2 Sequence 4, 3 Sequence 7, 3 Sequence 7, 3 Sequence 9, 3 Sequence 2, 3 Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Autonio
APPLICANT: Campos-Neto, Autonio
APPLICANT: Twardzik, Thomas S.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.8%; Score 486; DB 4; I
99.0%; Pred. No. 1.7e-48;
tive 0; Mismatches 1;
                                                                                                                    US-08-467-781-4
US-08-195-487-4
US-08-193-924-4
US-09-452-294-1
PCT-US93-06160-4
5510466-2
5510466-4
US-07-716-827C-5
US-08-452-592B-9
US-09-67-716-2
US-09-67-75-2
US-09-67-75-2
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NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNE: (206) 622-4900
TELEFRAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 115, Application US/08818112 Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 115: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 100 amino acids
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Best Local Similarity 99.0'
Matches 99; Conservative
         CITY: Seattle
STATE: Washington
COUNTRY: USA
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US-08-818-112-115
       STRANDEDNESS
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US-08-818-112-115
         Sequence 88, Appl
Sequence 89, Appl
Sequence 112, Appl
Sequence 112, Appl
Sequence 117, Appl
Sequence 98, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 95, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 93, Appl
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101.016 Million cell updates/sec
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Sequence 110, App
Sequence 115, App
Sequence 214, App
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492
1 MAEMKTDAATLGQEAGNFER.....VQYSRADEEQQQALSSQMGF
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/cgn2_6/ptodata/2/iaa/pcyt5_COMB.pep:*
                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-818-111-110

US-09-056-556-115

US-09-056-556-214

US-08-818-112-88

US-08-818-111-89

US-08-818-111-112

US-08-818-111-112

US-08-818-111-112

US-08-818-111-112

US-08-818-1112-96

US-09-056-556-96

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US-08-08-818-112-94

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Query Match I

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GENERAL INFORMATION:
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                                    MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
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                                                                                                                                                                                                                                                                                 APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Tedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 98.8%; Score 486; DB 4; Length 100; 1. Similarity 99.0%; Pred. No. 1.7e-48; 99; Conservative 0; Mismatches 1; Indels
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APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIA J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
                                                                                      E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
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REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            Sequence 110, Application US/08818111 Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-056-556-115
; Sequence 115, Application US/09056556
; Patent No. 6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-818-111-110
                                                                                                                                                                                                            US-08-818-111-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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Best Local Si
Matches 999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                    COMPOUNDS AND METHODS FOR THE PREVENTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOUNDS AND METHODS FOR THE PREVENTION AND
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                                                                                                                                                                                                                                                               COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                                                                                                                   ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDKESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 486; DB 4;
Pred. No. 1.7e-48;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 214, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
ITLE OF INVENTION: COMPOUNDS AI
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.88;
99.08;
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Best Local Similarity 99.0°
Matches 99; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                               98104-7092
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US-09-056-556-115
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Gaps

Length 95;

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6 TDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQ 65
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                                                                                                                                   Score 462; DB 4;
Pred. No. 8.8e-46;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                               66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 21(TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 682-4900 TELEFAX: (205) 682-6031 INFORMATION FOR SEQ ID NO: 89:
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98.9%;
                                                                                                                                     93.9%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
LENGTH: 95 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                       Query Match 93.9°
Best Local Similarity 98.9°
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Best Local Similarity
Matches 94; Conservi
                                                         linear
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                                                           ; TOPOLOGY:
US-08-818-112-88
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US-08-818-111-89
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: WedyLon, Raymond
APPLICANT: WedyLot, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                Length 802
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COUNTRY: USA

ZIP: 98104-7092

COMPUTER REDABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
HAPPLICATION DATA:
STELNG DATE: 13-MAR-1997
FILING DATE: 13-MAR-1997
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADÜRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ANKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
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Pred. No. 9.7e-47;
0; Mismatches 1
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                    us/09/056,556
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Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SED ID NO: 214:
SEQUENCE CHARACTERISTICS:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              97.8%;
                                    07-APR-1998
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                                                                                                                                                                                                                                                    LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.0°
Matches 98; Conservative
  CURRENT APPLICATION DATA:
                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                  linear
                                         FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-09-056-556-214
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US-08-818-112-88
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Netc, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 462; DB 4; Lengtn 5-
Pred. No. 8.8e-46;
                                                                                                                                                                                                                                                                                                                                                                   6300 Columbia Center, 701 Fifth Avenue
61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210121.417C6
                                                                                Sequence 89, Application US/08818111 Patent No. 6338852 GENERAL INFORMATION:
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOUNDS AND METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G.
APPLICANT: Reid, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dilloh, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%; Score 392; DB 4; Length 80; llarity 100.0%; Pred. No. 6.8e-38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
                                                                             E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                         FILING DATE: 13-MAR-1997
CLASSIFICATION
                                                                                                                                                                              ZIP: 98104-7092
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 112, Application US/08818111 Patent No. 6338852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SED ID NO: 117:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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TITLE OF INVENTION: CONTITLE OF INVENTION: ANI NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                               RY: USA
98104-7092
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Best Local Similarity
Matches 80; Conserv
                                                                                                                      Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                               ADDRESSEE:
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                                                                                                                                                           COUNTRY:
                                                                                                  STREET:
                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 88, Application US/09056556

Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed', Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Scelky, Vasir A.W.
APPLICANT: Compound C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 462; DB 4; Length 95;
Pred. No. 8.8e-46;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION:
CLASSIFICATION:
                                  61 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 KQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 88:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yequence 117, Application US/08818112;
Patent No. 6290969;
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Restky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos.Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.98;
98.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 95 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93.9
Best Local Similarity 98.9
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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98104-7092
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                                                                                                                               US-09-056-556-88
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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Gaps
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                                                                                                                                                                    1 ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Netc, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Twardiat, Thomas S.
APPLICANT: Twardiat, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.8%; Score 122; DB 4; Length 28; 100.0%; Pred. No. 1.1e-07; Live 0; Mismatches 0; Indels
                                                        Length 80;
                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center, 701 Fifth Avenue
                                                           Score 392; DB 4; 1
Pred. No. 6.8e-38;
                                             79.7%; St. 100.0%; Pred. No. 0. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210121.411C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 IRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 IRQAGVQYSRADEEQQQALSSQMGF 28
                                                                                                                                                                                                                                                                                                                                                                             Sequence 98, Application US/08818112
Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 21 TELECOMMUNICATION:
                                                                                                                                                                                                                                 81 VQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                     VQYSRADEEQQQALSSQMGF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                           Query Match 79.7's
Best Local Similarity 100.
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
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Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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US-09-056-556-117
                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-818-112-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           79.7%; Score 392; DB 4; Length 80; 100.0%; Pred. No. 6.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
SOFTWARE: PatentIn Release #1.0, Version #1.30
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206) 682-4900
TELEFHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Mak!, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/09/056,556
07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 VQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VQYSRADEEQQQALSSQMGF 80
                                                                                                                                                                                                                                                                                            LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      single
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FILING DATE: 07-APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches | 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-08-818-111-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-056-556-117
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Read, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COPPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 121; DB 4; Length 27
Pred. No. 1.4e-07;
0; Mismatches 2; Indels
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR/RIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATION NUMBER: 02/09/056,556
                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAS: (206) 682-6031
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARATTERICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J
REGISTRATION UNMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPERA: (206) 622-4900
TELEFERA: (206) 682-6031
INFORMATION FOR SEQ ID NO: 96:
                                                                                                                                         FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JMBER: US/09/056,556
07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 GAAGTAAQAAVVRFQEAANKQKQELDE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.68;
92.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.6 Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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US-08-818-112-96
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JS-09-056-556-96
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US-09-056-556-96
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                                                                                                                     APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
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APPLICANT: Seaiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREE: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.8%; Score 122; DB 4; Length 28; 100.0%; Pred. No. 1.1e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CARRATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/056,556 FILING DATE: 07-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 IRQAGVQYSRADEEQQQALSSQMGF 100
                                                              Sequence 98, Application US/09056556 Patent No. 6350456
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Patent No. 6290569
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 28 amino acids
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Best Local Similarity
Matches 25; Conserva
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                                                                                                        GENERAL INFORMATION:
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                                       08-09-056-556-98
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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Query Match 24.6%; Score 121; DB 4; Length 27; Best Local Similarity 92.6%; Pred. No. 1.4e-07; Matches 25; Conservative 0; Mismatches 2; Indels
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STATE: Washington
COUTRY: Gasttle
STATE: Washington
COMPUTER: BADDALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOUTWARE: PASTEM: PC-DOS/WS-DOS
SUSTAMARE: PASTEM: PC-DOS/WS-DOS
STATEM: J3-MAR-1997
CLASSIFICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION NUMBER: 210121.411C6
FELECOMMUNICATION INFORMATION:
TELEPROCE CHARACTERISTICS:
LENGTH: 27 amino acids
STEDAMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
STEDAMATION CALLS
STEDAMAT
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US-08-818-112-95
; Sequence 95, Application US/08818112
; Patent No. 6290969 |
; GENERAL INFORMATION;
APPLICANT: Reed, Steven G.
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Search completed: July 22, 2002, 01:12:22 Job time: 12129 sec

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Sequence 5, Application US/10140045
GENERAL INFORMATION:
APPLICANT: GIGQUEL.
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: ANDERSEN, PETER
APPLICANT: ANDERSEN, PETER B
TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MY
TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A
TITLE OF INVENTION: USING THE SAME
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Matches 100;
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1. (cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2. (cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3. (cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

4. (cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5. (cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

6. (cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7. (cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7. (cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
                                  Compugen Ltd
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US-10-080-170B-639

US-09-116-42A-6

US-09-116-42A-7

US-09-116-492A-7

US-09-116-492A-2

US-10-140-045-7

US-09-116-492A-12

US-10-140-045-8

US-10-140-045-8

US-10-140-045-8

US-10-116-492A-12

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US-09-116-492A-13

US-09-116-492A-13

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US-10-140-045-8

US-09-116-492A-13

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PCT-US02-12100-8
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
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Sequence 5. Application US/09116492A
; Sequence 5. Application US/09116492A
; GENERAL INFORMATION:
    APPLICANT: GICQUEL, BRIGITTE
    APPLICANT: ANDERSEN, PETER
    APPLICANT: ANDERSEN, PETER
    APPLICANT: ANDERSEN, PETER
    TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A
    TITLE OF INVENTION: USING THE SAME
    FILE REFERENCE: 0660-0137-27X
    CURRENT APPLICATION NUMBER: US/09/116,492A
    CURRENT FILING DATE: 1998-07-16
    PRIOR APPLICATION NUMBER: 60/252,631
    PRIOR FILING DATE: 1997-07-16
    NUMBER OF SEQ ID NOS: 39
    SOFTWARE: Patentin version 3:1
    SEQ ID NOS: 39
    SEQ ID NOS: 39
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US-60-360-039-5729
US-60-360-039-5241
US-60-360-039-5241
US-10-155-881-7665
PCT-US02-12378-478
PCT-US02-12378-485
US-10-124-805-485
US-10-124-805-485
US-60-360-039-2947
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APPLICANT: GICQUEL, BRIGITTE
APPLICANT: GICQUEL, BRIGITTE
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: RASMUSSEN, PETER B
TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MY
TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A
FILLE REPERENCE: 0660-0137-27X
CURRENT APPLICATION NUMBER: US/10/140,045
CURRENT FILING DATE: 2002-05-09
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR SEQ ID NOS: 39
         TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A
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APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: ASSMUSSEN, PETER
APPLICANT: RASMUSSEN, PETER
TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MITTLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 0660-0137-27X
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100.0%; Pred. No. 6.5e-19;
tive 0; Mismatches 0;
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100.0%; Pred. No. 6.5e-19;
iive 0; Mismatches 0;
  TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOG
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 0660-0137-27X
CURRENT APPLICATION NUMBER: US/09/116,492A
CURRENT APPLICATION NUMBER: 00/252,631
PRIOR FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 49
                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis US-09-116-492A-6
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Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
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APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: ANDERSEN, PETER
APPLICANT: RASMUSSEN, PETER B
TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MYCOB
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GENERAL INFORMATION:
APPLICANT: COLE, FA.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
CURRENT APPLICATION NUMBER: US/10/080,170B
CURRENT FILING DATE: 2002-06-10
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Pred. No. 3e-43;
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FILE REFERENCE: 0660-0137-27X
CURRENT APPLICATION NUMBER: US/10/140,045
CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US/09/116,492A
PRIOR FILING DATE: 1998-07-16
PRIOR PELICATION NUMBER: 60/252,631
PRIOR FILING DATE: 1997-07-16
NUMBER OF SEQ ID NDS: 39
SOFTWARE: PatentIn version 3.1
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US-10-140-045-5
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99.0%;
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Best Local Similarity
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PRIOR FILING DATE:
NUMBER OF SEQ IDENO
SOFTWARE:
SEQ ID NO 639
LENGTH: 100
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US-10-080-1708-639
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APPLICANT: BERTHET, FRANCIS XAVIER
APPLICANT: RANDERSEN, PETER
APPLICANT: PETERE
APPLICANTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, 1
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 0660-0137-27X
CURRENT APPLICATION NUMBER: US/20/116,492A
PRIOR APPLICATION NUMBER: US/20/116,492A
PRIOR APPLICATION NUMBER: 60/252,631
PRIOR FILING DATE: 1999-07-16
NUMBER OF SEQ. ID NOS: 39
SOFTWARE: PATENTIN VERSION 3.1
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GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170B
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40.0%; Pred. No. 2.6e-12;
Live 20; Mismatches 40;
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APPLICANT: GICQUEL, BRIGITTE; APPLICANT: BERTHET, FRANCOIS-XAVIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium leprae US-10-140-045-28
                                                                                                                                                      ; ORGANISM: Mycobacterium leprae US-09-116-492A-28
                               NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 100
       PRIOR FILING DATE: 1997-07-16
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Best Local Similarity 40.0%
Matches 40; Conservative
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                                                                                                                                 TYPE: PRT
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APPLICANT: ANDERSEN, PETER
APPLICANT: RASMUSSEN, PETER
TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MYCOE
TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, AS W
TITLE OF INVENTION: USING THE SAME
FILE REPERENCE: 060-0137-27X
CURRENT REPERENCE: 060-0137-27X
CURRENT PAPLICATION NUMBER: US/09/116,492A
CURRENT FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 60/252,631
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IVE FRAGMENTS, AS W
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Sequence 7, Application US/10140045

GENERAL INFORMATION:
APPLICANT: GLGQUELL BRIGITIE
APPLICANT: ANDERSEN, PETER
APPLICANT: RASMUSSEN, PETER
APPLICANT: ANDERSEN, PETER
TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGE
TITLE OF INVENTION: USING THE SAME
FILE OF INVENTION UNMBER: US/10/140,045
CURRENT APPLICATION NUMBER: US/09/116,492A
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
SSOFIWARE: PALENTIN VERSION 3.1

LENGTH: 42
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                                                                                                                                                                                                                                                                                                                                  Query Match 41.7%; Score 205; DB 5; Length 42; Best Local Similarity 100.0%; Pred. No. 1.2e-14; Matches 42; Conservative 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 1.2e-14;
les 42; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/116,492A CURRENT FILING DATE: 1998-07-16 PRIOR APPLICATION NUMBER: 60/252,631 PRIOR FILING DATE: 1997-07-16 NUMBER OF SEO ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT , , ORGANISM: Mycobacterium tuberculosis US-10-140-045-7
                                                                                                                                                                                                      TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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                                                                                                                              SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
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APPLICANT: GICOUEL, BRIGITTE
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: BERTHET, FERN
APPLICANT: ROBERION. PETER B
TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MY
TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 0660-0137-27X
CURRENT APPLICATION NUMBER: 05/09/116,492A
CURRENT FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 60/252,631
PRIOR FILING DATE: 1997-07-16
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APPLICANT: ANDERSEN, PETER
APPLICANT: RASMUSSEN, PETER
TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A TITLE OF INVENTION: USING THE SAME
TITLE OF INVENTION: USING THE SAME
TITLE OF INVENTION: USING THE SAME
TITLE OF INVENTION: USING THE SAME
CURRENT APPLICATION NUMBER: US/10/140,045
CURRENT APPLICATION NUMBER: US/09/116,492A
PRIOR APPLICATION NUMBER: US/09/116,492A
PRIOR APPLICATION NUMBER: 60/252,631
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Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 28; Conservative 0; Mismatches 0;
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             PRIOR APPLICATION NUMBER: US/09/116,492A
                                                                                                                                                                                                                                                                                                                                                                                                                                                73 STNIRQAGVQYSRADEEQQQALSSQMGF 100
                            PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 60/252,631
PRIOR FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VEFSION 3.1
SEQ ID NO 12
LENGTH: 28
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GENERAL INFORMATION:
APPLICANT: GICQUEL, BRIGITTE
APPLICANT: BERTHET, FRANCOIS-XAVIE
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Best Local Similarity 100.
Matches 20; Conservative
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SOFTWARE: PatentIn version
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GENERAL INFORMATION:
APPLICANT: GICQUELL
APPLICANT: GICQUELL
APPLICANT: BERTHHE, FRANCOIS-XAVIER
APPLICANT: ANDER&EN, PETER
APPLICANT: RASMUSER, DETER
APPLICANT: RASMUSER, DETER
TITLE OF INVENTION: USING THE SAME
TITLE OF INVENTION: USING THE SAME
FILE REPERENCE: 0650-0137-27X
CURRENT APPLICATION NUMBER: US/09/116,492A
CURRENT FILING DATE: 1998-07-16
PRIOR FILING DATE: 1997-07-16
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APPLICANT: RASMUSSEN, PETER
APPLICANT: RASMUSSEN, PETER B
TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MYCOE
TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, AS W
TITLE OF INVENTION: USING THE SAME
FILE REPERBURE: 060-0137-27X
CURRENT REPERBURE: 060-0137-27X
CURRENT PELLING DATE: 2002-05-08
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40.0%; Pred. No. 2.6e-12;
Live 20; Mismatches 40; Indels
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100.0%; Pred. No. 7.6e-08;
tive 0; Mismatches 0;
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US-09-116-492A-12
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2011-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 12
LENGTH: 100
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                                                                                                                                                                                   TYPE: PRT ORGANISM: Mycobacterium leprae
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Best Local Similarity 40.09
Matches 40; Congervative
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SOFTWARE: Patentin versic
SEQ ID NO 12
LENGTH: 28
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US-09-116-492A-12
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RESULT 15
US-09-116-492A-10
Sequence 10, Application US/09116492A
GENERAL INFORMATION:
APPLICANT: GICOUEL, BRIGITTE
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: WAS WISSEN, PETER B
TITLE OF INVENTION: TOTING THE SAME
FILLE REPRENCE: G660-0137-27X
CURRENT APPLICATION NUMBER: US/09/116,492A
CURRENT FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: US/09/116,492A
CURRENT FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 10
LENGTH: 16
TYPE: PATE OF INVENTION TOTING THE LUMBER OF SEQ ID NO 10
LENGTH: 16
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LENGTH: 16
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SEQ ID NO 10
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TYPE: PATE OF THE CALL OF THE CALL OF THE LUMBER OF SEQ ID NO 10
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                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Mycobacterium tuberculosis
US-10-140-045-8
PRIOR FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 20
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1 MAEMKTDAATLGQEAGNFER.....VQYSRADEEQQQALSSQMGF 100
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum DB seq length: 2000000000
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1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.	
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SUMMARIES

	; Description	hypothetical prote	hypothetical prote	0	hypothetical prote	Q.	hypothetical prote	~	ovtl protein - nem	probable PE protei	small heat shock p	a small heat shock	LcKin kinesin-rela	myosin heavy chain	myosin heavy chain	hypothetical prote		myosin heavy chain	hypothetical prote	conserved hypothet	keratin type II, m	uncharacterized sm	probable chemotaxi	conserved hypothet	keratin, type II,	hypothetical prote	tpr protein - huma	phycocyanin linker	rod-capping linker	apolipoprotein E p
		H70802	T10032	T35661	B59103	T38435	B70600	E70836	T43214	G70857	AB1439	AI1081	A47334	S33068	A59287	F75559	A61231	S21801	T44704	G87116	KRSHL2	696905	G83313	B75310	S05408	B89921	S33124	D29674		JC6549
	DB r			2										7		3		1	2	7						3				7
	Length	100	100	1186	410	75(	103	97	2022	6	6	6	95	527	194(	16.	1961	199	24	24.	206	10	56	. 528	49.	71	2094	8	8	31(
d	Quer <b>y</b> Matc <b>h</b>	98.86	38.0	18.8	18.6	æ	18.1	17.8		17.2	~	17.0	16.6	•		16.2		÷	16.1	•		15.9		15.5	•		•	15.1	15.1	15.1
	Score	486	187	92.5	91.5	80	æ	87.5	8		83.5			81	œ	79.5			79	79	79	78		76.5	97	75.5	75	4	74.5	74.5
	Result No.	1	7	ĸ	4	ស	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

RESULT T10032

hypothetical protein MLCB628.13c - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Accession: 110030
R;Eiglmeder, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A;Title: Use of an ordered cosmid library to deduce the genomic organization of Mycob A;Reference number: 216917; MUID:93188700
A;Reference number: 216917; MUID:93188700
A;Accession: T10032
A;Accession: T10032
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-100 < EIG>A;Cross-references: EMBL:X14967; NID:92370268; PIDN:CAA75210.1; PID:92370280

fcrA protein precu	hypothetical prote	kinesin [imported]	hypothetical prote	hypothetical prote	methyl-accepting c	methyl-accepting c	hypothetical prote	male-enhanced anti	hypothetical prote	hypothetical prote	fcrA 15 protein -	hypothetical prote	ferredoxinNADP+	ferredoxinNADP(+	periplasmic oligop
S57834	F83386	T51932	F96673	T16416	AF2849	E75590	D97626	T42722	T20971	T20978	S52536	D84335	S33479	AB2321	AD1824
7	7	7	~	N	~	~	~	~	~	~	~	~		~	7
387	880	929	1313	1956	754	756	768	1325	2241	2261	388	433	440	440	552
15.1	15.1	15.1	15.1	15.1	15.0	15.0	15.0	15.0	15.0	15.0	14.9	14.9	14.9	14.9	14.9
74.5	74.5	74.5	74.5	74.5	74	74	74	74	7.4	74	73.5	73.5	73.5	73.5	73.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT H70802	1
hypothet	hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV)
C; Date:	C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C; Access	C;Accession: H70802 B.Cole S.T.: Harris: Darkhill II: Carnier: T.: Churcher. C.: Harris: D.: Gordon
; Connoi	. R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandre	Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A; Author	Nacute 593, 257-348, 1370 A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title	A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A; Refere	A;Reference number: A70500; MUID:98295987
A: Status	A.Status: preliminary: nucleic acid sequence not shown; translation not shown
A; Molecu	A; Molecule type: DNA
A; Residu	A; Residues: 1-100 <col/>
A; Cross	A; Cross-references: GB: AL022120; GB: AL123456; NID: 93261558; PIDN: CAA17966.1; PID: 9296
A; Exper:	A;Experimental source: strain H37Rv
C;Genetics:	.cs:
A; Gene: Rv3874	Rv3874
Query Match	
Best Loc Matches	al Similarity 99.0%; 99; Conservative (
ΟÝ	] MAEMKIDAATLGQEAGNEBRISGDLKIQIDQVESTAGSLQGQWRGAAGTAAQAAVKKQE oU
QQ	1 MAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
Qy (	61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
Dp QC	61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100

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Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Recession: B70600; MUID:98295987
A.Accession: B70600
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                  Objections: Schizosaccharomyces power (Schizosaccharomyces power)
C;Species: Schizosaccharomyces power (Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O3-Dec-1999
C;Date: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O3-Dec-1999
C;Accession: T38435
S;McDougall, R.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
S;Refence number: 221793
A;Recreace number: 221793
A;Accession: T38435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Rv3905c - Mycobacterium tuberculosis (strain H37RV)
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                                                                                                                                                                                                                                                                                                              coiled coil protein - fission yeast (Schizosaccharomyces pombe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                                                                                     18.3%; Score 90; 28.2%; Pred. No.
                                                                                       63 NKQK-----QELDEISTNIRQAGVQYSRADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOKOELDEISTNIRQAGVQYSRADEEQQQAL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::|| :: :| :||:||:
550 KQAGENHYSNLSSDYETQIKSLESSL----
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Best Local Similarity
Matches 21; Conserv
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Matches 24; Conserv
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C;Species; Bacillus anthracis
C;Date: 12-NOv-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
C;Accessidn: B59103
C;Accessidn: Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
J. Bacteriol. 181, 6609-6515, 1999
A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbori
A;Reference number: A59091; MUID:99445483
A;Accession: B59103
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1186 <MUR>
A;Cross-references: EMBL:AL034447; PIDN:CAA22420.1; GSPDB:GN00070; SCOEDB:SC7A1.21
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A; Residues: 1-410 COKX>
A; Cross-references: GB:ARP065404; NID:94894216; PIDN:AAD32402.1; PID:94894314
A; Experimental source: strain Sterne
C; Genetics:
A; Genetics:
A; Gene: pX01-98
A; Gene: pX01-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable chromosome associated protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          686 AGRRRECAALVELGERRRAADREKSSVAQ---QLGRLAGQARGAAGEAERSAAAERAQ 742
                                                                                       Gaps
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                                                                                                                                                                                         1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE
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                          Length 100;
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                                                                                    40; Indels
                                                                                                                                                                                                                                                                          61 AANKOKOELDEISTNIRQAGVOYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                              61 AMQDQIRQLESIVDKLNRSGGNYTKTDDEANQLLSSKMNF 100
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0.68;
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|EALDKALTEVEELAE--RLAVAEEMPVEEEPDTAARDRL 779
                          Score 187; DB 2;
Pred. No. 3.7e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: T3561
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, Submitted to the EMBL Data Library, December 1998
A;Reference number: 221585
A;Accession: T35661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: SCOEDB:SC7Al.21
C;Superfamily: chromosome segregation protein SMC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
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                                                                                    20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.6%;
28.0%;
                          38.0%;
40.0%;
                                                                                       40; Conservative
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Matches | 32; Conservative
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                      Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                         g
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A; Residues: 733-866 cDON>
A; Cross-references: GB:J03995; NID:g159874; PIDN:AAA29412.1; PID:g159875
B; Ngozi, E.; Erondu, N.E.; Donelson, J.E.
Submitted to the EMBL Data Library, April 1990
A; Description: Characterization of a myosin-like antigen from Onchocerca volvulus.
A; Reference number: S27825
A; Molecule type: mRNA
B; Residues: 733-874, E', 876-916, 'S', 918-1038, 1040-1047, 'S', 1049-1283, 'E', 1285-1347,'' A; Cross-references: EMBL:M30398; NID:g159876; PIDN:AAA29413.1; PID:g159877
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable PE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-011-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G7085;
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete gence A; Reference number: A70500; MulD:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross_references: GB:AL021287; GB:AL123456; NID:93261508; PIDN:CAA16105.1; PID:e123A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      small heat shock protein of Clostridium acetobutylicum homolog lin0049 [imported] - T C; Species: Listeria innocua C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C; Accession: AB1439 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloe C; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi D.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1752 LDEEKRTMENILHETALQREAIESSLNALERENKELHRNCAQLQQQIAQLELENGNRLIQ 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.7%; Score 87; DB 2; 25.5%; Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.2%; Score 84.5; DE Best Local Similarity 34.9%; Pred. No. 0.6; Matches 29; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AANKOKOELDEISTNIRQAGVOYSRADEEQQQALSSQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 QAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAAGTYVAAD --- AAAASSYTGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ovt1
C;Keywords: leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 25; Conserv
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A; Residues: 733-874, FE, 876-916, 'S', 918-1038,1040-1047, 'S', 1049-1283, 'E', 1285-1363 < ERO>
A; Residues: 733-874, 'E', 876-916, 'S', 918-1038, 1040-1047, 'S', 1049-1283, 'E', 1285-1363 < ERO>
A; Cross-references: GB: M30398
A; Note: the sequence is revised in GenBank entry ONGANTML, release 115, (PIDN: AAA29413.1
R; Donelson, J.E.; Duke, B.O.L.; Moser, D.; Zeng, W.; Erondu, N.E.; Lucius, R.; Renz, A.;
Mol. Biochem. Parasitol. 31, 241-250, 1988
A; Reference number: A54513
A; Accession: A54513
A; Accession: A54513
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL021930; GB:AL123456; NID:g3261524; PIDN:CAA17362.1; PID:e125247
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0287
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C; Species: Onchocerca volvulus.
C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Jun-2000
C; Accession: T41214; A44939; A54513; S27825
R; Triteeraprapab, S.; Richie, T.L.; Tuan, R.S.; Shepley, K.J.; Dinman, J.D.; Neubert, T. R, Triteeraprapab, S.; Richie, T.L.; Tuan, R.S.; Shepley, K.J.; Dinman, J.D.; Neubert, T. A; Triteeraprapab, S.; Affile: Molecular cloning of a gene expressed during early embryonic development in Onc A; Reference number: 222341; MUID:95287898
                                                                                                                                                                                                                                                                                                                                                Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: E70836

A;Accession: E70836

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-97 (COL>
                                                                                                                                                                                                              probable transcription regulator Rv0287 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999
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A/Molecule type: mRNA
A) Residues: 1-202 cPR1
A) Residues: 1-202 cPR1
A) Residues: 1-202 cPR1
A) Reperimental Source: specific_host Homo sapiens
B) Experimental Source: specific_host Homo sapiens
B) Enondu, N.E.; Donelson, J.E.
Mol. Biochem. Parasitol. 40, 213-224, 1990
A) Fittle: Characterization of a myosin-like antigen from Onchocerca volvulus.
A) Reference number: A44939; MUID:90301142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 FAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDVAQANLG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87.5; DB 2; Length 97;
Pred. No. 0.32;
8; Mismatches 43; Indels
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N;Alternate names: myosin-like antigen
              78 QAGVQYSRADEEQQQALSSQMGF 100
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34.9%;
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Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T43214
                                                                                                                                                                                                                                                                                                                              C; Accession: E70836
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--- ESTAGSLOGOWRGAAGTAA 51

955 97

Length 955;

5,

DB

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Myosin heavy chain - fluke (Schistosoma mansoni) (fragment)
Nylternate names: surface antigen, 200K
C;Species: Schistosoma mansoni
C;Date: 22-Nov-1993 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C;Accession: S33068
R;Soisson, L.M.A.; Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M.A.;Reference number: A46514; MUID:9305636
A;Title: Induction of protective immunity in mice using a 62-kDa recombinant fragment A;Reference number: A46514; MUID:9305636
A;Molecule type: MRNA
A;Residues: 1-527 <SOI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI>A;COI
A;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA;COICA
A;Title: Molecular characterization of a kinesin-related antigen of Leishmania chagas A;Reference number: A47334; WUID:93133867
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R;Weston, D.S.; Schmitz, J.; Kemp, M.: Kunz, W.
Mol. Blochem. Parasitol. 58, 161-164, 1993
A;Title: Cloning and sequence characterization of a complete myosin heavy chain cDNA A;Reference number: A59287; MUID:93211444
A;Accession: A59287
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                         A; Experimental source: MHOM/BR/82/B4-2.C1
A;Note: sequence extracted from NCBI backbone (NCBIN:122864, NCBIP:122865)
S; Superfamilly: unassigned kinesin-related proteins; kinesin motor domain homology C; Keywords: ATP; nucleotide binding; P-loop
F;13-998/Domain: kinesin motor domain homology <KMOT>
F;12-129/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Schistosoma mansoni
C;Date: 09-Jun_2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAA 62
                                                                                                                                                                                       A; Residues: 1-955 <BUR>
A; Residues: 1-955 <BUR>
A; Cross-references: GB:L07879; NID:g308884; PIDN:AAA29254.1; PID:g308885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 QAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELASQLEATAAAKSSAEQDR - - ENTRAALEQQLRDSEERAAELASQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.6%; Score 81.5; C
29.2%; Pred. No. 14;
Live 15; Mismatches
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Best Local Similarity
Matches 31; Conserv
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Best Local Similarity
                                                                                                                 A; Status: preliminary
                                                                                                                                                            DNA
                                                                              A; Accession: A47334
                                                                                                                                                        A; Molecule type:
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                           A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ov, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a small heat shock protein of Clostridium acetobutylicum homolog lmo0056 [imported] - Li
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession Al1081
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
5cience 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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R; Burns Jr., J.M.; Shreffler, W.G.; Benson, D.R.; Ghalib, H.W.; Badaro, R.; Reed,
Proc. Natl. Acad. Sci. U.S.A. 90, 775-779, 1993
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-97 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC95282.1; PID:g16412470; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A47334
LCKin kinesin-related antigen - Leishmania chagasi (fragment)
C;Species: Leishmania chagasi
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
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Pred. No. 0.74;
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Best Local Similarity 25.5%; Pred. No. 0.74
Matches 26; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches
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25.5%;
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849-852, 2001
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A; Residues: 1-97 <GLA>
                                                                                                                                                                                   A; Accession: AB1439
A; Status: preliminary
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Best Local S
Matches 26
Science
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5,

Gaps

45;

Length 527;

Lys

residue 346 as

-1

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Nypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75559
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
K;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A;S550; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-163 <WHI>
A; Residues: 1-163 <WHI>
A; Cross-references: GB: AE001873; GB: AE000513; NID: g6457764; PIDN: AAF09701.1; PID: g645777
B; Experimental source: Strain R1
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAA 62
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A; Molecule type: mRNA
A; Residues: 1-1940 (MES>
A; Cross-references: GB:L01634; PIDN:AAA29905.1
A; Experimental source: strain Brazilian LE
C; Genetics:
A; Gene: MYH
A; Gene: MYH
C; Superfamily: myosin heavy chain; myosin motor domain homology
F; 82-752/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                    Length 1940;
                                                                                                                                                                                                                                                                                                    Query Match
16.5%; Score 81; DB 2; Length 194
Best Local Similarity 21.9%; Pred. No. 33;
Matches 21; Conservative 24; Mismatches 45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 1095 KELQTRIQELEEDLEAERAARSKAEKSRQQ-LESEL 1129
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Job time: 10123 sec
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A; Map position: 1
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OM protein - protein search, using sw model

Run on: July 22, 2002, 01:13:29 ; Search time 23.86 Seconds
(without alignments)
162.278 Million cell updates/sec

102.2/0 MILIION CELL UPUALES
US-09-462-480-5
cre: 492
1 MAEMKTDAATLGGEAGNFER.....VQYSRADEEQQQALSSQMGF 100

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	E	033084 mycobacteri	_	-	S	Q9cbs6 mycobacteri		-			P12270 homo sapien		Q9hhc2 halobacteri		anabaena	P58558 anabaena sp	drosophil		P11396 mastigoclad	P22251 campylobact	068032 rhodobacter	P40457 saccharomyc					61	P15492 vibrio chol	Ŋ	6	P42638 schistosoma	18	P33741 halobacteri
SUMMARIES	ID	CF10_MYCTU	CF10_MYCLE	ES6D_MYCTU	ANT1_ONCVO	KINL_LEICH	YT27_MYCLE	MYH9_HUMAN	K2M2_SHEEP	FENR_ANAVA	MYH9_RAT	TPR_HUMAN	PYS1_ANASP	GRPE_HALME	G160_MOUSE	FENR_ANASO	FENR_ANASP	KINH_DROME	PHP_DROME	PYS1_MASLA	FLA2_CAMJE	SBCC_RHOCA	YIO9_YEAST	C11D_HUMAN	K2M3_SHEEP	BPHC_PSES1	MYH9_CHICK		HLYB_VIBCH	PYS1_SYNEL	Y4FA_RHISN		MCPD_ENTAE	HTR1_HALN1
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P33292 pichia past	P75247 mycoplasma	Q13751 homo sapien	P80703 galleria me	P13276 manduca sex	P02567 caenorhabdi	P12608 synechococc	P21758 bos taurus	Q9pg89 xylella fas	P39285 escherichia	Q9nqx4 homo sapien	P12845 caenorhabdi
PEX5_PICPA	CLPB_MYCPN	LMB3_HUMAN	APL3_GALME	APL3_MANSE	MYSD_CAEEL	IRPA_SYNP7	MSRE_BOVIN	RMUC_XYLFA	YJEP_ECOLI	MY 5C_HUMAN	MYSC_CAEEL
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# ALIGNMENTS

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SEQUENCE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLIKE-21128732; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruthert S., Seeger K., Simon S., Simmonds M., Selton J., Squares R., Barrell B.G.;
                                                                                                                                                                             Gaps
                                                                                                                                                                                                 2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61
                                                                                                                                                                                                                          1 AEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 60
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                                                                                                                                                                           ;
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  Score 481; DB 1; Length 99;
Pred. No. 4.2e-37;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
859B484F7EFE5A8A CRC64;
                                                                                                            99 AA; 10663 MW; EBCAE6A996C5489D CRC64;
                                                                                                                                                                                                                                                  62 ANKOKOELDEISTNIROAGVOYSRADEEQOQALSSOMGF 100
                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
10 kba culture filtrate antigen cfpl0 homolog,
MLO050 OR MLCB628.13C.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                          AA.
 or send an email to license@isb-sib.ch).
                       EMBL, AF004671; AAC83445.1; -. EMBL, AAC022120; CAA17966.1; -. EMBL, AE007190; AAK48356.1; -. TIGR; MT3988; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y14967; CAA75210.1; -.
EMBL; AL583917; CAC29558.1; -.
Leproma; ML0050; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 AA; 10833 MW;
                                                                                                                                                  97.8%;
99.0%;
                                                                                                                                                                          98; Conservative
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                         Tuberculist; Rv3874; -.
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                                                                                                                                                   Query Match
Best Local Similarity
                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=TN;
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INIT_MET 0
SEQUENCE 99 AA;
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STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s:
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                                                                                                                                                                                                  1 AEMITEAAILTQQAAQFDQIASGLSQERNFVDSIGQSFQNTWEGQAASAALGALGREFDEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gold S.T., Brosch R., Pathill J., Garnier T., Churcher C., Harris I Gordon S.Y., Brosch R., Pathill J., Garnier T., Churcher C., Harris I Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Squares R., Schlon S., Squares S., Squares R., Techlon S., Stoares S., Squares R., Poliology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                        2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA
                                                                               ;
           Length 99;
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103 Aa; 10460 MW; 3994E272A7BDFF02 CRC64;
                                                                               40;
                                                                                                                                                                                                                                                                                                     62 ANKOKOELDEISTNIROAGVOYSRADEEQOQALSSOMGF 100
       37.0%; Score 182; DB 1; 39.4%; Pred. No. 3.9e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                           61 MQDQIRQLESIVDKLNRSGGNYTKTDDEANQLLSSKMNF
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                                                                            20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103
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RV3905C OR MT4024 OR MTCY15F10.06.
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MEDLINE-98295987; PubMed-9634230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
Query Match
Best Local Similarity 39.4%
Matches 39; Conservative
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1812 LTNKQREEYDKFAQNMRTEKIQIERIIENRERSLKSRI 1849
                                                                 KINL_LEICH
P46865;
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MEDLINE-95287898; PubMed-7770081;
Tritecrapraph S., Richle T.L., Tuan R.S., Shepley K.J., Dinman J.D.,
Neubert T.A., Scott A.L.;
"Molecular cloning of a gene expressed during early embryonic development in Onchocerca volvulus.";
Mol. Blochem. Parasitol. 69:161-171(1995).
                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Gaps
                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LGQEAGNFERISGDLKTQIDQVESTAGSLQGQ----WRGAAGTAÄQAAVV-----RFQE 60
                                           4 MKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAAN 63
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                          :::|:|:|:|:|:|:|:|
LRVEPAVMQGFAASLDGAAEHLAVQLAELDAQVGQMLGGWRGASGSAYGSAWELWHRGAG
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 733-866 FROM N.A. MEDLINE=89127417; PubMed=2464764; MEDLINE=89127417; PubMed=2464764; Donelson J.E., Duke B.O.L., Moser D., Zeng W., Erondu N.E., Luclus R., Renz A., Karam M., Flores G.Z.; "Construction of Onchocerca volvulus cDNA libraries and partial characterization of the CDNA for a major antigen."; Mol. Biochem. Parasitol. 31:241-250(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.7%; Score 87; DB 1; Length 2022; 25.5%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
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COILED COIL (POTENTIAL).
MW; B7132AACF1520317 CRC64;
                      Indels
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Pred. No. 0.098;
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                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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     23.1%; Pred. No.
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                                                                                       64 KOKOELDEISTNIRQAGVQYSRADEEQQQAL 94
                                                                                                           EVQLGLSMLAAAIAHAGAGYQHNETASAQVL 97
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                                                                                                                                                                                                                                                                         Onchocerca.
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                      21; Conservative
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01-NOV-1995 (Rel. 32,
30-MAY-2000 (Rel. 39,
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HSSP; P02633; 3ICB.
Antigen; Coiled coil
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2022 AA;
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Matches 25; Conserv
         Best Local Similarity
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P21249;
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                                                                                                                                                         ANT1_ONCVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                             67
                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EMKTDAATLGQEAGNFERISGDLKTQIDQV------ESTAGSLQGQWRGAAGTAA 51
                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5669;
                                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>
۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).
7 x 39 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                   Burns J.M. Jr., Shreffler W.G., Benson D.R., Ghalib H.W., Badaro Reed S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular characterization of a kinesin-related antigen of
Leishmania chagasi that detects specific antibody in African and
American visceral leishmaniasis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 81.5; DB 1; Length 955;
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSP; P1,112.

InterPro; IPR001752; ...

InterPro; IPR00125; Kinesin; 1.

SMART; SM00129; KISC; 1.

PR0SITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.

PROSITE; P550067; KINESIN_MOTOR_DOMAIN2; 1.

PROSITE; P550067; KINESIN_MOTOR_DOMAIN2; 1.

PROSITE; P550067; KINESIN_MOTOR_DOMAIN2; 1.

COILED COIL (POTENTIAL).

COILE COIL (POTENTIAL).

COILE COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106168 MW; 8CA76815BE84C6E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 QAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
DEVELOPMENTAL STAGE: PREDOMINANT IN AMASTIGOTES.
                                                    01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
Kinesin-like protein K39 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PARTIAL)
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-MHOM/BR/82 / ISOLATE BA-2;
MEDLINE-93133867; PubMed-8421715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L07879; AAA29254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 31; Conserva
                                                                                                                                                                                                       Leishmania chagasi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                955 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                   MEDLINE-21128732; PubMed=11234002;
Cole S.T., Eiglmeder K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyk S., Hornsby T., Jagels K., Lacroix C., MacLean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AEMKTDAATLGQEA----GNFERISGDLKTQIDQVESTAGS----LQGQWRGAAGTAA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MXH9_HUMAN STANDARD; PRT; 1960 AA.

92579; 06805; 1
15-DEC-1998 (Rel. 2), Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
Myosin heavy obdin, nonmuscle type A (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo <mark>sapiens (Human).</mark>
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.1%; Score 79; DB 1; Length 245; 25.7%; Pred. No. 1.9; tive 20; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 QAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEE---QQQALSSQ 97
                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 protein; Complete proteome.
245 AA; 27087 MW: C984D9A5FA49697A CRC64;
                                                                                                                                                                                                                                                                                                                 SIMILARITY: STRONG, TO M.TUBERCULOSIS RV2927C.
                                                                                                                                                                                                                                                                                           "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                        245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AL583923; CAC30614.1; ALT_INIT.
Leproma; MI1661; -
Hypothetical protein; Complete proteom
SEQUENCE 245 AA; 27087 MW; C984D9A
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL023635; CAA19194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 25.77
Matches 28; Conservative
        STANDARD;
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                            NCBI_TaxID=1769;
       YT27_MYCLE
Q9CBS6; 069467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606
                                                                                                                                                                                                                                                                     squares S., St
Barrell B.G.;
                                                                                                                                                              STRAIN-TN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type MYH9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYH9_HUMAN
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RA PUDLINE-20077165; pubMed-110591208.

RA PUDLIAN - 1, WINTA RA. COLLING JE. B. BURKKACH, R. BEDDER, C. BILDER, C. BALLER, C. MAIR L. J. ANIECOUGH R. N. BEDDER, C. BALDER, C. BALLER, C. BALDER, C. BALLER, C.
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us-09-462-480-5.rsp

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                                                                                                                                                                                                                                                                                                      Seri M., Cusano M., Gangarossa S., Caridi G., Bordo D., Lo Nigro C., Ghiggeri G.M., Ravazzolo R., Savino M., Del Vecchio M., d'Apolito M., Iolascon A., Zelante L.L., Savola A., Balduini C.L., Noris P., Magrini U., Belletti S., Heath K.E., Babcock M., Glucksman M.J., Aliprandis E., Bizzaro N., Desnick R.J., Martignetti J.A.; "Mutations in MYH9 result in the May-Hegglin anomaly, and Fechtner and
                                                                                                                                                                             VARIANTS MHA ILE-1155 AND LYS-1841.
MEDLINE-20428193; PubMed=10973260;
Kelley M.J., Jawien W., Ortel T.L., Korczak J.F.;
"Mutation of MYB9, encoding non-muscle myosin heavy chain A, in May-Hegglin anomaly.";
Nat. [Genet. 26:106-108(2000).
-i- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                               SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY
                                     VARIANTS MHA/FTNS/SBS K-93; C-702; C-1165; H-1424 AND K-1841. MEDLINE-20428192; PubMed-10973259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
nmuscle myosin MYH9.";
. J. Hum. Genet. 67:1121-1128(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin_N.
Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002017; Spectrin.
InterPro; IPR001609; myosin_head.
Pfam, PF00612; IQ; 1.
                                                                                                                                          Sebastian syndromes.";
Nat. Genet. 26:103-105(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 282215; CAB05105.1; -. EMBL; M81105; AAA59888.1; -. EMBL; M69180; AAA61765.1; -. EMBL; M31013; AAA36349.1; -. HSSP; P08799; ILVK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000048;
InterPro; IPR004009;
  nonmuscle myosin MYH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153640;
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                                                                                                                                                                                                                                                                                  CAPPING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605249;
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Gaps
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type II microfibrillar, component 7C.
Ovis arises (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                       71;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1960;
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
SPRODO355; myosin_head; 1.
SMART; SM0015; IQ; 1.
SMART; SM0242; MYSc; 1.
PROSITE; PS5096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
Colled coll; Alkylation; Multigene family; Disease mutation;
                                                                                                                                    ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                       29; Indels
                                                                                                                                                                                                                                                                                                                                                                       588F84BB8C106E6F CRC64;
                                                                                                                                                                                                                                                              /FTIG=VAR_010796.
E -> K (IN MHA).
/FTIG=VAR_010797.
EAI -> RGH (IN REF. 3).
T -> S (IN REF. 3).
T -> M (IN REF. 4).
C -> Y (IN REF. 4).
                                                                                               IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 AGSLQGQWRGAAGTAAQAAVVRFQE------AANKQ---
                                                                                                                                                                                            R -> H (IN DFNA17).
/FTId=VAR_010793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E -> EE (IN REF. 2
T -> A (IN REF. 2)
S -> G (IN REF. 2)
                                                                                                                                                                                                                                                                                                                              KG -> GR (IN REF.
                                                                                                                                                                  /FTId=VAR_010791.
                                                                                                                                                                                                                                            /FTId=VAR_010795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KQELDEISTNIRQAGVQYSRADEEQQQALSSQ 97
                                                                                      MYOSIN HEAD-LIKE
                                                                                                                   ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                                                                                                          R -> C (IN FTNS)
/FTId=VAR_010792
                                                                                                                                                                                                                        FTIG=VAR_010794
                                                                                                                                                                                                                                                       D -> H (IN FTNS)
                                                                                                                                                         N -> K (IN MHA)
                                                                                                                                                                                                                 T -> I (IN MHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 AA
                                                                                                                                                                                                                                                                                                                                                                                                    16.0%; Score 78.5; 21.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                      23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LGQEAGNFERISGDLK --- TQIDQV ------
                                                                                                                                                                                                                                                                                                                                                                          Σ
                                                                                                                                                                                                                                                                                                                                                                        226531
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 21.79
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                      778
808
1926
181
676
694
704
                                                                                                                                                                                                                 1155
                                                                                                                                                                                                                                    1165
                                                                                                                                                                            702
                                                                                                                                                                                              705
                                                                                                                                                                                                                                                       1424
                                                                                                                                                                                                                                                                          1841
                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                  1240
1350
1764
1771
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                                                                                                                                             704
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660
869
                                                                                                                                                                            702
                                                                                                                                                                                               705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K2M2_SHEEP
P15241;
                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                             Deafness
                                                                                      DOMAIN
DOMAIN
DOMAIN
NP_BIND
DOMAIN
MOD_RES
MOD_RES
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                                                                                                                                                                            VARIANT
                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                        /ARIANT
                                                                                                                                                                                                                                                                          /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
K2M2_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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5

[1] SEQUENCE.

myosin\_head; 1.

PF02736; myosin\_head; PF02736; Myosin\_N; 1.

P fam; Pfam;

31.g

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ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 NFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNI 76
                                                                                                                                                                                                               PRESENT IN ALL VERFEBRATE EPITHELIAL CELLS.

-!- MISCELLANBOUS: THE LOW-SULFUR PROTEINS, DERIVED FROM THE MICROFIBRILLAR FRACTION OF WOOL EXTRACTS, ARE COMPOSED OF TWO FAMILIES, EACH CONSISTING OF 4 HOMOLOGOUS SUBUNITS: THE TYPE I COMPONENTS (8C-1, 8C-2, 8A & 8B) AND THE TYPE II COMPONENTS (5, 7A, 7B, AND 7C).

-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                      Sparrow L.G., Robinson C.P., McMahon D.T.W., Rubira M.R.;
The amino acid sequence of component 7c, a type II intermediate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAINS-PCC 7937 / ATCC 28413;
Mannan R.M., Matthijs H.C.P., Pakrasi H.B.;
"Cloning and molecular characterization of the petH gene in the cyanobacterium Anabaena variabilis ATCC 29413.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.4%; Score 76; DB 1; Length 491; 22.9%; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A801771FE3831ABE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (Rel. 41, Last annotation update)
Ferredoxin--NADP reductase (EC 1.18 1.2) (FNR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Intermediate filament; Coiled coil; Keratin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COIL 2.
C -> G OR S.
C -> S.
F -> Y.
S -> D OR N.
Q -> H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COIL 1B.
LINKER 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINKER 1.
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MEDLINE-90026244; PubMed-2803231;
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InterPro; IPR001664; IF.
InterPro; IPR003054; Keratin_II.
                                                                    filament protein from wool,";
Biochem. J. 261:1015-1022(1989).
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PROSITE; PS00226; IF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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Q44549;
01-NOV-1997 (
01-NOV-1997 (
01-MAR-2002 (
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SEQUENCE
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FENR_ANAVA
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-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALCHALLCAL COLLED COLLS.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SNQGAFEGAANVESGSRVFVYEVVGMRQNEETDQTNYPIRKSGSVFIRVPYNRMNQEMQR 61
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Choi O.H., Park C., Itoh K., Adelstein R.S., Beaven M.A.;
Submitted (JUL-1995) to the EMBL/Cenbank/DDB datebases.
-!- FUNCTION: CELLULA WYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
                                                                                                                                -! - SUBCELLULAR LOCATION: MAY BE BOUND TO THE THYLAKOID MEMBRANE OR
                                                                                                                                                           ANCHORED TO THE THYLAKOID-BOUND PHYCOBILISOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
LoCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases. 
 -!- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
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InterPro; IPR001685; CpcD.
InterPro; IPR0013097; FAD_binding.
InterPro; IPR001433; Oxidored_FAD.
Pfam; PF001677; FAD_binding; 1.
Pfam; PF001677; FAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
ProDom; PF00175; NAD_binding; 1.
ProDom; PF00175; PR0071; FPNCR.
ProDom; PD002828; CpcD; 1.
Oxidoreductase; Flavoprotein; NADP; FAD; Thylakoid; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 440;
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660BAA2DCF59BBB6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.3%; Score 75.5; DI 30.0%; Pred. No. 7.3; tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              -!- SIMILARITY: WITH OTHER SPECIES FNR.
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48826 MW;
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Best Local Similarity 30.0%
Matches 18; Conservative
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                                                             ferredoxin + NADPH.
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Q62812;
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RESULT 12
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ID PYS1_ANASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93064711; PubMed-1437155; Mitchell P.J., Cooper C.S.; The human tpr gene encodes a protein of 2094 amino acids that has extensive coiled-coil regions and an acidic C-terminal domain."; Oncogene 7:2329-2333(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------KQELDEISTNIRQAGVQYSRADEEQQQALSSQ 97
                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1961;
                                                                                                                                                                                                                                                                                                                                             ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
W; 9B9876D9681FB19E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels
                                                                                                                                                                                                                                                          PROSITE; PS50096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                             CÓILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                         MYOSIN HEAD LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0cT-1989 (Rel. 12, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-0cT-2001 (Rel. 40, Last annotation update)
Nucleoprotein TPR.
                                                                                                                                                                                                                                                                                                                                                                                                15.3%; Score 75.5; DB 22.8%; Pred. No. 35; ative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2349 AA.
                                                                                                                                                                                                                                                                               Coiled coil; Alkylation; Multigene family.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN
                                                                                                                         InterPro; IPR000048; IQ.
InterPro; IPR000048; IQ.
InterPro; IPR0019298; Myosin_N.
InterPro; IPR001509; Myosin_Leail.
InterPro; IPR001509; Myosin_head.
Pfam; PF000613; IQ; 1.
Pfam; PF001063; Myosin_Head; 1.
Pfam; PF01576; Myosin_Lail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000135; Myosin_head; 1.
SWART; SM0015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS, AND CHARACTERIZATION.
MEDLINE-95096166; Pubmed-7798308;
                                                                                                       EMBL; U31463; AAA74950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                  AA;
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                   P10587; 1BR1
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704
1961
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SEQUENCE
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                                                                                                                                                                                    Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T., Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.; "Tpv. a large coiled coil protein whose amino terminus is involved in activation of encogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";

J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                                                                                                                                                                                                                                                COMPONENTS, INCLUDING P62.
--- TISSUE SPECIFICITY: HIGHEST IN TESTIS, LUNG, THYMUS, SPLEEN AND BRAIN, LOWER LEVELS IN HEAST, LIVER, AND KIDNEY.
--- DISEASE: INVOLVED IN TUMORIGENIC REARRANGEMENTS WITH THE MET, TRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 DAATLGQEAGNFE-----RISG------DLKTQIDQVESTAGSLQGQWRGAA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.2%; Score 75; DB 1; Length 2349; 26.2%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNVEQYQAMVISLEESLINKEKQVIEEVRKNIE---VRLKESAEFQTQ 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265600 MW; AFDD6885CEDCA9EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 GTAA--QAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Mismatches
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POLY-ASP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COILED
                                                                                                                                                                           MEDLINE-88262257; PubMed-3387099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X66397; CAA47021.1; -. EMBL; Y00672; CAA68681.1; -. PIR; S00928; S00928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coiled coil; Proto-oncogene;
Nuclear protein; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Conservative
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1196
1196
11354
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1476
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1933
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12295
2295
2349 AA
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                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=87246520; PubWed=3109890;
Belknap W.R., Haselkorn R.;
"Cloning and light regulation of expression of the phycocyanin operon of the cyanobacterium Anabaena.";
         01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Phycobilisone 8.9 kDa linker polypeptide, phycocyanin-associated, rod
CL-8.9/R) (Rod capping linker protein).
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-21134097; PubMed-11237320;
Cai Y.A., Murphy J.T., Wedemayer G.J., Glazer A.N.;
"Recombinant phycobiliproteins. Recombinant C-phycocyanins equipped with affinity tags, oligomerization, and biospecific recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 GOWRGAAGTAAQAA--VVRFQEAANKQKQELDEISTNIRQAG-----VQYSRADEEQQQ
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-21595285; PubMed-11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashina K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shinpo S., Sugimoto M., Takazawa M., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
-1- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Indels
                                                                                     Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phycobilisome; Photosynthesis; Complete proteome.
SEQUENCE 80 AA; 8895 MW; 52DF2D7DEF5444D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.1%; Score 74.5; DB 1; 35.6%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
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                                                                                                                                                                                                                                                                                                         Anal. Biochem. 290:186-204(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X05239; CAA28865.1; -. EMBL; AF178757; AAG09319.1; -. EMBL; AP003582; BAB72489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; D29674; D29674.
InterPro; IPR001685; CpcD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD002828; CpcD; 1.
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                                                                                                                                                                                                        EMBO J. 6:871-884(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01383; CpcD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                NCBI_TaxID=103690;
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16-OCT-2001
16-OCT-2001
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GRPE_HALME
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                                                                                                                                                                                                                                                                                         Kazi A.S., Nair C.K.K.;
"Organization of the DNAK locus of the archeabacterial halophile,
"Organization of the DNAK locus of the archeabacterial halophile,
Haloferax mediterranei.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF
DNAK HELPES TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECYCLE
MORE EFFICIENTLY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GRPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoantigen.";

DNA Seq. 7:71-82(1997).

-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR

-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR

-!- FUNCTION EDEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLOGICALLY

DETECTABLE MALE ANTIGEN (SDM).

-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN BE
                                                                    Halobacterium mediterranei (Haloferax mediterranei).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloferax.
NCBI_TaxID=2252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CD-1; TISSUE-Testis;
MEDLINE-97217683; PubMed=9063644;
Kondo M., Sutou S.;
"Cloning and molecular characterization of cDNA encoding a mouse male-enhanced antigen-2 (Mea-2): a putative family of the Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26673 MW; 1B2959577A2D1FC7 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Golgin-160 (Male-enhanced antigen-2) (MEA-2).
GOLGA3 OR MEA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.1%; Score 74.5; DB Best Local Similarity 25.0%; Pred. No. 4.8; Matches 18; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00773; GRPEPROTEIN.
PROSITE; PS01071; GRPE; FALSE_NEG.
GrpE protein (HSP-70 cofactor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF069527; AAC23114.1; -.
InterPro; IPR000740; GrpE.
Pfam; PF01025; GrpE; 1.
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 33500 / R4;
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129 KKROQOIKERAT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 NKQKQELDEIST 74
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P55937;
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Hermoso J.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                             201 AAAAQHQDQNQEANGEVRSRRDSICSSVSMESSLAEPQDELLQILKDKRRLEGQVEALSL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sancho J., Peleato M.L., Gomez-Moreno C., Edmondson D.E.; "Purification and properties of ferredoxin-NADP+ oxidoreductase from the nitrogen-fixing cyanobacteria Anabaena variabilis.";
                                                                                                                                                                                                                                                                                              26; Gaps
                                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fillat M.F., Bakker H.A.C., Weisbeek P.J.;
"Sequence of the ferredoxin-NADP(+)-reductase gene from Anabaena PCC
          LEYDIG CELLS, SPERMATGGONIA, OR SPERMATOCYTES.
SIMILARITY: HIGH, TO HUMAN GOLGIN-160.
CAUTION: IT IS UNCERPAIN WHETHER MET-1, MET-19 OR MET-30 IS THE
                                                                                                                                                                                                                                                                                                                       -----SLQGQWRGAAG
  NO EXPRESSION IN
                                                                                                                                                                                                                                                                                                                                                                                    261 EASQA----LQEKAELQAQ-LAALSTRL-QAQVEHSHSSQQKQDSLSSEV 304
                                                                                                                                                                                                                                                                     Score 74; DB 1; Length 1325;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                              34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anabaena sp. (strain PCC 7119).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                      POLY-ALA.
W; 3230636962C687B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      49 TAAQAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQM
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MEDLINE-97045988; Pubmed-8890910;
Serre L., Vellieux F.M.D., Medina M., Gomez-Moreno C.,
  SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1994 (Rel. 30, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ferredoxin--NADP reductase (EC 1.18.1.2) (FNR)
                                                                                                                                                                                                                                                           15.0%; Scor.
24.5%; Pred. No. 31,
... 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 AA
                                                                                                                                                                                                                                                                                                                      9 ATLGQEAGNFERISGDLKTQIDQVESTAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arch. Biochem. Biophys. 260:200-207(1988).
                                                                                                                                                                                                           Spermatogenesis; Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 18:7161-7161(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 137-440 FROM N.A. MEDLINE-91088322; Pubmed-2124680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=1403.46;
MEDLINE-88132819; PubMed=3124746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-93344523; PubMed-8343609;
                                                                                                                                                                                                                                  149880 MW:
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(Rel. 30, Last sequ
(Rel. 41, Last anno
 FOUND IN SPERMATIDS DURING
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Best Local Similarity 24.53
Matches 27; Conservative
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1325 AA;
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                                                INITIATOR.
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This small the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7119 ferredoxin NADP+ reductase revealed by x-ray crystallography."; Proteins 38:60-69(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: MAY BE BOUND TO THE THYLAKOID MEMBRANE OR ANCHORED TO THE THYLAKOID-BOUND PHYCOBILISOMES.
-i- SIMILARITY: WITH OTHER SPECIES FNR.
-i- SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER PROTEIN CPCD.
                                                                                                                                                                                                                                                                         Martinez-Julvez M., Hermoso J., Hurley J.K., Mayoral T., Sanz-Aparicio J., Tollin G., Gomez-Moreno C., Medina M.; Krôle of Argl00 and Arg264 from Anabaena PCC 7119 ferredoxin-NADP-reductase for optimal NADP+ binding and electron transfer."; Biochemistry 37:17680-17691(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ferredoxin-NADP+ reductase and ferredoxin from the cyanobacterium Anabaena: looking for the elusive ferredoxin molecule.";
Acta Crystallogr. D 56:1408-1412(2000).
-i- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized
Fontecilla-Camps J.C., Frey M.;

**ray structure of the ferredoxin:NADP+ reductase from the cyanobacterium Anabaena PCC 7119 at 1.8-A resolution, and crystallographic studies of NADP+ binding at 2.25-A resolution.";
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MEDLINE=20508220; Pubmed=11053838;
Morales R., Kachalova G., Vellieux F., Charon M.-H., Frey M.;
"Crystallographic studies of the interaction between the
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ProDom; PD002828; CpcD; 1.
Oxidoreductase; Flavoprotein; NADP; FAD; Thylakoid; Membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 137-440.
MEDLINE=20114461; PubMed=10651039;
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InterPro; IPR001433; Oxidored_FAD.
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PIR; S13103; S13103.
PIR; S33479; S13479.
PIR; S15150; S15150.
PDB; IQUE; 15-MAY-97.
PDB; IBJK; 18-NOV-98.
PDB; IBJK; 15-DEC-99.
PDB; IEWY; 07-FEB-01.
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Length 440;

DB 1;

14.9%; Score 73.5;

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Best Local Similarity 30.0%; Pred. No. 11;
Matches 18; Conservative 15; Mismatches 22; Indels
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Search completed: July 22, 2002, 01:20:15 Job time: 406 sec

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X MEDLINE=9700351; PubMed=8843436;

A Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,

A Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,

A Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,

A Kinashi H., Hopwood D.A.;

T a set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

R EMBL, ALO34447; CAA22420.1; -.

R InterPro; IPR003439; ARC_Transportr.

R InterPro; IPR003405; SMC_C.

R InterPro; IPR003405; SMC_N.

R InterPro; IPR003405; SMC_N.

R InterPro; IPR003405; SMC_N.

R InterPro; PR003405; SMC_N.
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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NCBI_TaxID=1902;
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1 MAEMKTDAATLGQEAGNFER.....VQYSRADEEQQQALSSQMGF
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Copyright (c) 1993 - 2000 Compugen Ltd
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Matches 29; Conserv
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                NCBI_TaxID=4896;
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J. Bacteriol. 181:6509-6515(1999).
                                                                                   Gaps
                                                                                                      2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTA--AQAAVVRFQ 59
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Pfam; PF02463; SMC_N; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
SEQUENCE 1186 AA; 128723 MW; CB11027815373E99 CRC64;
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 87.3 KDA PROTEIN C27D7.02C IN CHROMOSOME I. SPRC27D7.02C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 AA; 45798 MW; F10BC04607575C7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                  Plasmid virulence plasmid PX01.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                  18.8%; Score 92.5; DB 2; 32.3%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                   60 EAANKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQM 98
                                                                                                                                                                                                                                    410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 AA
                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.6%; Score 91.5; D 28.0%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
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                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99445483; PubMed=10515943;
                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF065404; AAD32402.1; -. InterPro; IPR001680; WD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Conservative
                                                                    Best Local Similarity 32.3
Matches 32; Conservative
                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                        Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1392;
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-STERNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid.
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                                                                                                                                                                                                                                                                                                                                                                                            20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 QEAG--NFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 97;
                                                                                                                                                                                                                                                                                                                                         DB 3; Length 750;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
McDougall R., Wood V., Barrell B.G., Rajandream M.A.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases-!-SIMILARITY: SOME, TO THE C-TERMINAL OF YEAST USO1. EMBL; AL009227; CAA15821.1; --Interpro; IRR000237; GRIP. Pfam; PF01465; GRIP; I. Hypothetical protein.
                                                                                                                                                                                                                                                      87264 MW; A469AD95C5787042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; Complete proteome.
AA; 9778 MW; 927527DA610A1637 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 9.8 ROTEIN.
RV0287 OR MTV035.15.
                                                                                                                                                                                                                                                                                                                                                                                         23;
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                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                   No. 5.9;
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                                                                                                                                                                                                                                                                                                                                      18.3%; Score 90; 28.2%; Pred. No.
                                                                                                                                                                                                  POLY-LYS.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 ELKLKLNEANKKY-----QELAIS 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 EISTNIRQAGVQYSRADEEQQQALS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98295987; Pubmed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence.";
Nature 393:537-544(1998).
EMBL; AL021930; CAA17362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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EMBL; AL596163; CAC95282.1; -. ListiList; LIN00049; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
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                                                                                                                                                             Complete proteome. SEQUENCE 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 1.
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Q921B9;
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Q921B9
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Mature 393:537-544(1998).

EMBL: ALO21287: CAA16105.1; -.
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                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQANLG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9842 MW; BA9BCB3180EC17F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84.5; DB 16;
Pred. No. 1.9;
7; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 AA
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                                                                                                                                                                                                                                                                                                                       MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 QAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / SEROVAR 6A;
EAAGTYVAAD---AAAASTYTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34.9%;
Matches 29; Conservative
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                                                                                              PRELIMINARY;
                                                                                                                                                                                             RV3020C OR MTV012.34C.
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria innocua.
                                                                                                                                                                       PE-FAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN.
                                                                                                                                                                                                                                                          NCBI_TaxID=1773;
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Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Rondslek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Vazquez-Boltand J.-K., Voss H., Wehland J., Cossart P., Comparative genomics of Listeria species."; Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sandblad L., Hunziker A., Cordes V.C.; "Evolutionarily conserved mouse tpr is a single-copy gene located chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.0%; Score 83.5; DB 16; Length 97; Best Local Similarity 25.5%; Pred. No. 2.3; Matches 26; Conservative 20; Mismatches 39; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.9%; Score 83; DB 11; Length 1200; 27.1%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Conservative 16; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       960 SNVEQYRAMVISLEDSLNKEKQVIEEVHKNIE---VRLKESAEFQTQ 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC_2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ298076; CAC40701.1; -. NON_TER 1200 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 GTAAQ--AAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NUCLEAR PORE COMPLEX-ASSOCIATED PROTEIN TPR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                           97 AA; 11342 MW; 5CEE89D26C1BA775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ANKOKOELDEISTNIROAGVOYSR---ADEEQQQALSSOMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
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4

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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 002456;
                                                                                                                                                                                                                                                                                                                                                                                                         002456
                                                                                                                                                                                                                                                                                                                                                           RESULT 10
Q02456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9RY46
                                                                                                                                                                                            Вb
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A strand M.;

Induction of protective immunity in mice using a 62-kDa recombinant if ragment of a Schistosoma mansoni surface antigen.";

J. Immunol. 149:3612-3620(1992).

BMBL; X65591; CAA46548.1;

RISEP, PAT733; IMDC.

InterPro; IPR001043; IQ.

InterPro; IPR001048; IQ.

InterPro; IPR001609; Myosin_head.

InterPro; IPR000533; Tropomyosin.

R InterPro; IPR000533; Tropomyosin.

R InterPro; IPR000531; Tropomyosin.

R Pfam; PF00063; IQ; 2.

Pfam; PF00063; III).

PRIMTS; PR00194; TROPOMYOSIN.

PRINTS; PR00194; TROPOMYOSIN.

PRINTS; PR00194; TROPOMYOSIN.

PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          026589;
01-NOV-1996 (TTEMBLrel. 01, Created)
01-NOV-1996 (TTEMBLrel. 01, Last sequence update)
01-DEC-2001 (TTEMBLrel. 19, Last annotation update)
MYOSIN II HEAVY CHAIN (FRAGMENT).
Schistosoma mansoni (Blood fluke).
Eukartota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomacoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                       MEDLINE-99097579; PubMed-9880904;
Kim E., Kim S.H., Choi C.S., Park Y.I., Kim H.R.;
"Cloning and expression of apolipophorin-III from the common cutworm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 TDANAKAKTALEQARQNLEKTAEDLRKSHPDVERQAGELRTKLQAAVQNTAQEVQKLAKE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
APOLP-III.
Spodoptera litura.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
NCEI_TaxID=69820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 TDA-----ATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
STRAIN-PUBERTO RICAN;
MEDLINE-93056536; PubMed=1431131;
Soisson L.M., Masterson C.P., Tom T.D., McNally M.T., Lowell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                         Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                1582; AAC63377.1; -.
188 AA; 20649 MW; 7A8AE366DF8E432C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61622 MW; AF075D13EB249B4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AANKQKQELDEISTNIRQAGVQYSRADEEQQ----QALSSQ 97
                                                                                                                                                                                                                                                                                                                                                                                                    16.8%; Score 82.5; DB 5; 26.7%; Pred. No. 5.9; Live 20; Mismatches 45;
                                                                                                                                                                                                                                                             Spodoptěra litura.";
Arch. Insect Blochem. Physiol. 39:166-173(1998).
EMBL; AF094582; AAC63377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00182; GLNA_ADENYLATION; UNKNOWN_1.
PROSITE; PS50096; IQ; 1.
1 1.
SEQUENCE 528 AA; 61622 MW; AF075D13EB249B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-PUERTO RICAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00015; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amory L.M.;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         026589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
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Q26589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                  337 KLEGDLKATQETVDDLERVKRDLEEQLRRKEAEIGGLSGKFEDEQGLVAQ----LQRKI 391
                                                                                                               3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAINBRAILLIAN LE;
MEDLINE-93211444; Pubbed-8459827;
MEDLINE-93211444; Pubbed-8459827;
Weston D.S., Schmitz J., Kemp M., Kunz W.;
"Clothing and sequence characterization of a complete myosin heavy chain cDNA from Schistosoma mansoni.";
MOL Biochem. Parasitol. 58:161-164(1993).
EMBL; L01644; AAA29905.1;
HSSP; P08799; IMND.
                                                           . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 9
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          Length 528;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222379 MW; 10FC4EAE208CA365 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.5%; Score 81; DB 5; 1
ilarity 21.9%; Pred. No. 1.1e+02;
Conservative 24; Mismatches 45.
          DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1095 KELQTRIQELEEDLEAERAARSKAEKSRQO-LESEL 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; D08/99; IMND:
InterPro; IPR004069; Chemotaxis_transducer.
InterPro; IPR001637; GlnA_adenyltn.
InterPro; IPR001648; IQ.
InterPro; IPR004009; Myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR004009; Myosin_Lail.
Pfam; PF00061; IQ. 2.
Pfam; PF00061; IQ. 2.
Pfam; PF00063; Myosin_Lail.
Pfam; PF00163; Myosin_Lail.
PRINTS; PR00193; MYOSIN_Lail; I.
PRINTS; PR00193; MYOSIN_Lail; I.
PRNART; SM00015; IQ: 1.
SMART; SM00015; IQ: 1.
                                                                                                                                                                                                                                                    392 KELQTRIQELEEDLEAERAARSKAEKSRQQ-LESEL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00182; GLNA_ADENYLATION; UNKNOWN_1 PROSITE; PS50096; IQ; 1.
        ch 16.5%; Score 81; DB 5
1 Similarity 21.9%; Pred. No. 25;
21; Conservative 24; Mismatches
                                                                                                                                                                                                                      63 NKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 NKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1940 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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16.5%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1940 AA;
        Query Match
Best Local Similarity
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6183;
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S.

49;

Length 1999;

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9 ATLGQEAGN-----FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRF 58
                                                                                                                                                                                                                                                                   59 QE-----AQELDEISTNIRQAGVQY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 NFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             evolutionary conservation of the hair type II keratin intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              filament gene family.";
Development 114:417-433(1992).
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression, structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.1%; Score 79; DB 6; Length 508; 22.9%; Pred. No. 36;
                                                                                                                                      16.2%; Score 79.5; DB 11; Length 123.1%; Pred. No. 1.5e+02;
cive 26; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Mismatches 39; Indels
                                                                                          SEQUENCE 1999 AA; 231456 MW; 090C181D55727B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coiled coil; Intermediate filament; Keratin.
SEQUENCE 508 AA; 55245 MW; 3E728AA9512F96F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ol-nov-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NIT-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                            508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92274852; Pubmed-1375545; Powell B., Crocker L., Rogers G.; "Hair follicle differentiation:
                ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 QRLTAEVENAKCQNSKLEAAVTQ 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X62509; CAA44368.1; ..
InterPro; IPR001664; IF.
InterPro; IPR003054; Keratin_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01276; TYPE2KERATIN. PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 RQ--AGVQYSRADEEQQQALSSQ
 PRINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00038; filament; 1
                                                                                                                                                                        31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
                             SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                               1880 EEAEEEAQRANASR 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 84 SRADEEQQQALSSQ 97
                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9940;
                                                                              Myosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                            028582
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                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
Q28582
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                                                                                                                                                                          Matches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ILGQEAGN------FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20036896; PubMed-10567266; White O., Eisen J.A., Heldelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamadhevan J.J., Lam P., McDonald L., Pitterback T., Zalewski C., Makadova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sun W., Chantler P.D.; "Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain and its differential expression within the central
                                                                                                          Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 163;
                                                                                                                                                                                                                                                                                                               Gendme sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                              al protein; Complete proteome.
163 AA; 17830 MW; AOAC12CE20534D9C CRC64;
             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEURONAL MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery March 16.2%; Score 79.5; DB 16; Best Local Similarity 22.7%; Pred. No. 9.3; Matches 22; Conservative 16; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 FQEAANKOKQELDEISTNIRQAGVQYSRADEEQQQAL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1999 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nervous system[see comments].";
J. Mol. Biol. 224:1185-1193(1992).
HSSP; P10587; 1BR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00048; IQ.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectfin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=BRAIN;
MEDLINE=92235856; PubMed=1569576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00612; IQ; 1.
PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 2.
                                                            HYPOTHETICAL 17.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                               ans R1.";
286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                               AE001873; AAF09701.1;
DR0105; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                           Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                         NCBI TaxID-1299;
                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEOUENCE
                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             063731;
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Pfam;
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063731
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Gaps

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Ragland J., Yamauchi Y., Sato R., Wells M.A., Hamano K., Tsuchide K.;
"CDNA and Deduced Amino Acid Sequence of Apolipophorin-III from Agrius
concolyuli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Douette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Snith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:483-4838(2001).
EMBL, AE007518; AAK78034.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 04, Last sequence update)
APOLIPOPHORIN-III (FRACMINT).
Agrius convolvuli (morning glory sphinx moth).
Eukaryota; Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Sphingiodea; Sphingidae; Sphinginae; Agrius.
                                                                                                                                           Clostridium acetobutylicum,
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                            01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
UNCHARACTERIZED SMALL CONSERVED PROTEIN, HOMOLOG OF YFJA/YUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%; Score 78; DB 16; Length 103; 21.3%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.7%; Score 77; DB 5; Length 178; 25.0%; Pred. No. 17; ative 21; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF001632; AAB61280.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 APOLIPOPHORIN-III.
19648 MW; E4DA3C4DA4341E85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  103 AA; 11764 MW; 41B2E22D3DF36D6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 AA.
                  103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Mismatches
                                                                                                                                                                                                                                         STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AANKQKQELDEISTNIRQAGVQYSRADEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 GMQRHCNMIGELIKELQETAKEFTKLDNE
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.7%
Best Local Similarity 25.0%
Matches 21; Conservative
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Best Local Similarity 21.39
Matches 19; Conservative
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE 103 AA
                                                                                                                                                                          Clostridium.
NCBI_TaxID=1488;
                                                                                                           B.SUBTILIS.
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CHAIN
SEQUENCE
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097MZ2
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11 LGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELD 70

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88 LEQARQNVEKTAEELRKAHPEVEKEANALKDKLQAAVQTTVQESQKLAKEVASNMEETNQ 147
qq
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71 EISTNIRQAGVQYSRADEEQQQAL ò

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Search completed: July 22, 2002, 01:19:31 Job time: 427 sec

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

sw model OM protein - protein search, using

5, 2001, 11:41:11 ; Search time 130.35 Seconds (without alignments) 46.509 Million cell updates/sec July Run on:

1 MAEMKTDAATLGQEAGNFER.....VQYSRADEEQQQALSSQMGF 100 US-09-462-480-5 Title: Perfect score:

Sedneuce:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

412676 seqs, 60623988 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:\*/SIDS8/gcgdata/geneseqp/AA2000.DAT:\* . DAT: \* /gcgdata/geneseg/geneseqp/AA1996.DAT:\* /SIDS8/gcgdata/geneseg/genesegp/AA2001.DAT:\* gcgdata/geneseq/geneseqp/AA1992.DAT:\* | SIDS8|gcgdata/geneseq/geneseqp/AA1982.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	M. tuberculosis LH M. tuberculosis im	Mycobacterium tube M. tuberculosis an	M. tuberculosis and tuberculosis by 3	Mycobacterium tube M. tuberculosis fu	Mycobacterium anti Mycobacterium tube M. tuberculosis fu
ID	AAY03705 AAW81706	) AAW64339 ) AAY39136	_	A A	AAY3063 AAY3024 AAY30224
DB	20	19	22	19	19 20 20
Query Match Length DB ID	100	100	100	100 802	802 802 802
Query Match	100.0	98.8 98.8	98.8 98.8	98.8 97.8	97.8 97.8 97.8
Score	492	486 486	486 486	486	481 481 481
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22 23 17	AAW64321 AAY32097 AAY39118 AAY38981 AAW32454 AAW32386 AAW32386	AAW64340 AAY39137 AAY38994 AAX03706 AAX03707 AAY03712 AAW32460 AAW31698	AAW32458 AAW81696 AAX39126 AAW32457 AAW32459 AAW81695	0 0 0 10 D
20 20 20 11 18 19	19 18 18 18	100 100 100 100 100 100 100	1788 1788 1788 1788	20 20 118 20
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7.7.8.8.8.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.		20.2 20.2 24.8 24.8		
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### ALIGNMENTS

AAY03705 standard; Protein; 100 AA. AAY03705 RESULT

(first entry) 07-JUN-1999 AAY03705; 

M. tuberculosis LHP polypeptide.

ESAT-6 protein; antigenic protein; LHP; Mycobacterium tuberculosis; immunogen; vaccine; bacteria; tuberculosis; regulatory; synergistic; immune response.

Mycobacterium tuberculosis.

WO9904005-A1.

98WO-IB01091 16-JUL-1998; 28-JAN-1999.

(INSP ) INST PASTEUR. (STAT-) STATENS SERUM INST.

97US-0052631.

16-JUL-1997;

Rasmussen PB; Andersen P, Berthet F, Gicquel B,

WPI; 1999-132249/11. N-PSDB; AAX29168, AAX29171.

New nucleic acid containing regulator and LHP gene of Mycobacterium tuberculosis – useful in vaccines, for diagnosis, and for expression

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of heterologous proteins

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Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                    Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                             M. tuberculosis immunogenic polypeptide Tb38-IN.
          Claim 17; Page 64; 88pp; English
                                                                                                                                                                                                                                          AAW81706 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                              97US-0818112.
96US-0730510.
                                                                                                                                                                                                                                                                                                                                                   97WO-US18293
                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                     Similarity
                                                                                                                            100 AA;
                                                                                                                                                                                                                                                                   27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                   07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                               13-MAR-1997;
                                                                                                                                                                                                                                                                                                                          WO9816646-A2
                                                                                                                                                                                                                                                                                                                                                                     11-0CT-1996;
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                                                                                                                                                           100;
                                                                                                                                                                                                                                                       AAW81706;
                                                                                                                            Sequence
                                                                                                                                              Query Match
                                                                                                                                                     Best Local
Matches 10
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                                                                                                                                                                                                                               RESULT
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100.0%; Score 492; DB 20; 100.0%; Pred. No. 2.1e-46; ive 0; Mismatches 0;

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This polypeptide comprises a partial sequence of Mycobacterium tuberculosis antigen Tb38-IN. It is encoded by genomic DNA isolated from a M. tuberculosis strain H37Rv genomic library using a probe derived from clone Tb38-I (see AAV44384). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64201-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or an immunogenic portion of polypeptides, recombinant expression vectors and transformed or pransfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.
This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a methor for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccins and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                     1 MAEMKIDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                             New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                    Length 100;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis; infection; diagnosis; antigen; Tb37-FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                  Score 486; DB 19;
Pred. No. 9.6e-46;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis antigen Tb38-IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 145; 250pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW64339 standard; Protein; 100
                                                                                                                                                                                                                      98.8%;
99.0%;
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Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 99; Conserv
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11-0CT-1996;
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                                                                                                                                                              Sequence
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                                                                                       requiatory expression signals of the ESAT-6 protein as well as an open regulatory expression signals of the ESAT-6 protein as well as an open regulatory expression signals of the ESAT-6 protein as well as an open trading frame coding for an antigenic protein LHP from Mycobacterium tuberculosis. Host cells comprissing the polynuclectide are used for the recombinant expression of the protein. The recombinant polypeptide can be used as immunogens and vaccines, to protect against bacteria of the turber immunogenic proteins of the bacteria or their fragments, specifically ESAT-6; and (b) for diagnosing tuberculosis infection by detection of specific antibodies. The regulatory region present in the polynuclectide may be used to express almost any heterologous protein in mycobacteria, particularly as a fusion with polyhistidine. The two provide a synergistic increase in ability to induce a protective immune response. The present sequence represents the LHP polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Example 3B; Page 138-139; 230pp; English

WPI; 1998-261042/23.

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Sequence

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                               Gaps
                                                          1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                          New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
                               ö
 Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vedvick TS;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton R;
                                                                                                                                                                                                                                                                                                                M. tuberculosis antigen Tb38-IN amino acid sequence.
                                                                                                                                  61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC, Hendrickson RC, Hou
SG, Skeiky YAW, Twardzik DR,
 Score 486; DB 19;
Pred. No. 9.6e-46;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 133-134; 299pp; English.
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                                                                                                                                                                                                                       AAX39136 standard; Protein; 100
98.8%;
ilarity 99.0%;
Conservative
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98US-0025197
                                                                                                                                                                                                                                                                                                                                                                          Immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A,
Lodes MJ, Reed
                                                                                                                                                                                                                                                                                05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                    W09942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-1999
 Query Match
Best Local Sim
Matches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                     AAY39136;
                                                                                                                                                61
                                                                                                                                                                                                           AAY39136
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This invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                     M. tuberculosis recombinant antigen protein Tb38-IN
             61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AANKOKOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 486; DB 20;
Pred. No. 9.6e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 179; 323pp; English.
                                                                                         ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB35218 standard; Protein; 100 AA.
                                                                                         AAY38993 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.8%;
99.0%;
                                                                                                                                                                                                                                                                                                                  99WO-US03265
                                                                                                                                                                                                                                                                                                                                            98US-0072596
                                                                                                                                                                                                                                                                                                                                                         98US-0024753
                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527416/44.
                                                                                                                                                                                               Antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA;
                                                                                                                                                                                                            immunity
                                                                                                                                                                                                                                                              WO9942118-A2
                                                                                                                                                                                                                                                                                                                  17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                         18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                            05-MAY-1998;
                                                                                                                                            05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                        26-AUG-1999
                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB35218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                  AAY38993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                S
61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT (AAB35218 ID AAB31XX AAC AAB31XX
                                                                             AAX38993
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Length 100;

Score 486; DB 20; Pred. No. 9.6e-46; 0; Mismatches 1;

98.88; 99.08;

Query Match Best Local Similarity

Conservative

66

Matches

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The present sequence is that of the Mycobacterium tuberculosis MTBN4 protein. This is 1 of 8 proteins, i.e. MTBN1-8 (see AAB891842-9), encoded by 8 open reading frames (see AAA89013-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. WTBN1-8 represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these MTBN polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic (vaccine) methods, including genetic vaccination methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 486; DB 22;
Pred. No. 9.6e-46;
0; Mismatches 1;
                                                       (PUBL-) PUBLIC HEALTH RES INST NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. tuberculosis fusion protein TbF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW81746 standard; Protein; 802 AA
                                                                                                                                                                                                                                                      Claim 11; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0818112.
96US-0730510.
                    99US-0132505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US18293
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Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.0
Matches 99; Conservative
                                                                                                                         WPI; 2001-007153/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AA;
                                                                                                                                             N-PSDB; AAA89038
                  04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-1997;
11-OCT-1996;
                                                                                           Gennaro ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW81746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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AAW81746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences for members of the esat-6 gene family from Mycobacterium tuberculosis. These proteins include Rv0287, Rv1036c, Rv1037c, Rv3346c, Rv3248c, Rv2543c, Rv3005c, Rv3444c, Rv3444c, Rv3405c, Rv3890c, Rv3890c, Rv3905c. These can be used to produce vaccines against, and in the diagnosis of, tuberculosis (TB) infection. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide encoded by a member of the esat-6-gene family for immunizing against and diagnosis of tuberculosis -
                                                                      Tuberculosis; TB; vaccine; esat-6 gene family; Rv0287; Rv1036c;
Rv1037c; Rv2346c; Rv2348c; Rv2653c; Rv2654c; Rv3020c; Rv3444c;
Rv3445c; Rv3890c; Rv3891c; Rv3904c; Rv3905c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis; BCG; vaccine; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 486; DB 22;
Pred. No. 9.6e-46;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis protein MTBN4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 65; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB19845 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                   M tuberculosis Rv3874 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.8%;
99.0%;
                                                                                                                                                                                                                                                                                     99DK-0001020.
                                                                                                                                                                                                                                                    13-JUL-2000; 2000WO-DK00398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2000; 2000WO-US12257
                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                           (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                             Skjot R;
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-091923/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 AA;
                                                                                                                                                                               WO200104151-A2.
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                                                                                                                                                                                                                                                                                     13-JUL-1999;
15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                             Andersen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-2001
                                                                                                                                                                                                                18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB19845;
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AAB19845 RESULT

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Gaps

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Length 100; 1; Indels ö

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composed of Mycobactrium tuberculosis antigens TDRA3 (see AAW64295), composed of Mycobactrium tuberculosis antigens TDRA3 (see AAW64325), 38 kDa antigen (see AAW64364), TDS8-1 (see AAW64321) and DPEP (see AAW64322). It was produced by PCR amplification (see AAW6450-57) of the appropriate antigen DNA sequences, cloning into an expression vector, and expression in E. coli. TDF-2 can be used for serodiagnosis of tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising antigenic or liminunogenic portions of M. tuberculosis antigens, or fusion proteins, DNA sequences encoding such polypeptides, recombinant expression vectors and host cells. Also claimed are methods and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a recombinant Mycobacterium tuberculosis tetra-antigen fusion protein, termed TbF-2, composed of the antigens TDRa3, 39RD, Tb58-1 and DPEP. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AA220198) comprising the 4 coding sequences. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuberculosis; antigen; fusion protein; TbF-2; TbRa3; 38kD; Tb38-1; DPEP; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                      designated TbF-2,
                                                                                                                                                                                                                                                                                                                                                      Length 802;
                                                                                                                                                                                                                                                        kits for detecting M. tuberculosis infection in a patient
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis antigen fusion protein TbF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ANKOKOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 481; DB 19;
Pred. No. 4.3e-44;
                        This polypeptide comprises a fusion protein,
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campos-Neto A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 5G-J; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY32063 standard; Protein; 802
                                                                                                                                                                                                                                                                                                                                                      97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0056556.
98US-0223040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                        Query Match 97.8%
Best Local Similarity 99.0%
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW, Alderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-601610/51.
                                                                                                                                                                                                                                                                                                 802 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ20198
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30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2000
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                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                    This sequence represents the fusion protein TDF-2 which is composed of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogenic polypeptides from Mycobacterium tuberculosis (MT). This protein is used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of TB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                  Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGGWRGAAGTAAQAAVVRFQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection; diagnosis; 38 kDa antigen; TbRa3; DPEP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
  Houghton R, Lodes MJ;
1k DR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                    97.8%; Score 481; DB 19; 99.0%; Pred. No. 4.3e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ANKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium antigen TbF2 protein fusion.
                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Page 223-226; 250pp; English.
Campos-Neto A, Dillon DC, Houghto
Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.
                                                                                                                                                                                             Disclosure; Page 208-211; 230pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW64379 standard; Protein; 802
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96US-0729622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 99.0 98; Conservative
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Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-251292/22.
N-PSDB; AAV55801.
                                                         WPI; 1998-261042/23
                                                                                                                                                                                                                                                                                                                                                                           802 AA;
                                                                             N-PSDB; AAV64567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis;
Tb38-1; TbF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409816645-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-0CT-1996;
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                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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AAY39225 are used in the exemplification of the present invention.

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M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to
                                                                                                                                                                                                                                                                                     425 aemktdaatlaqeagnferisgdlktqidqvestagslqgqwrgaagtaaqaavvrfqea 484
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                    2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGGWRGAAGTAAQAAVVRFQEA 61
antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antigens from Mycobacterium tuberculosis useful in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
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                                                                                                                                                                                     Length 802;
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R, Vedvick TS;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis fusion protein TbF-6 amino acid sequence.
                                                                                                                                                                                    Score 481; DB 20;
Pred. No. 4.3e-44;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                    62 ANKOKOELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                     Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 37; Page 271-273; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY39224 standard; Protein; 802
                                                                                                                                                                                  97.88;
99.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1999 (first entry)
                                                                                                                                                                         Query Match
Best Local Similarity 99.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
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                                                                                                                                     802 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Mycobacterium
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                                                                                                    components
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                                                                                                     Gaps
                                                                                                                                                              425 aemktdaatlageagnferisgdlktgidgvestagslgggwrgaagtaagaavvrfgea 484
                                                                                                                                  2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
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                                                                         Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton R;
, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                       M. tuberculosis fusion protein TbF-2 amino acid sequence.
                                                                                                    Indels
                                                                      Score 481; DB 20; I
Pred. No. 4.3e-44;
0; Mismatches 1;
                                                                                                                                                                                          62 ANKOKOELDEISTNIRQAGVOYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                        Campos-Neto A, Dillon DC, Hendrickson RC, Hor
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 205-208; 299pp; English.
                                                                                                                                                                                                                                                                                                AAY39176 standard; Protein; 802
                                                                        97.8%;
99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0072967
98US-0025197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                   Query Match
Best Local Similarity 99.0
Matches 98; Conservative
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                             802 AA;
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Length 802;

DB 20;

97.8%; Score 481;

Query Match

Best Local Matches 9

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This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEA 61
                                                                                                                                       Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ANKOKOELDEISTNIRQAGVOYSRADEEQQQALSSOMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 481; DB 20;
Pred. No. 4.3e-44;
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
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                                                                                                          M. tuberculosis fusion protein TbF-2
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 AAY39033
ID AAY39033 standard; Protein; 802
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99.0%;
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98US-0024753.
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Best Local Similarity 99.00,
"when 98; Conservative
                                                                                                                                                                                    Mycobacterium tuberculosis.
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N-PSDB; AAZ19156.
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18-FEB-1998;
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                                              AAY39033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
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                                                                                                                                                                                                                                                                                                                                     Antigen; diagnosis; detection; infection; antibody; immunisation;
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               Indels
 Pred. No. 4.3e-44;
; Mismatches 1;
                                                                                                    Score 481; DB 20;
Pred. No. 4.3e-44;
0; Mismatches 1;
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 10; Page 316-318; 323pp; English.
                                                                                                                                                                                                                                                                                                         M tuberculosis fusion protein TbF-6.
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Similarity 99.0%;
98; Conservative
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98US-0024753.
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                                                                                                                                                                                                                                                                           (first entry)
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N-PSDB; AAZ19245.
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Best Local Similarity
Matches 98; Conserv
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                                                                                                                                                                                                                                                                                                                                                        immunity
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18-FEB-1998;
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26-AUG-1999

vaccine;

AAY39081;

AAY39081

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Houghton R; R, Vedvick TS;

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Indels

Sequence

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Length 802;

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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or ancistications). The present sequence represents a M.tuberculosis antigen, Tb38-1. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus BSAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                     New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention, or treatment of tuberculosis, also
                                                                                                                                                                                                                  Skeiky YAW;
                                                                                                                                                                                                                  Reed SG,
                                                                                                                                                                                                                 Campos-neto A, Dillon DC, Houghton R,
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 124; 168pp; English.
                                                                                                               95US-0523436.
95US-0533634.
96US-0620874.
96US-0659683.
                                                                     96WO-US14674
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                                                                                                                                                                                      (CORI-) CORIXA CORP
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                                                                                                               01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
            WO9709428-A2
                                                                   30-AUG-1996;
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                                        13-MAR-1997
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Score 462; DB 18; Length 95; Pred. No. 3.7e-43; 0; Mismatches 1; Indels

93.9%;

Query Match 93.9 Best Local Similarity 98.9 Matches 94; Conservative

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Appl Appl App Appli

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47; Indels 13; Gaps
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                                                                                                                                                     Sequence 41,
Sequence 41,
Sequence 168
Sequence 8,
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                             US-08-968-685A-10
US-08-460-512-7
US-08-742-923A-4
PCT-US94-01149-55
PCT-US94-01149-55
PCT-US94-01149-57
US-08-45-518-6
US-08-45-41
US-08-234-613-41
US-08-745-308-18
US-08-745-598-8
US-08-745-598-8
US-08-745-598-8
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US-08-260-582-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.6%; Score 81.5; DE Best Local Similarity 29.2%; Pred. No. 0.4; Matches 31; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08006676B
Sequence 1, Application US/08006676B
Sequence 1, Application US/08006676B
Sequence 1, Application US/08006676B
Sequence 1, Application US/08006676B
SEREME 1 ENVORMATION: Diagnosis of Leishm NUMBER OF SEQUENCES: SADERS: ADDRESSE: Jeffrey B. Oster STREET: 8339 SE 57th Street CITY: Mercet Island STATE: Washington COUNTRY: USA
ZIP: 98040-4906
COMPUTER READABLE FORM: COMPUTER READABLE FORM: MINDOWS COMPUTER: WASHINGTON COMPUTER: WASHINGTON STATE: WASHINGTON UNMBER: US/08/006,676B
FILING DATE: WASHINGTON: A 35 SETILNG DATE: WASHINGTON: A 32 SETILNG DATE: APPLICATION NUMBER: 32,585
REFERENCE/DOCKET NUMBER: 32,585
REFERENCE/OCKET NUMBER: 32,585
TELEPHONE: C206) 232 7845
TELEPHONE: C206) 232 7845
TELEPHONE: SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
TTYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
552
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885
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; MOLECULE TYPE: protein
US-08-006-676B-1
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Sequence 7, 1
Sequence 9, 1
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Patent No. 5
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-144-121-2
US-08-735-893-2
US-08-470-950-4
US-08-470-950-4
US-08-470-950-4
US-08-483-924-4
US-08-483-924-4
US-08-483-924-4
US-08-452-5928-9
US-08-83-85-7
US-08-95-7
US-09-067-351-2
US-09-067-351-2
US-08-966-318-5
US-08-765-106-8
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US-08-428-414A-3
PCT-US94-00324-1
US-08-144-121-3
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                                                                                                                                                                                                                                                                                                               193259 segs, 20144635 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein – protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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492
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REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 50
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 955 amino acids
                                                                                                                                                            SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
COUNTRY: USA
                      Washington
                                                                                                                                     OPERATING SYSTEM:
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Best Local Similarity
Matches 31; Conserv
                                                            98104-7092
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US-08-428-414A-3
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-US94-00324-1
                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08428414A
Patent No. 5912166
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TITLE OF INVENTION: LEISHMANIASIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                        APPLICANT: Reed, Steven G.
TITLE OF INVENTION: A 230Kd Antigen Present in Leishmania
TITLE OF INVENTION: Species
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       ZIP: 98101

ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: FOPPPY disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh Operating System 7.1

SOFTWARE: Microsoft Word for Macintosh 5.1a

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        912 ELASQLEATAAAKSSAEQDR--ENTRAALEQQLRDSEERAAELASQ 955
912 ELASQLEATAAAKSSAEQDR--ENTRAALEQQLRDSEERAAELASQ 955
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EMKTDAATLGQEAGNFERISGDLKTQIDQV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08/006,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/006,676
FILING DATE: JANUARY 15, 1993
CLASSIFICATION: 435
                                                                                             Sequence 2, Application US/082845
Patent No. 5719263
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Conservative
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Best Local Similarity
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                                                                          US-08-282-845-2
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852 DRESTRATLEQOLRESEERAAELASQLESTTAAKMSAEQDRESTRATLEQOLRDSEERAA 911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9400324
GENERAL INFORMATION:
APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.6%; Score 81.5; Di 29.2%; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word, version 5.1a SOFTWARE: Microsoft Word, version 5.1a CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/00324 FILLING DATE:
                                                                                                                                                                                                    NAME: Kadlecek, Ann T.
REGISTRATION NUMBER: 39,244
REFERENCE/DOCKET NUMBER: 210121.407
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRAPATERISTICS:
                                                                                               APPLICATION NUMBER: US/08/428,414A FILING DATE: 21-APR-1995 CLASSIFICATION: 436 AND THE NUMBER: Radlecek, Ann T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,676
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
IBM PC compatible
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958 EDVVGNLRQGTVALQEAQDTMQGTSRSLRLIQDRVAEVQQVLGQQKLVTSMTKQLGDFWT 1017
                                                                                                                                                                                                                               60; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08735893
Patent No. 5914317
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Wagman, David W.
TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: BOSTON
STATE: Massachusetts
                                                                                                                    DB 1; Length 1147; 4.8;
                                                                                                                                                               45; Indels
                                                                                                                                                                                                                                                                                    (MGH-0780.1) MGP-021DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                          68 ELDEISTNIRQAGVQYSRADE----EQQQALSSQMGF 100
                                                                                                                                                               23; Mismatches
                                                                                                                       Score 73;
Pred. No.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/144,121
FILING DATE: 27-007-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MYETS, Paul L.
REFERENCE/DOCKET NUMBER: (MGH-0780.1)
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION FOR SEC 1D NO: 3:
                                                                                                                                                                                                     4 MKTDAATLGQEAGNFERISG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1147 amino acids
                                                                                                                    Query Match
Best Local Similarity 18.5%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
                       Domain
766..1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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LOCATION:
FEATURE:
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                   ; NAME/KEY:
; LOCATION:
US-08-144-121-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-735-893-3
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                                                                                                                                                                                                                                                                                                                        3 EMKTDAATLGQEAGNFERISGDLKTQIDQV------ESTAGSLQGQWRGAAGTAA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-144 121-3
Sequence 3, Application US/08144121
Patent No. 5610031
GENERAL INFORMATION:
APPLICANT: Burgeson, Robert E.
APPLICANT: Wagman, David W.
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                     DB 5; Length 955;
                                                                                                                                                                                                                                                                                                                                                                                                                                               912 ELASQLEATAAAKSSAEQDR -- ENTRAALEQQLRDSEERAAELASQ 955
                                                                                                                                                                                                                                                                                                                                                                                                           52 QAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPPRATIES: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021
TELECOMNUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1147 amino acids
                                                                                                                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                              Score 81.5;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/144,121
FILING DATE: 27-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
                     (206) 587-0430
                             TELEFAX: (206) 233-064-0430
TELEFAX: (206) 233-0645
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           Query Match 16.6%;
Best Local Similarity 29.2%;
Matches 31; Conservative 1:
                                                                                               LENGTH: 955 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                    ; MOLECULE TYPE: protein PCT-US94-00324-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
412..765
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02109
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LOCATION:
FEATURE:
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FEATURE:
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; NAME/KET: DOMBIN 	976 EDVVGNLRQGTVALQEAQDTMQGTSRSLRLIQDRVAEV
	OY 68 ELDEISTATROAGYOYSRADEEQOQALSSOMGF 100 :: :  : : : :  : : : : :  :  :        Db 1036 RMEELRHQARQOGAEAVOAOCLAEGASEOALSAORGE 1072
Ouery Match 14.8%; Score 73; DB 2; Length 1147; Best Local Similarity 18.5%; Pred. No. 4.8; Matches 29; Conservative 23; Mismatches 45; Indels 60; Gaps 4;	SULT 8
4 MKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQW 43 	US-08-735-893-2; Sequence 2, Application US/08735893; Pattent No. 5914317.
	TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
SNLRQGTVALQEAQDTMQGTSRS ISTNIRQAGVQYSRADEEQ	: 14 ESS: E & COCKFIELD
:::::      : :  :       : :	; STREET: 60 State Street, suite 510 ; CITY: BOSTON ; STATE: Massachusetts ; COUNTRY: United States
RESULT 7 US-08-144-121-2 Sequence 2, Application US/08144121 Patent No 5610031	OKL
NERAL INFORMATION: APPLICANT: Burgeson, Robert E.	OPERATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICANT: Wagman, David W. TITLE OF INVENTION: B1k CHAIN OF LAMININ AND METHODS OF USE NUMBER OF SEQUENCES: 14	င်းမြောက်
CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510	Q I E
ല E	; FILING DATE: 27-OCT-1993 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION:
ZIP: 02109 COMPUTER READALE FORM:	; NAME: Myers, Paul L. REGISTRATION NUMBER: 35,965 MATERIAL AND
patible -DOS/MS-DOS	CATION INFORM (617) 227-
SOFTWARE: Patentin Release #1.0, Version #1.25 DRRENT APPLICATION DATA:	; TELEFAX: (617) 227-5941 ; INFORMATION FOR SEQ ID NO: 2:
APPLICATION NUMBER: US/08/144,121 FILLING DATE: 27-07-1993	ωΞ
CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: MYGTS, Paul L.	; TYPE: amino acid ; TOPOLOGY: Incar : MOLECHIE TYPE: nrotein
REGISTRATION NUMBER: 35,965 . REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021	
H S	14.88:
TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 2:	4.8; ches 45; Inde
SEQUENCE CHARACTERISTICS: LENGTH: 1165 amino acids	AATLGOEAGNFERISGDLKTOIDOVESTAGSLOGG
TYPE: amino acid TOPOLOGY: linear	916 LPIDSATVLOKMNETOATAARLPNVDLVLSOTKODIGGARRLOAFAEERRSRAHAVEGOV
Α.	44 RGAAGTAAOAAOVVRPOEAANKOK
Outery Marcn Best Local Similarity 18.5%; Pred. No. 4.8; Marches 29; Conservative 23; Marches 45; Indels 60; Gaps 4;	OY 68 ELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
MKTDAATLGOEAGNFERISGDLKTOIDOVESTAGSLOGOW 43	Db 1036 RWEELRHQARQGGAEAVQAQQLAEGASEQALSAQEGF 1072
LPNVDLYLSOTKODIGGARRIOAEAEEARSRAHAVEGOV	RESULT 9

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417 TLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERG-------HFEE----EKQQL 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08467781
Patent No. 5780596
GENERAL INFORMATION:
APPLICANT: TOURATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2101;
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COMPOURS: IBM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/467,781
CLASSIFICATION: 424
                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 25.0%; Pred. No. 10;
Conservative 19; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: TESTA, HURWITZ & THIBEAULT 125 HIGH STREET
                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDWUND R
RESISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
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                                                                                                    06-JUN-1995
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 21; Conserva
                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                    amino acid
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US-08-470-950-4
                                                                                                          FILING DATE:
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STATE:
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APPLICANT: TOURATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT
           Sequence 4, Application US/08466390
Patent No. 5686562
GENERAL INFORMATION:
APPLICANT: TOUKATION:
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.8%; Score 73; DB 1; Length 2101;
Best Local Similarity 25.0%; Pred. No. 10;
Matches 21; Conservative 19; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,390
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: TESTA, HURWITZ & THIBEAULT STREET: 125 HIGH STREET CITY: BOSTON STAFF.
                                                                                                                                                                                                      E: TESTA, HÜRWITZ & THIBEAULT
125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                           ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
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US-08-470-950-4
US-08-466-390-4
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Query Match
Best Local Similarity 25.0%
Matches 21, Conservative
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                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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02109
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PCT-US93-06160-4
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                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                           12; Gaps
                                                                                                                                                     10 TLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQEL 69
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                   DB 1; Length 2101;
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%; Score 73; DB 1; Length 2101; 25.0%; Pred. No. 10;
                                                                                                                     Indels
                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                   Query Match 14.8%; Score 73; DB 3
Best Local Similarity 25.0%; Pred. No. 10;
Matches 21; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
STREET: 53 STATE STREET
STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/901 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/195,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTP-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  465 SSLITDLOSSISNLSQAKEELEQA 488
                                                                                                                                                                                                                       70 DEISTNIRQAGVQYSRADEEQQQA 93
                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08195487
Patent No. 5783403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 DEISTNIRQAGVQYSRADEEQQQA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: PITCHER ESQ, EDMUND R REGISTRATION NUMBER: 27,829 REPERENCE/DOCKET NUMBER: MTF TELECOMMUNICATION INFORMATION: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.8°
Best Local Similarity 25.0°
Matches 21; Conservative
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INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-467-781-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-195-487-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
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RESULT 13
SEQUENCE 4 APPLICATION US/08483924
SEQUENCE 4 APPLICATION:
APPLICANT: TOUKAITY: CARY
APPLICANT: TOUKAITY: CARY
APPLICANT: TOUKAITY: CARY
APPLICANT: TOUKAITON:
APPLICANT: TOUKAITON:
APPLICANT: TOUKAITON:
APPLICANT: TOUKAITON: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURMITZ 6 THIBEAULT
STREET: 125 HIGH STREET
STREET: 125 HIGH STREET
COUNTRY: USA
ZIP: MA
COUNTRY: USA
ZIP: MA
COUNTRY: USA
ZIP: MA
COUNTRY: USA
STATE: MA
COUNTRY: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PLOPEN COMPATION:
MADIUM TYPE: FLORM IN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,924
FILIG DATE: ON JUN-1995
CLASSIFICATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
TELEROMMUNICATION NUMBER: 27,829
TELEROMMUNICATION NUMBER: MTP-013
TELERAX: (617) 248-7100
TELERAX: (617
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COMPUTER READABLE FORM:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 TLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQEL 69
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Best Local Similarity 26.5%; Pred. No. 3.3;
Matches 22; Conservative 14; Mismatches 36; Indels II.
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14.8%; Score 73; DB 5; Length 2101;
Best Local Similarity 25.0%; Pred. No. 10;
Matches 21; Conservative 19; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5510466
APPLICANT: KREIGER, MONTY; KODAMA, TATSUHIKO
TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19930621
CLASSIFICATION:
                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENTH: 2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,400
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 SSLITDLQSSISNLSQAKEELEQA 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 997,113
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 391,486
FILING DATE: 09-A06-1989
APPLICATION NUMBER: 272,002
FILING DATE: 15-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein
PCT-US93-06160-4
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 349
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5510466-2
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| : ||:| :| 221 ASAEIKSLDEKQVYLEQEIKGEM 243

Search completed: July 5, 2001, 11:46:57 Job time: 311 sec

us-09-462-480-5.rpr

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	Ltd.	
4.5	Compugen Ltd	
GenCore version 4.5	- 2000	
GenCore	(c) 1993	
	Copyright	

OM protein - protein search, using sw model

Run on:

July 5, 2001, 11:42:21; Search time 79.63 Seconds (without alignments) 95.661 Million cell updates/sec

Perfect score:

US-09-462-480-5 492 1 MAEMKTDAATLGQEAGNFER......VQYSRADEEQQQALSSQMGF 100 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ			SOMMAKIES	
Result No.	Score	Query Match	Query Match Length	DB		Description
-	486	98.8	100	•	H70802	hypothetical prote
7	187	38.0	100	~	T10032	
æ	92.5	18.8	1186	7	T35661	0
4	91.5	18.6	410	~	B59103	hypothetical prote
ស	06	18.3	750	7	T38435	Ω
9	88	18.1	103	7	B70600	
7	87.5	17.8	97	7	E70836	
8	87	17.7	2022	7	T43214	ovtl protein - nem
6	•	17.2	76	~	G70857	probable PE protei
10	81.5	16.6	955	~	A47334	LcKin kinesin-rela
11	81	16.5	527	~	S33068	myosin heavy chain
12	81	16.5	1940	7	A59287	myosin heavy chain
13	•	16.2	163	7	F75559	hypothetical prote
14	79.5	16.2	1961	Н	A61231	>
15	79.5	16.2	1999	Н	S21801	myosin heavy chain
16	79	16.1	245	7	T44704	hypothetical prote
17	79	16.1	508	Н	KRSHL2	
18	77	15.7	561	7	G833118	probable chemotaxi
19	76.5	15.5	528	~	875310	conserved hypothet
20	97	15.4		7	S05408	keratin, type II,
21	75	15.2		7	S33124	tpr protein - huma
22	•	15.1	80	~	D29674	phycocyanin linker
23	74.5	15.1	316	7	JC6549	apolipoprotein E p
24		15.1	387	7	S57834	forA protein precu
25	4	15.1	880	ď	F83386	
26	4	15.1	929	7	T51932	0
27	4	15.1	1313	~	F96673	
28	74.5	15.1	1956	<b>?</b>	T16416	hypothetical prote
53	74	15.0	756	N	E75590	-

male-enhanced anti	nypornetical prote hypothetical prote	fcrA 15 protein -	hypothetical prote	ferredoxinNADP+	unknown protein [1	kinesin heavy chai	keratin-like prote	tail fiber protein	phage lambda-relat	hypothetical prote	nuclear mitotic ap	8.9K linker polype	Fc gamma (IgG) rec	flagellin A - Camp
T42722	T20971 T20978	S52536	D84335	S33479	н96760	A31497	138025	T14650	T14968	T13606	A42184	A24691	A33939	A39228
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1325	2261	388	433	440	745	975	257	860	978	1589	2101	80	405	576
15.0	15.0	14.9	14.9	14.9	14.9	14.9	14.8	14.8	14.8	14.8	14.8	14.7	14.7	14.7
74	74	73.5	73.5	73.5	73.5	73.5	73	73	73	73	73	72.5	72.5	72.5
30	31 32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1 H70802 hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis	C;Date: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: H70802 R;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mathire, 303, 53-54, 1908	A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987 A; Accession: H70802	A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-100 <col/> A;Cross-references: GB:AL022120; GB:AL123456; NID:g3261558; PIDN:CAA17966.1; PID:g296 C;Genetics: A;Genetics: Ry3874
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Gaps ö Length 100; Indels Query Match 98.8%; Score 486; DB 2; Best Local Similarity 99.0%; Pred. No. 3.1e-37; Matches 99; Conservative 0; Mismatches 1; g

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hypothetical protein MLCB628.13c - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 13-Aug-1999 #text\_change 21-Jul-2000
C;Accession: T1003
R;Eiglmeier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A;Title: Use of an ordered cosmid library to deduce the genomic organization of Mycob A;Reference number: 216917; MUID:93188700
A;Accession: T10032
A;Accession: T10032
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-100 <EIG>

A;Cross-references: EMBL:Y14967; NID:92370268; PIDN:CAA75210.1; PID:92370280

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hypothetical protein Rv3905c - Mycobacterium tuberculosis (strain H37RV)

hypothetical protein Rv3905c - Mycobacterium tuberculosis

c;Species: Mycobacterium tuberculosis

c;Date: 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: B70600

Rocassion: B70600

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A; Residues: 1-103 <COL>
A; Cross-references: GB:294121; GB:AL123456; NID:g3261736; PIDN:CAB08096.1; PID:e31227
A; Experimental source: strain H37RV
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                      T38435

Colled coil protein - fission yeast (Schizosaccharomyces pombe)

Colled coil protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dac-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T38435

R;McDougall, R; Wood, V; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, December 1997

A;Reference number: Z21793

A;Accession: T38435

A;Accession: T3843
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                                     - RFYOMF
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|| || || :
-QWSGASSD---
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; Pred. No. 0.19;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Mismatches
64 KQKQELDEISTNIRQAGVQYSRADEEQQQAL 94
                                                                                                                                                                  598 ELKLKLNEANKKY -----QELAIS 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::|| ::|| :||:
550 KQAGENHYSNLSSDYETQIKSLESSL---
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23.1%;
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Matches 24; Conservative
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Best Local Similarity
Matches 21; Conserva
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R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
B;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
Bacteriol. 181, 6509-6515, 1999
A;Title: A;Hills anthracis plasmid harbori
A;Reference number: A59091; MUID:99445483
A;Accession: B59103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, December 1998
A; Reference number: 221585
A; Reference number: 735661
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A;Residues: 1-1186 <MUR>
A;Cross-references: EMBL:AL034447; PIDN:CAA22420.1; GSPDB:GN00070; SCOEDB:SC7A1.21
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A;Residues: 1-410 <-OKI>
A):Cross_rreferences: GB:AR065404; NID:94894216; PIDN:AAD32402.1; PID:94894314
A;Experimental source: strain Sterne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Jun-2000
C;Accession: T35661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Bacillus anthracis
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         686 AGRRRECAALVEELGERRRAADREKSSVAQ---QLGRLAGQARGAAGEAERSAAAAERAQ 742
                                                                                                                         Gaps
                                                                                                                                                                                                    1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein pX01-98 - Bacillus anthracis virulence plasmid pX01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable chromosome associated protein - Streptomyces coelicolor
                                     Length 100;
                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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EALDKALTEVEELAE--RLAVAEEMPVEEEPDTAARDRL 779
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                                 Score 187; DB 2;
Pred. No. 2.7e-10;
); Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 EAANKOKOELDEISTNIRQAGVOYSRADEEQOOALSSOM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: SCOEDB:SC7Al.21
C;Superfamily: chromosome segregation protein SMC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.8%; Score 92.5; 32.3%; Pred. No. 1.
            38.0%; Scorv
40.0%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain A3(2)
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                                                                                                                Conservative
                                     Query Match
Best Local Similarity
Matches 40; Conserv
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A;Genome: plasmid
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Best Local S
Matches 26
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A; Residues: 733-866 A; Cross-references: GB:J03995; NID:g159874; PIDN:AAA29412.1; PID:g159875
A; Cross-references: GB:J03995; NID:g159874; PIDN:AAA29412.1; PID:g159875
B; Mgozi, E.; Erondu, N.E.; Donelson, J.E.
submitted to the EMBL Data Library, April 1990
A; Description: Characterization of a myosin-like antigen from Onchocerca volvulus.
A; Reference number: S27825
A; Mccession: S27825
A; Mccession: S27825
A; Mclecule type: mRNA
A; Residues: 733-874, 'E', 876-916,'S', 918-1038, 1040-1047,'S', 1049-1283,'E', 1285-1347,'E
C; Genetics:
A; G
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
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A; Title: Molecular characterization of a kinesin-related antigen of Leishmania chagas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-97 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable PE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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C;Species: Leishmania chagasi
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1752 LDEEKRTMENILHETALQREAIESSLNALERENKELHRNCAQLQQQIAQLELENGNRLIQ 1811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 2022; 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LGQEAGNFERISGDLKTQIDQVESTAGSLQGQ----WRGAAGTAAQAAVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.2%; Score 84.5; DB 2;
34.9%; Pred. No. 0.45;
tive 7; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1812 LTNKQREEYDKFAQNMRTEKIQIERIIENRERSLKSRI 1849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.7%; Score 87; DB 25.5%; Pred. No. 7.5; iive 22; Mismatches
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Best Local Similarity
Matches 25; Conserv
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les 29; Conserv
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C;Species: Onchocerca volvulus
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Jun-2000
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Jun-2000
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Jun-2000
R;Triteeraprapab, S.; Richie, T.L.; Tuan, R.S.; Shepley, K.J.; Dinman, J.D.; Neubert, T. Mol. Biochem. Parasitol. 69, 161-171, 1995
MA;Title: Molecular cloning of a gene expressed during early embryonic development in Ond A;Reference number: 222341; MUID:95287898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL021930; GB:AL123456; NID:g3261524; PIDN:CAAL7362.1; PID:e125247
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0287
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A;Title: Construction of Onchocerca volvulus cDNA libraries and partial characterization A;Reference number: A54513; MUID:89127417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #Molecule type: mRNA
A; Residues: 733-874,'E',876-916,'S',918-1038,1040-1047,'S',1049-1283,'E',1285-1363 <EROY
A;Cross-references: GB:M30398
                                                                                                                                                                                                                                               probable transcription regulator Rv0287 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature: 393, 537-544, 1998
A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MUID: 98295987
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R)Erondu, N.E.; Donnelson, J.E.
MAOI. BIOChem. Parasitol. 40, 213-224, 1990
A)Title: Characterization of a myosin-like antigen from Onchocerca volvulus. A)Reference number: A44939; MUID:90301142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A;Residues: 1-2022 <TRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 87.5; DB Pred. No. 0.24; B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ovtl protein - nematode (Onchocerca volvulus)
N;Alternate names: myosin-like antigen
                  67 EVQLGLSMLAAAIAHAGAGYQHNETASAQVL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 QAGVQYSRADEEQQQALSSQMGF 10Q
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34.9%;
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Best Local Similarity
Matches 29; Conserva
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A; Molecule type: mRNA

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A;Gene: MYH
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;82-752/Domain: myosin motor domain homology <MMO>
                    A; Cross-references: GB:L01634; PIDN:AAA29905.1
A; Experimental source: strain Brazilian LE
C; Genetics:
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Best Local Similarity 22.7
Matches 22; Conservative
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A; Molecule type: DNA
A; Residues: 1-163 <WHI>
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A; Molecule type: mRNA
A; Residues: 1-715 <SIM>
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Best Local S
Matches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myosin heavy chain - fluke (Schistosoma mansoni) (fragment)
N.Alternate names: surface antigen, 200K
C; Species: Schistosoma mansoni
C; Species: Schistosoma mansoni
C; Species: 22.Nov-1933 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C; Accession: S33068
R; Soisson, L.M.A.; Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M.J.; Immunol. 149, 3612-3620, 1992
A; Title: Induction of protective immunity in mice using a 62-kDa recombinant fragment of A; A; Accession: S33068
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A;Accession: A59287
                                                                                                       A,Cross-references: GB:L07879; NID:g308884; PIDN:AAA29254.1; PID:g308885
A,Experimental source: MHOW/BK/BA/2,C.1
A;Note: sequence extracted from NCB1 backbone (NCBIN:122864, NCBIP:122865)
C;Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology
C;Stywords: APP, nucleotide binding; P-loop
F;13-398/Domain: kinesin motor domain homology <KMOT>
F;12-129/Region: nucleotide-binding motif A (P-loop)
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C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
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                                                                                                                                                                                                                                                                                                           Length 955;
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A;Note: the authors translated the codon CAA for residue 346 as
C;Superfamily: myosin heavy Chain; myosin motor domain homology
C;Keywords: ATP; surface antigen
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A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
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C; Accession: A59287
R; Weston, D.S.; Schmitz, J.; Kemp, M.; Kunz, W.
Mol. Biochem. Parasitol. 58, 161-164-1993
                                                                                                                                                                                                                                                                                                           16.6%; Score 81.5; 29.2%; Pred. No. 10
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21.9%; Pred. No.
A; Reference number: A47334; MUID: 93133867
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                                                           A; Molecule type: DNA
A; Residues: 1-955 <BUR>
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A; Residues: 1-527 <SOI>
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                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                     31;
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A;Cross-references: GB:AE001873; GB:AE000513; NID:g6457764; PIDN:AAF09701.1; PID:g645
A;Experimental source: strain R1
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C;Date: 12-May-1994 #sequence_revision 14-Jul-1994 #text_change 19-Jan-2001
C;Date: 12-May-1994 #sequence_revision 14-Jul-1994 #text_change 19-Jan-2001
C;Accession: A61231; A34876; 152562; I61692
R;Simons, M.; Wang, M.; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelste Circ. Res. 69, 530-539; 1991
A;Title: Human nonmuscle myosin heavy chains are encoded by two genes located on diff A;Reference number: A61231; MUID:91316803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Baccasion: F7559
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Wanatheyan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896
A;Accession: F75559
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                                                                                                                                                                3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin type 9; NMMHC-A
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         Length 1940;
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                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
16.5%; Score 81; DB 2;
llarity 21.9%; Pred. No. 25;
Conservative 24; Mismatches 4
                                                                                                                                                                                                                                                                                             1095 KELQTRIQELEEDLEAERAARSKAEKSRQQ-LESEL 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 FQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQAL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOEAAONAREKAODVRANVHESAODFRAGAOEQAOTL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 79.5; D
; Pred. No. 2.3;
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin heavy chain nonmuscle form A - human N;Alternate names: cellular myosin heavy chain; N;Contains: myosin ATPase (EC 3.6.1.32)
                                                                                                                                                                                                                                                      63 NKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQM
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C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleo
F; 84-763/Domain: myosin motor domain homology <AMOT>
F; 174-181/Region: nucleotide-binding motif A (P-loop)
F; 541-575/Region: actin binding #status predicted
F; 653-675/Region: actin binding #status predicted
F; 836-1999/Domain: coiled coil #status predicted <COI>
   A;Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian br
A;Reference number: S21801; MUID:92235856
                                                                                                                                                     A;Cross-references: EMBL:X62659
R;Sun, W.; Chantler, P.D.
Biochem. Blophys. Res. Commun. 175, 244-249, 1991
A;Title: A unique cellular myosin II exhibiting differential expression in the cerebr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1820 EEQLDNETKERQAACKOVRRTEKKLKDVLLQVDDERRNAEQYKDQADKASTRLKQLKRQL 1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ATLGQEAGN-----FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---KQELDEISTNIRQAGVQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1277-1999/Region: light meromyosin
F;125/Modified site: N6.N6.N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;693,703/Active site: Cys #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
F;1943/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.2%; Score 79.5; Ellarity 23.1%; Pred. No. 35; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                          A; Reference number: PN0013; MUID:91151356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001, 11:48:30
                                                                                                                                                                                                                                                                                                       A; Accession: PN0013
A; Molecule type: mRNA
A; Residues: 1914-1998,'I' <SU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|| |:| ;:
1880 EEAEEEAQRANASR 1893
                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: brain
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                                                                                            A; Molecule type: mRNA
A; Residues: 1-1999 <SUN>
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Best Local Similarity
Matches 31; Conserv
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e: 369 sec
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                                                                  A; Accession: S21801
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Job time:
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C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Reywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Saez, C.G.; Myers, J.C.; Shows, T.B.; Lelnwand, L.A.
Proc. Natl. Acad. Sci. US.A. 87, 1164.1168, 1990
A;Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through alterr
A;Reference number: A34876; MUID:90138958
                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 715-1961 CSAE>
A; Cross-references: GB:M31013; NID:g18035; PIDN:AAA36349.1; PID:g189036
A; Cross-references: GB:M31013; NID:g18035; PIDN:AAA36349.1; PID:g189036
R; Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.A.
Blood 78, 1825-1833, 1991
A; Tetle: Cellular myosin heavy chain in human leukocytes: isolation of 5' CDNA clones,
A; Reference number: 152562; M0ID:92003925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ů,
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N;Alternate names: myosin II
N;Contains: myosin ArPasse (EC 3.6.1.32)
C;Species: Rattus norvegicus (Norway rat)
C;Bate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: $21801; PN0013; $18134
R;Sun, W.; Chantler, P.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1821 EEQLDNETKERQAACKQVRRTEKKLKDVLLQVDDERRNAEQYKDQADKASTRLKQLKRQL 1880
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A; Cross-references: GB:M69180; NID:9189029; PIDN:AAA61765.1; PID:9189030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: L29141; NID: 9457249; PIDN: AAA20904.1; PID: 9531134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F)84-764/Domain: myosin myotor domain homology 
F)84-764/Domain: myosin myotor domain homology 
F)174-181/Region: myotor domain homology 
F)174-181/Region: actin binding #status predicted
F)52-565/Region: actin binding #status predicted
F)52-565/Region: actin binding #status predicted
F)837-1938/Domain: coiled coil #status predicted <COI>
F)837-1277/Domain: coiled coil #status predicted <COI>
F)1278-1961/Domain: light meromyosin #status predicted <LMM>
F)199-1961/Domain: carboxyl-terminal <CBT>
F)125/Modified site: ATP (LY9) #status predicted
F)68/Anding site: ATP (LY9) #status predicted
F)694,704/Active site: Cys #status predicted
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23.1%; Pred. No. 50,
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J. Mol. Biol. 224, 1185-1193, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 16.2
Best Local Similarity 23.1
Matches 31; Conservative
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A; Residues: 182-218 <BEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: I61692
                                                                                                                                                        A; Accession: A34876
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A;Gene: GDB:MYH9
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 5, 2001, 11:43:21; Search time 41.8 Seconds (without alignments) 81.951 Million cell updates/sec Run on:

US-09-462-480-5 492 1 MAEMKTDAATLGQEAGNFER......VQYSRADEEQQQALSSQMGF 100 Title: Perfect score: Sequence:

93435 segs, 34255486 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	49 onchocer	P46865 leishmania	P35579 homo sapien	ovis	Q44549 anabaena va	P12270 homo sapien	anaba	7							P25691 ovis aries	7	-		P15492 vibrio chol		P55439 rhizobium s	P42638 schistosoma	P21823 enterobacte			~	_		P80703 galleria me		P02567 caenorhabdi	260	P21758 bos taurus
SUMMARIES	ΩI	ANT1_ONCVO	KINL_LEICH	MY SN_HUMAN	K2M2_SHEEP	FENR_ANAVA	TPR_HUMAN	PYS1_ANASP	G160_MOUSE	FENR_ANASO	KINH_DROME	PHP_DROME	PYS1_MASLA	FLA2_CAMJE	YIO9_YEAST	K2M3_SHEEP	BPHC_PSES1	MYSN_CHICK	MESE_LEUME	HLYB_VIBCH	PYS1_SYNEL	Y4FA_RHISN	TPM2_SCHMA	MCPD_ENTAE	HTR1_HALHA	HTR1_HALN1	PEX5_PICPA	CLPB_MYCPN	LMB3_HUMAN	APL3_GALME	APL3_MANSE	MYSD_CAEEL	IRPA_SYNP7	MSRE_BOVIN
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æ	Query	17	16.6		15.4	15.3	15.2	15.1	•	14.9	4	14.8			14.7		14.5		•			14.3			4	÷.	4	4	14.1	٠.	4	4		13.9
	Score	_	81.5	78.5	7	75.5	75	74.5	7	e,		73	72.5	72.5	72.5	72	71.5	71.5	71	71	70.5	70.5	70	70	70	70	70	70	69.5	69	69	S	68.5	
	Result No.	1	7	ო	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33

P39285 escherichia P12845 caenorhabdi	Q9zeq8 erwinia chr P48667 homo sapien	P48668 homo sapien	P30141 streptococc	006942 streptococc	P/9955 xenopus lae P06536 rattus norv	P13538 gallus gall	Q10973 mycobacteri
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68.5	68 68	68	67.5	67.5	67.5	67.5	49
34 35	36 37	38	40	41	4 4	44	45

# ALIGNMENTS

STA	01-NOV-1995 (Rel. 32, 30-MAY-2000 (Rel. 39, MAJOR ANTIGEN.		RP 11)  RX MIJ.  RX MEDLINE-95287898; PubMed-7770081;  RA Triteeraprapab S., Richie T.L., Tuan R.S., Shepley K.J., Dinman J.D.,  RA Neubbert T.A., Scott A.L.;  RA Neubert T.A. Scott A.L.;  RT "Molecular cloning of a gene expressed during early embryonic  RT development in Onchocerca volvulus.";  RM Mol. Biochem. Parasitol. 69:161-171(1995).		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. CC the European Bioinformatics Institute. There are no restrictions on its cc use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cc entities requires a license agreement (See http://www.isb-sib.ch/announce/cc or send an email to license@isb-sib.ch).		Ouery Match 17.7%; Score 87; DB 1; Length 2022; Best Local Similarity 25.5%; Pred. No. 3.2; Matches 25; Conservative 22; Mismatches 41; Indels 10; Gaps 2;
R A H A D		00000	x	* * * * * * * * * * * * * * * * * * * *		) U O O O X F F F F V	

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11 LGQEAGNFERISGDLKTQIDQVESTAGSLQGQ----WRGAAGTAAQAAVV-----RFQE 60

912 ELASQLEATAAAKSSAEQDR--ENTRAALEQQLRDSEERAAELASQ 955

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NCBI_TaxID=9606;
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                MYSN_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P17119; 3KAK..

R HSSP; P17119; 3KAK..

R InterPro; 1PR00175; -.

DR PF00225; Kinesin; 1.

DR PROSITE; P50067; KINESIN_MOTOR_DOMAIN1; 1.

DR PROSITE; P50067; KINESIN_MOTOR_DOMAIN2; 1.

KW MOTOR protein; Microtubules; ATP-binding; Coiled coil; Repeat.

KW MOTOR protein; Microtubules; ATP-binding; Coiled coil; Repeat.

FT DOMAIN 426 >955 COILED COIL (POTENTIAL).

122 129 ATP (POTENTIAL).

7 X 39 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRESTRATLEQOLRESEERAAELASQLESTTAAKMSAEQDRESTRATLEQOLRDSEERAA 911
                                                                                                                                                                                                                                                                                                             Burns J.M. Jr., Shreffler W.G., Benson D.R., Ghalib H.W., Badaro R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 EMKTDAATLGQEAGNFERISGDLKTQIDQV-----ESTAGSLQGQWRGAAGTAA 51
                                                                                                                                                                                                                          Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                           "Molecular characterization of a kinesin-related antigen of Leishmania chagasi that detects specific antibody in African and American visceral leishmaniasis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 955;
                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
-i- DEVELOPMENTAL STAGE: PREDOMINANT IN AMASTIGOTES.
-i- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8CA76815BE84C6E9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                             1812 LINKOREEYDKFAQNMRTEKIQIERIIENRERSLKSRI 1849
61 AANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQM 98
                                                                                                                                    ou mov-1995 (Rel. 32, Created) - 01-NOV-1995 (Rel. 32, Last sequence update) 10-CT-1996 (Rel. 34, Last annotation update) MINESIN-LIKE PROTEIN K39 (FRAGMENT).
                                                                                                     955 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.6%; Score 81.5; D
29.2%; Pred. No. 4.5;
Live 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PARTIAL)
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-MHOM/BR/82 / ISOLATE BA-2;
MEDLINE=93133867; Pubmed=8421715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                               (Rel. 32, Created)
(Rel. 32, Last sequ
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                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    955
955 AA;
                                                                                                                                                                                                           Leishmania chagasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                        NCBI_TaxID=5669;
                                                                                                                                 01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 31;
                                                                                                    KINL_LEICH
                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                             Reed S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
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                                                                        RESULT 2
KINL_LEICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN SUBDNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBDNITS (MHC), 2 ALKALI LIGHT CHAIN SUBDNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC.2).

DOMAIN: THE RODLIKE TAIL SCOURENE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K., Gdula D., Adelstein R.S., Weir L., "Human nonmuscle myosin heavy chains are encoded by two genes located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 714-1960 FROM N.A.
MEDLINE=90138958; PubMed=1967836;
Sacz C.G., Myers J.C., Shows T.B., Leinwand L.A.;
Lindman nonmuscle myosin heavy chain mRNA: generation of diversity through alternative polyadenylylation.";
Proc. Natl. Acad. Sci. U.S.A. 87:1164-1168(1990).
-i- FUNCTION: CELLULAR WOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS, CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBFRAGMENT (S2).
SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST
MYSN_HUMAN STANDARD; PRT; 1960 AA.
P35579; 060805;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYOSIN HEAVY CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M. Arnaout M.A., Clayton L.K., Tenen D.G.; "Cellular myosin heavy chain in human leukocytes: isolation of 5'
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA clones, characterization of the protein, chromosomal localization, and upregulation during myeloid differentiation."; Blood 78:1826-1833(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-715 FROM N.A. MEDLINE=91316803; PubMed=1860190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-1337 FROM N.A. MEDLINE-92003925; Pubmed-1912569;
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EMBL; M81105; AAA5988.1; -.
EMBL; M69180; AAA61765.1; -.
EMBL; M31013; AAA86349.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Circ. Res. 69:530-539(1991).
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                            TYPE A) (NMMHC-A). MYH9.
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PRESENT IN ALL VERTEBRATE EPITHELIAL CELLS
                                                                                                                                                                                                         Intermediate filament; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53681 MW;
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                                                                                                                                                                                          PROSITE; PS00226; IF; 1.
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416
491
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284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          284
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                                                                                                                                                                                                                                                                CALMODULIN-BINDING (BY SIMILARITY).
CALMODULIN-BINDING (BY SIMILARITY).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
EAI -> RGH (IN REF. 3).
T -> S (IN REF. 3).
T -> M (IN REF. 4).
C -> Y (IN REF. 4).
KG -> GR (IN REF. 4).
KG -> GR (IN REF. 2).
T -> A (IN REF. 2).
T -> A (IN REF. 2).
S -> G (IN REF. 2).
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01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotate)
01-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                       GLOBULÁR HEAD (S1).
RODLIKE TAIL (S2 AND LAM DOMAINS)
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1960;
                                                                                                                                                    ; Actin-binding; Alkylation; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          588F84BB8C106E6F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KQELDEISTNIRQAGVQYSRADEEQQQALSSQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.0%; Score 78.5; D
21.7%; Pred. No. 18;
iive 23; Mismatches
                                                                                                                                                                                                                                                     ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGQEAGNFERISGDLK ---TQIDQV -----
                                                                                                                                                                         Multigene family; Calmodulin-binding
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                           InterPro; IPR000049; -.
InterPro; IPR001699; -.
InterPro; IPR001509; -.
Pfam; PF00612; IQ; I.
Pfam; PF001576; Myosin_tail; I.
Pfam; PF00193; Myosin_head; I.
PRINTS; PR00193; MYOSINEAVY.
PROSITE; PS50096; IQ; I.
Myosin; Coiled coil; Actin-bindii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P15241;
01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         226531
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Best Local Similarity 21.77
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Caprinae; Ovis.
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HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1960
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1764
1771
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q.R
                                                                                                                                                                                                                                                                                                                                | coil; Heptad repeat pattern; Keratin.
BLOCKED.
MISCELLANEOUS: THE LOW-SULFUR PROTEINS, DERIVED FROM THE MICROFIBALLLAR FRACTION OF WOOL EXTRACTS, ARE COMPOSED OF TWO FAMILIES, BACH CONSISTING 0F 4 HOWOLOGOUS SUBUNITS: THE TYPE I COMPONENTS (8C-1, 8C-2, 8A & BB) AND THE TYPE II COMPONENTS (5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: MAY BE BOUND TO THE THYLAKOID MEMBRANE CANCHORED TO THE THYLAKOID-BOUND PHYCOBILISOMES.
-!-.SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mannan R.M., Matthijs H.C.P., Pakrasi H.B.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!-.CATALYTIC ACTIVITY: REDUCED FERREDOXIN + NADP(+) = OXIDIZED
                                                                                                        7A, 7B, AND 7C).
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
--- INTERPRO: IPR001664; -.
--- INTERPRO: IPR003054; -.
--- INTERPRO: ITPEZERERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBL_TaxID=1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 76; DB 1; Length 491; 22.9%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A801771FE3831ABE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
FERREDOXIN--NADP REDUCTASE (EC 1.18.1.2) (FNR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        illarity 22.9%; Pred. No. 6.9; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COIL 2.
C -> G OR S.
C -> S.
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LINKER 12.
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TAIL.
COIL 1A.
LINKER 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q -> H.
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUNCTION: COMPONENT OF THE CYTOPLASMIC FIBRILS OF THE NUCLEAR PORE COMPLEX INDLICARED IN NUCLEAR PROTEIN IMPORT: ITS AMINO TERMINUS IS INVOLVED IN ACTIVATION OF ONCOGRNIC KINASES.
SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF THE NUCLEAR PORE COMPLEX. THE ASSEMBLY OF THE NPC IS A STREWISE PROCESS IN WHICH TRP-CONTAINING PERIPHERAL STRUCTURES ASSEMBLE AFTER OTHER COMPONENTS, INCLUDING P62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS, AND CHARACTERIZATION.

MEDLINE=95096166; PubMed=7798308;
Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T.,
Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.;

"Tpr, a large coiled coil protein whose amino terminus is involved in activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";
J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                         38 SLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG-----VQYSRADEEQQQ 92
                                                                                                                                                                                                                                                                                                                                                                                           2 SNQGAFEGAANVESGSRVEVYEVVGMRQNEETDQTNYPIRKSGSVFIRVPYNRMNQEMQR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=93064711; Pubmed=1437155;
Mitchell P.J., Cooper C.S.,
"The human tpr gene encodes a protein of 2094 amino acids that has extensive colled-coll regions and an acidic C-terminal domain.";
Oncogene 7:2329-2333(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                             CPCD-LIKE.
NADP (RIBOSE PART) (BY SIMILARITY)
660BAA2DCF59BB6 CRC64;
                                                                                                                             InterPro; IPR001685; -.
InterPro; IPR001685; -.
Pfam; PP01383; CpcD; 1.
Pfam; PP0175; oxidored_fad; 1.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; NADP; FAD; Thylakoid membrane;
                                                                                                                                                                                                                                                                                                                  Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          King H.W.S., Tempest P.R., Merrifield K.R., Rance A.J.; "tpr homologues activate met and raf."; Oncogene 2:617-619(1988).
                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                  15.3%; Score 75.5; DI 30.0%; Pred. No. 6.8; tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2349 AA
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MEDLINE-88262257; PubMed=3387099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                          48826 MW;
                                                                                                  EMBL; L26346; AAA91046.1; -.
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                              306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1989 (Rel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens (Human)
                                                                                                                                                                                                                                                                          440 AA;
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOPROTEIN TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel
01-OCT-2000 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                 HSSP; P21890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPR_HUMAN
P12270;
                                                                                                                                                                                                                                                           NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
TISSUE SPECIFICITY: HIGHEST IN TESTIS, LUNG, THYMUS, SPLEEN AND BRAIN, LOWER LEVELS IN HEART, LIVER, AND KIDNEY.
DISEASE: INVOLVED IN TUMORIGENIC REARRANGEMENTS WITH THE MET, TRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Belknap W.R., Haselkorn R.; "Cloning and light regulation of expression of the phycocyanin operon of the cyanobacterium Anabaena."; embo J. 6:871-884(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       900 EIATLKOHLSNMEVQVASOSSORTGKGOPSNKEDVDDLVSQLRQTEEQVNDLKERLKTST 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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1-APR-1998 (Rel. 07, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
PHYCOBILISOME 8.9 KDA LINKER POLYPEPTIDE, PHYCOCYANIN-ASSOCIATED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2349;
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBL_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFDD6885CEDCA9EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 GTAA - - QAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQ 92
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                                                                                                                                                                                                                                                                                                                                                                         protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLU.
POLY-ASP.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                    Heptad repeat pattern; Coiled coil;
Chromosomal translocation; Nuclear p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 DAATLGQEAGNFE-----RISG----
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MEDLINE-87246520; PubMed-3109890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265600 MW;
                                                                                                                                                                                                                                                                EMBL; X66397; CAA47021.1; -. EMBL; Y00672; CAA68681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   595
                                                                                                                                                                                                                                                                                                         PIR; S00928; S00928
MIM; 189940; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                           OR RAF GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1833
1957
2295
2349
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Best Local S
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INSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO EXPRESSION IN LEXDIG CELLS, SPERMATOGONIA, OR SPERMATOCYTES.

SIMILARITY: HIGH, TO HUMAN GOLGIN-LAW, MET-19 OR MET-30 IS THE CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq. 7:71-82(1997).
FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 GOWRGAAGTAAQAA--VVRFQEAANKQKQELDEISTNIRQAG-----VQYSRADEEQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Cloning and molecular characterization of cDNA encoding a mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  male-enhanced antigen-2 (Mea-2): a putative family of the Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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149880 MW; 3230636962C687B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                               Phycobilisome, Photosynthesis.
SEQUENCE 80 AA, 8895 MW; 52DF2D7DEF5444D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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15-DEC-1998 (Rel. 37, Last annotation update)
GOLGIN-160 (MALE-ENHANCED ANTIGEN-2) (MEN-2).
GOLGA3 OR MERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74.5; DI
Pred. No. 1.4;
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MGD; MGI:96958; Golga3.
Spermatogenesis; Developmental protein.
201
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MEDLINE=97217683; PubMed=9063644;
Kondo M., Sutou S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%;
35.6%;
                                                                                                                                                                                                                                                    EMBL; X05239; CAA28865.1;
PIR; D29674; D29674.
InterPro; IPR001685; -.
Pfam; PF01383; CpcD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
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1325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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DNA Seq. 7:7
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P55937;
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Matches
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Fillat M.F., Flores E., Gomez-Moreno C.;
Homology of the N-terminal domain of the petH gene product from
Anabaena sp. PCC 7119 to the CpcD phycobilisome linker polypeptide.";
Plant Mol. Biol. 22:725-729(1993).
                                                                                                            201 AAAAQHQDQNQEANGEVRSRRDSICSSVSMESSLAEPQDELLQILKDKRRLEGQVEALSL 260
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sancho J., Peleato M.L., Gomez-Moreno C., Edmondson D.E.; "Purification and properties of ferredoxin-NADP+ oxidoreductase from the nitrogen-fixing cyanobacteria Anabaena variabilis."; Arch. Biochem. Blophys. 260:200-207(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91088322; Pubmed-2124680; Fillat M.F., Bakker H.A.C., Welsbeek P.J.; "Sequence of the ferredoxin-NADP(+)-reductase gene from Anabaena PCC 7119.";
                                                                         ----SLQGQWRGAAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLUIAR LOCATION: MAY BE BOUND TO THE THYLAKOID MEMBRANE OR ANCHORED TO THE THYLAKOID-BOUND PHYCOBILISOMES.
-!- SIMILARITY: WITH OTHER SPECIES FNR.
-!- SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBILISOME LINKER PROTEIN CPCD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99119196; PubMed=9922134;
Martinez-Julvez M., Hermoso J., Hurley J.K., Mayoral T.,
Sanz-Aparicio J., Tollin G., Gomez-Moreno C., Medina M.;
Role of Arg100 and Arg264 from Anabaena PCC 7119 ferredoxin-NADP+
reductase for optimal NADP+ binding and electron transfer.";
Biochemistry 37:17680-17691(1998).
-:- CATALYTIC ACTIVITY: REDUCED FERREDOXIN + NADP(+) = OXIDIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 137-440.
MEDLINE=97045988; PubMed=8890910;
MEDLINE=97045988; PubMed=8890910;
MEDLINE=97045988; PubMed=8890910;
Montecilla-Camps J.C., Frey M.;
"X-ray structure of the ferredoxin:NADP+ reductase from the granobacterium hanbaena PCC 7119 at 1.8-A resolution, and crystallographic studies of NADP+ binding at 2.25-A resolution.";
J. Mol. Biol. 263:20-39(1996).
                                      26;
                                                                                                                                                                    DB 1; Length 1325;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena
NCBL_TaxID=1168;
                                                                                                                                                49 TAAQAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQM 98
                                      Indels
                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 146-440.
                                                                                                                                                                                                                                                                                                             01-MAY-1991 (Rel. 18, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FERREDOXIN--NADP REDUCTASE (EC 1.18.1.2) (FNR).
                                                                                                                                                                                                                                                                              440 AA
                                    23; Mismatches
                                                                         9 ATLGQEAGNFERISGDLKTQIDQVESTAG-----
15.0%; Score 74; 24.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 18:7161-7161(1990).
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88132819; PubMed-3124746;
                                                                                                                                                                                                                                                                                                                                                                                                            Anabaena sp. (strain PCC 7119).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 137-440 FROM N.A.
                                    27; Conservative
                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 152-183.
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                      Matches
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLQCQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG-----VQYSRADEEQQQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNOGAFDGAANVESGSRVFVYEVVGMRQNEETDQTNYPIRKSGSVFIRVPYNRMNQEMQR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93030741; PubMed=1384131;
Gho M., McDonald K., Ganetzky B., Saxton W.M.;
Effects of kinesin mutations on neuronal functions.";
Science 258:313-316(1992).
-!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
-1- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
                                                                                                                                                                                                                                                                                                                                                                                               CPCD-LIKE.
NADP (RIBOSE PART) (BY SIMILARITY).
I -> L (IN REF. 3).
8E1FG1D0F09338B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89168428; PubMed-2522352;
Yang J.T., Laymon R.A., Goldstein L.S.B.;
"A three-domain structure of kinesin heavy chain revealed by sequence and microtubule binding analyses.";
Cell 56:879-889(1989).
                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0371; FPNCR.
Oxidoreductase; Flavoprotein; NADP; FAD; Thylakoid membrane;
Phycobilisome; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 73.5; Di
; Pred. No. 10;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                    ; oxidored_fad; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              48865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%;
30.0%;
                                                                                                                         EMBL; X72394; CAA51088.1; -. EMBL; X54039; CAA37973.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                   InterPro; IPR001433; -.
InterPro; IPR001665; -.
InterPro; IPR001709; -.
Pfam; PF01383; CpcD; 1.
Pfam; PF00175; oxidored_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                       A27581; A27581.
S13103; S13103.
S33479; S33479.
S35150; S35150.
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1QUF; 17-SEP-97.
1BJK; 18-NOV-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINESIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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SEQUENCE FROM N.A.
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Best Local Simil
Matches 18; C
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P17210;
                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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This
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                                                                                                                                                                                        PIR;
PIR;
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DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF

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                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00225; Kinesin, ...
PRINTS; PR00380; KINESINHEAVY.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor_protein; Microtubules; ATP-binding; Coiled coil.
Motor_protein; MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION, AND A SMALL GLOBULER C-TERMINAL DOMAIN WHICH INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS), VESICLES AND MEMBRANOUS ORGANELLES.

MISCELLANGOUS: WUTANT FLIES DISPLAY IMPAIRED ACTION POTENTIAL PROPAGATION AND NEUROPREAST IMPAIRED ACTION POTENTIAL DROCHOATIONS, BUT ARE STILL CAPABLE OF TRANSPORTING CERTAIN SINGERRANDES, INCLUDING SYNAPTIC VESICLES, TO THE NERVE TERMINAL. SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            618 ISKMKTEAKNIAQRCSNMETQQADSNKKISEYEKDLGEYRLLISQHEARMKSLQESMR-- 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTAAQAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRAD-----EEQQQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9966CBC35BA74FD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MICROTUBULE-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1589 AA.
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; Pred. No. 24;
19; Mismatches
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MEDLINE-92146957; PubMed-1346609;
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24.8%;
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HSSP, P56536; ZKIN.
Flybase; FBqn0001308; Khc.
InterPro; IPR001752; -.
Pfam; PF00225; Kinesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Conservative
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180
92
975 AA;
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01-OCT-2000
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P39769:
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SEQUENCE
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Best Local :
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PHYCOBILISOME 8.9 KDA LINKER POLYPEPTIDE, PHYCOCYANIN-ASSOCIATED, ROD (ROD CAPPING LINKER PROTEIN).
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                                                                                                                                                           NCBI_TaxID=1191;
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                                                                                                                                                 **MEDLINE-92039031; PubMed=1937015;
A Deatrick J., Daly M., Randsholt N.B., Brock H.W.;
Deatrick J., Daly M., Randsholt N.B., Brock H.W.;
Deatrick J., Daly M., Randsholt N.B., Brock H.W.;
Deatrick J., Daly M., Randsholt N.B., Brock H.W.;
Detentially encodes two homologous zinc-finger proteins.";
Gene 105:185-195(1991).

- FUNCTION: BINDS TO POLYTENE CHROMOSOMES. SEEMS TO INTERACT WITH PROTEINS ALREADY BOUND TO PROMOTER COMPLEXES AND MAY BE A NEGATIVE REGULATING THE EXPRESSION OF SEGMENTATION GENES. PLAYS A ROLE IN REGULATING THE EXPRESSION OF OTHER PAIR-RULE GENES SICH AS EVE, FTZ, AND H.

- SUBCELLULAR LOCATION: NUCLEAR.
- SUBCELLULAR LOCATION: NUCLEAR.
- ITISSUE SPECIFICITY: SALIVARY GLANDS.
- SIMILARITY: TO MOUSE EARLY DEVELOMENT REGULATOR PROTEIN RAE-28.
- SIMILARITY: TO MOUSE EARLY DEVELOMENT REGULATOR PROTEIN RAE-28.
- SIMILARITY: TO MOUSE EARLY DEVELOMENT REGULATOR PROTEIN RAE-28.
- CHILL SIMILARITY: TO MOUSE EARLY DEVELOMENT REGULATOR PROTEIN RAE-28.
   Decamillis M., Cheng N.S., Pierre D., Brock H.W.; "The polyhomeotic gene of Drosophila encodes a chromatin protein that shares polytene chromosome-binding sites with Polycomb.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAEMKTDAATLGQEAGNFERISGDL-----KTQIDQVESTAG-----SL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> A (IN REF. 2).
A6DF0CF9106E1891 CRC64;
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D -> A (IN REF. 2).
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(Rel. 11, Last sequence update)
(Rel. 25, Last annotation update)
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SER/THR-RICH.
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GLN-RICH.
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M.
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PIR; S23632; S23632.
FlyBase; FBgn0004861; ph-p.
Interpro; IPR01160; -.
Pfam; PF00536; SAM; 1.
Zinc-finger; Developmental pr
                                                                                                 Genes Dev. 6:223-232(1992).
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1589 AA;
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01-APR-1993
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         RRITER REPRESENTATION OF THE PROPERTY OF THE P
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Blooinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
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J. Biol. Chem. 265:17798-17804(1990).
-!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
-!- SUBUNIT: HEPEROPOLYMER OF FLAA AND FLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                Fuedlistaller P., Suter F., Zuber H.;
"Linker polypeptides of the phycobilisome from the cyanobacterium wastigocladus laminosus: amino-acid sequences and relationships.";
Biol. Chem. Hoppe-Seyler 366:993-1001(1985).
-: SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.7%; Score 72.5; DB 1; Length 80; 29.3%; Pred. No. 2.1;
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                                                                                                                                           SEQUENCE FROM N.A.
Kufer W., Hoegner A., Eberlein M., Mayer K., Buchner A.,
Gottschalk L.;
                                                                                                                                                                                                                                                        Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
Mastigocladus laminosus (Fischerella sp.).
Bacteria; Cyanobacteria; Stigonematales; Fischerella
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01-6CT-1996 (Rel. 34, Last sequence update) .
10-CCT-2000 (Rel. 40, Last annotation update)
FLAGELLIN A.
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                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86050914; PubMed-3933528;
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Matches 22; Conservative
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                                                                                                                            9 ATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVR----FQEAANKQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 NFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDE----- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
01-MAY-1992 (Rel. 22, Last sequence)
01-MAY-1992 (Rel. 22, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPONENTS (8C-1, 8C-2, 8A & 8B) AND THE TYPE I COMPONENTS (8C-1, 8C-2, 8A & 8B) AND THE TYPE II COMPONENTS (5, 7A, AND 7C).

SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coiled coil; Heptad repeat pattern; Keratin.
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                     Length 1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 502;
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                                                                            Indels
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8734C8230550CE68 CRC64;
                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                 502 AA.
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                     ; Score 72.5; E
; Pred. No. 53;
18; Mismatches
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Pred. No. 16;
                                                                                                                                                                                                                                                                  838 TTIEKLSSEIENLDKELRKTKFQYKFLDQ 866
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LINKER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKER 12
                                                                                                                                                                                                                                 -----KQELDEISTNIRQAGVQYSRADE 88
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PROSITE; PS00226; IF; 1.
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23.0%;
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                                                                         Conservative
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                     Query Match
Best Local Similarity
Matches 20; Conserv
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 AALKTTAANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITV 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Barrell B.G., Badcock K., Copsey T., Dear S., Devilin K., Fraser A.,
Gentles S., Hanlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.,
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
HYPOTHETICAL 195.1 KDA PROTEIN IN DNA43-UBII INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 575;
SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   523 TQVNV----KAAESQIRDVDFASESANYSKANILAQSGSYAMAQANSSQ 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AQAAVVRFQEAANKQKQELD--EISTNIRQAGVQYSRADEEQQQALSSQ 97
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71F192EFD0AF0DC7 CRC64;
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Pred. No. 17;
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Pfam; PF00669; Flagellin_N; 1.
PRINTS; PR00207; FLAGELLIN.
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59398 MW;
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26.68;
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InterPro; IPR001029; -.
InterPro; IPR001492; -.
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Best Local Similarity
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SEQUENCE 16
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SEQUENCE
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YIO9\_YEAST

RESULT

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Matches

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Search completed: July 5, 2001, 11:51:41 Job time: 500 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 5, 2001, 11:42:57; Search time 123.78 Seconds (without alignments) 106.887 Million cell updates/sec

US-09-462-480-5 492 1 MAEMKTDAATLGQEAGNFER......VQYSRADEEQQQALSSQMGF 100 Title: Perfect score: Sequence:

Scoring table:

425026 seqs, 132305027 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

425026

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

10: sp\_plant:\* 11: sp\_rodent:\* 12: sp\_unclassified:\* 13: sp\_vertebrate:\* 14: sp\_virus:\* sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\* sp\_mhc:\* sp\_organelle:\* sp\_phage:\* SPTREMBL\_16:\*
.: sp\_archea:\*
?: sp\_bacteria:\* sp\_mammal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	1	Description	069739 mycobacteri	033084 mycobacteri	Q9zbq2 streptomyce	Q9x367 bacillus an	042657 schizosacch	005440 mycobacteri	053692 mycobacteri	053267 mycobacteri	077248 spodoptera			Q9ry46 deinococcus	Q63731 rattus norv	069467 mycobacter1	Q28582 ovis aries	002415 agrius conv	P78386 homo sapien	Q9nsb1 homo sapien	Q91016 pseudomonas
SUMMARIES			_		^1	_	_	_	۵,	_	_	_			1	_	٠.				
SON		) a	069739	033084	<b>09ZBQ2</b>	09x367	042657	005440	053692	053267	077248	026589	002456	<b>Q9RY46</b>	063731	069467	028582	002415	P78386	Q9NSB1	910160
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0912c3 streptomyce 09rsj1 deinococcus 09fsj1 rhizobium m 09fsj1 chizobium m 09fsj1 streptococc 09fsj4 streptococc 09fsj4 paracoccus 04374 pomo sapten 091360 arabidopsis 06fsj2 rattus norv 09fsj6 arabidopsis 06fsj2 rattus norv 09fsj6 arabidopsis 09fsj6 arabidopsis 09fsj7 mectria hae 08fsj6 arabidopsis 09fsj7 mus musculu 09fyf3 mus musculu 09fyf3 mus musculu 09fyf3 mus musculu	Q53474 streptococc
2 Q9L2C3 2 Q9RSJ1 2 Q9RSJ1 2 Q9RSJ1 2 Q9XJAB 4 Q4ZJ4 1 Q9LJ6 11 Q62812 11 Q62812 11 Q62812 11 Q62812 2 Q9RD24 2 Q9RD24 2 Q9RD24 2 Q9RD24 2 Q9RD26 2 Q9RD26 3 P78718 5 Q9RSB3 3 P78718 4 Q9NSB3 1 Q9QYT3 1 Q9QYT3 5 Q9TW65	2 053474
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# ALIGNMENTS

033084;

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RESULT 033084

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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 wb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL: AL034447; CAA22420.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okinaka R.T., Cloud K., Hamton O., Hoffmaster A., Hill K.K., Keim P., Koehler T., Lamke G., Kumano S., Mahillon J., Manter D., Martinez Y., Ricke D.O., Svensson R., Jackson P.J., The sequence and organization of px01, the large Bacillus anthracis plasmid harboring the Anthrax toxin genes.";

J. Bacteriol. 0:0-0(1999).

EMBL: AF065404; AAD32402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  686 AGRRRECAALVEELGERRRAADREKSSVAQ---QLGRLAGQARGAAGEAERSAAAAERAQ 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTA--AQAAVVRFQ 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 410;
                    Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                Pfam; PF00463; SMC_N; 1.
Pfam; PF02483; SMC_C; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
GROTIE: 1186 AA; 128722 MW; CB11027815373E99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid virulence plasmid PX01.
Bacteria: Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 EAANKQKQELDEISTNIRQAGVQYSRADEEQQQALSSQM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91.5; DB 2;
Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.5; Di
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
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                                                                                        STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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28.0%;
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32.3%;
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                                                                                                                                                                                                                                InterPro; IPR001066; -.
                                                                                                                                                                                                                                                                   InterPro; IPR003395; -
InterPro; IPR003405; -
                                                                                                                                                                                                                                                     InterPro; IPR001687; -
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Best Local Similarity
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                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                      1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                          SEQUENCE FROM N.A.
MEDILTE=93188700; Pubmed-8446027;
Eiglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
"Use of an ordered cosmid library to deduce the genomic organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAEMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBL_TaxID=1902;
                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Eiglmeier K., Garnier T., De Rossi E., Fsihi H., Cole S.T.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 187; DB 2; Length 100;
; Pred. No. 2e-10;
20; Mismatches 40; Indels
 Score 486; DB 2; Length 100;
                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murphy L., Harris D.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Mycobacterium leprae.";
Mol. Microbiol. 7:197-206(1993).
Mal. Microbiol. 7:197-206(1993).
SEQUENCE 100 AA; 10964 MW; 460EE12F876EC383 CRC64;
                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                  Pred. No. 4e-38;
; Mismatches
                                                                                                                                                                                                                                                                     100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1186 AA
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                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                     PRT;
                                    ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.0%;
40.0%;
98.8%;
99.0%;
                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.09
Matches 40; Conservative
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                        SIMILARITY TO SMALL. Mycobacterium leprae.
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                   :66
 Query Match
                    Best Local
Matches 9
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Gaps

7;

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21;

SC7A1.21

Murphy

Q9ZBQ2

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RESULT 092BQ2

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"Deciphering the biology o complete genome sequence." Nature 393:537-544(1998).
                                EMBL; Z94121; CAB08096.1;
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                      Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 053267;
                                                                                                                                                                                                                                                                                053692
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053267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-9825987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglimeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      550 KQAGENHYSNLSSDYETQIKSLESSL-----TNSQAECVSFQEKINELNSQID 597
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 QEAG--NFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                          18.3%; Score 90; DB 3; Length 750; 28.2%; Pred. No. 1.8; Live 18; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Indels
                                                                                                                          01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 87.3 KDA PROTEIN C27D7.02C IN CHROMOSOME I.
                                                                                                                                                                                                                                                                A469AD95C5787042 CRC64;
                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  005440 PRELIMINARY; PRT; 103 AA. 005440; 01-JUL-1997 (TrEMBLrel. 04, Created) 01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) HYPOTHETICAL 10.5 KDA PROTEIN.
                                                                                           750 AA
                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
                       63 NKQK-----QELDEISTNIRQAGVQYSRADE
                                                                                                                                                                                                                                                                                                                                                  POLY-LYS.
POLY-SER.
                                                                                                                  Created)
                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           598 ELKLKLNEANKKY-----QELAIS 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 EISTNIRQAGVQYSRADEEQQQALS 95
                                                                                                                                                                                                                                                                                                                                                                          87264 MW;
                                                                                                              01-JAN-1999 (TrEMBLrel. 09, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Conservative
                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     Hypothetical protein
                                                                                                                                                                                                            Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                             682 (
750 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1773;
                                                                                                                                                                                                                     NCBI_TaxID=4896;
                                                                                                                                                             SPAC27D7.02C
                                                                                                                                                                                                                                                       STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                        042657
                                                                  RESULT
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SITALINE-90295987; PubMed=9634230; Carnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigluneber K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Olail M.A., Rajandream M.A., Rogers Y., Seeger K., Skelton S., Squres S., Sqares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Paylor K., Whitehead S., Barrell B.G.; Perly Rochering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHERICAL 9.8 KDA PROTEIN.
RVO287 OR MIVO35.15.
Mycobacterium tuberculosis.
Bacteria, Firmicutes; Actinobacteriae; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAAN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 FAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDVAQANLG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.8%; Score 87.5; DB 2; Length 97; ilarity 34.9%; Pred. No. 0.33; Conservative 8; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                               18.1%; Score 89; DB 2; Length 103; llarity 23.1%; Pred. No. 0.25; Conservative 22; Mismatches 48; Indels
                                                                                                                                                                 ll protein.
103 Aa; 10460 MW; 3994E272A7BDFF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9778 MW; 927527DA610A1637 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 EVQLGLSMLAAAIAHAGAGYQHNETASAQVL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 KOKQELDEISTNIRQAGVQYSRADEEQQQAL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 QAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL021930; CAA17362.1;
TubercuList; Rv0287; -.
Hypothetical protein.
SEQUENCE 97 AA; 9778 MW;
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Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Induction of protective immunity in mice using a 62-kDa recombinant
fragment of a Schistosoma mansoni surface antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STAIN-PUBETRO RICAN;
MEDLINE-93056536; Pubmed-1431131;
Solsson L.M., Masterson C.P., Tom T.D., McNally M.T., Lowell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 AA; 61622 MW; AF075D13EB249B4C CRC64;
                                                                                                                                                                                                                                                                                         (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                              148 VASNVEETNEKLAPKLKEAYENFSKHVEEVQKKVHEAASKQ 188
                             61 AANKOKQELDEISTNIRQAGVQYSRADEEQQ----QALSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.5%; Score 81; DB 5; 21.9%; Pred. No. 8.5; tive 24; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00194; TROPOMYOSIN.
PROSITE; PS00182; GLNA_ADENYLATION; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 KELQTRIQELEEDLEAERAARSKAEKSRQQ-LESEL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 NKOKQELDEISTNIRQAGVQYSRADEEQQQALSSQM 98
                                                                                                                                                                                                                528 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1940 AA.
                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                         OT-MAR-2001 (TIEMBLEEL 16, Last an MYOSIN II HEAVY CHAIN (FRAGMENT).
Schistosoma mansoni (Blood fluke).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Immunol. 149:3612-3620(1992).
EMBL; X65591; CAA46548.1; -.
HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001637; -. InterPro; IPR001837; -. Pfam; PF00063; myosin_head; 1. Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin_tail; 1.
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01,
16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Conservative
                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000048; -.
                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-PUERTO RICAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6183;
                                                                                                                                                                                                                                                                                         01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                Schistosoma
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SEQUENCE
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Q02456
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                                                                                                                                                                                                                                                                              PERINHJ7RV;
MEDLINE-9829590; PubMed-9634230;
MEDLINE-9829590; PubMed-9634230;
Goldon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeiter R., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Seeger K., Skelton S., Squares S., Sqares J.,
Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Kim E., Kim S.H., Choi C.S., Park Y.I., Kim H.R.;
"Cloning and Expression of Apolipophorin-III from the Common Cutworm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNIR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQANLG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
NCBI_TaxID=69820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDA----ATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQE 60
                                                                                                                    Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63377.1; -. 20649 MW; 7A8AE366DF8E432C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9842 MW; BA9BCB3180EC17F2 CRC64;
                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84.5; DB 2;
Pred. No. 0.62;
7; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.8%; Score 82.5; DB 5; 26.7%; Pred. No: 2; tive 20; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spodoptera litura.";
Arch. Insect Biochem. Physiol. 0:0-0(1998).
EMBL: AF094582; AAC63377.1;
  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 QAGVQYSRADEEQQQALSSQMGF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAAGTYVAAD---AAAASSYTGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL021287; CAA16105.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.2%;
06,
06,
14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, APOLIPOPHORIN-III PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.8%
Best Local Similarity 26.7%
Matches 27; Conservative
                  (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
  01-JUN-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                      RV3020C OR MTV012,34C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rv3020c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spodoptera litura.
                                                                           PE-FAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       077248
077248;
01-NOV-1998
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculist;
                                                   01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S:
Matches 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Length 528; 45; Indels

[1] SEOUENCE

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Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 LGQEAGN-------FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                        White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffatk K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sun W., Chantler P.D.; "Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain and its differential expression within the central
                                                                                                                                                                                                                                     Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.2%; Score 79.5; DB 2; Length 163; 22.7%; Pred. No. 3.2; ive 16; Mismatches 46; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 AA; 17830 MW; AOAC12CE20534D9C CRC64;
                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) NEURONAL MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TQEAAQNAREKAQDVRANVHESAQDFRAGAQEQAQTL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1999 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 FQEAANKOKQELDEISTNIRQAGVQYSRADEEQQQAL
                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20036896; PubMed-10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system[see comments].";
J. Mol. Biol. 224:1185-1193(1992).
HSSP; P10587; 1BR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92235856; PubMed-1569576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00063; myosin_head; 1.
                                                                                                                                               HYPOTHETICAL 17.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 2.
PRINTS; PR00193; MYOSINHEAVY.
Probom; PD000355; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001873; AAF09701.1;
TIGR; DR0105; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000048; -.
InterPro; IPR001609; -.
InterPro; IPR002017; -.
InterPro; IPR002928; -.
                                                                                                                                                                                                                      Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
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les 22; Conserv
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE
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Matches
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              ACCOOR REPARED DE LA SERVICIO DE LA COOR A DEL COORDA DEL COORDA DE LA COORDA DEL COOR
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                                   Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EMKTDAATLGQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | InterPro; | IPR0000122; | IPR0000122; | InterPro; | IPR0000122; | IPR0000122; | IPR0000122; | IPR000122; | IPR000122; | IPR000122; | IPR000123; | IPR001237; | IPR00123; | IPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NONHELICAL TAILPIECE.
ATP (BY SIMILARITY).
FOR ATPASE ACTIVITY (POTENTIAL)
FOR ATPASE ACTIVITY (POTENTIAL)
WH. 10FC4EAE208CA365 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 81; DB 5; Length 1940; 21.9%; Pred. No. 36; Live 24; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : : : | : : | : : : | 1.095 KELQTRIQELEEDLEAERAARSKAEKSRQO-LESEL 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
Schistosoma mansoni (Blood fluke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      692 69
1940 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                           NCBI_TaxID=6183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     682
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DOMAIN NP\_BIND ACT\_SITE

ACT\_SITE SEQUENCE

Matches

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ò a RESULT 12 Q9RY46 ID Q9RY46 **Q9RY46** 

94

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77 RQ--AGVQYSRADEEQQQALSSQ 97
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Job time: 469 sec
                                                                                                                                                                                            family.";
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                                                                                                                              70 ADSMVSSATTESESLLSHARAEADRILSDAKSOVDRMASEARQHSERMLGDAREESIRIA 129
                                                                                      49; Gaps
                                                                                                              ATLGQEAGN-----FERISGDLKTQIDQVESTAGSLQGGWRGAAGTAAQAAVVRF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDIANGE-8446027;
MEDIANE-93188700; PubMed-8446027;
Eiglimeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
"Use of an ordered cosmid library to deduce the genomic organization
                                                                                                                                                                 ------KQELDEISTNIRQAGVQY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AEMKTDAATLGQEA-----GNFERISGDLKTQIDQVESTAGS----LQGQWRGAAGTAA 51
                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                             Length 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 TVAKREYEASLNRAQSECDRL---IENGNISYEKAIQEGIKEQQKLVSQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 245;
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 QAAVVRFQEAANKQKQELDEISTNIRQAGVQYSRADEE---QQQALSSQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                        090C181D55727B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Hamlin N., Churcher C.M.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27087 MW; C984D9A5FA49697A CRC64;
                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 27.1 KDA PROTEIN.
                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                             DB 11;
                                                                                                                                                                                                                                                                                                            245 AA.
                                                            Query Match 16.2%; Score 79.5; DI Best Local Similarity 23.1%; Pred. No. 51; Matches 31; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.1%; Score 79; 25.7%; Pred. No. E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Mycobacterium leprae.";
Mol. Microbiol. 7:197-206(1993).
EMBL; ALO23635; CAA19194.1; -.
Hypothetical protein.
SEQUENCE 245 AA; 27087 MW; C'
                        1999 AA; 231456 MW;
                                                                                                                                                                 59 QE-----AANKQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                             1880 EEAEEEAORANASR 1893
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                   84 SRADEEQQQALSSQ 97
SMART; SM00015; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 28; Conserv
                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
Q28582
ID Q28582
AC Q28582;
DT 01-NOV-1
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069467
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evolutionary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00038; filament; 1.
PRINTS; PR01276; TYPEZKERATIN.
PROSITE; PS00226; IF; 1.
Colled coil; Heptat pettern; Intermediate filament; Keratin.
SEQUENCE 508 AA; 55245 MW; 3E728AA9512F96F7 CRC64;
                                                                                                                                                 Ovis aries (Sheep).
Wakaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development 114:417-433(1992).
-!- SIMILARITY: TO THE INTERMEDIATE FILAMENT FAMILY.
EMBL; X62509; CAA44368.1; -.
InterPro: IPR001664: -.
InterPro: IPR003054; -.
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) HAIR TYPE II KERATIN INTERMEDIATE FILAMENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9940;
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17 NFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDEISTNI 76 Query Match 16.1%; Score 79; DB 6; Length 508; Best Local Similarity 22.9%; Pred. No. 13; Matches 19; Conservative 23; Mismatches 39; Indels

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5, 2001, 11:50:46 331 ORLTAEVENAKCONSKLEAAVTQ 353

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